GenCore version 5.1.6

OM protein - nucleic search, using frame_plus_p2n model

Run on: June 12, 2003, 20:08:49 ; Search time 1995 Seconds
(without alignments)
3603.205 Million cell updates/sec

Title: US-09-705-500A-3
Perfect score: 1268
Sequence: 1 MLQNSAVLLVLVISASATHE.....NLRGEEDSPSHIKRTSHESA 247

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
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-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
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-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1268	100.0	741	6	E37712	E37712 Osteogenesi
2	1268	100.0	741	6	E39295	E39295 Novel prote
3	1268	100.0	771	6	AR055558	AR055558 Sequence
4	1268	100.0	771	6	AR091578	AR091578 Sequence
5	1268	100.0	840	9	HSU46768	U46768 Human stann
6	1268	100.0	2481	9	BC029044	BC029044 Homo sapi
7	1268	100.0	3901	9	HSU25997	U25997 Homo sapien
8	1234	97.3	1232	10	MMU47815	U47815 Mus musculu
9	1234	97.3	2341	10	BC021425	BC021425 Mus muscu
10	1231	97.1	1004	10	RNU62667	U62667 Rattus norv
11	1228	96.8	4183	10	AF099098	AF099098 Mus muscu
12	1199	94.6	834	4	AF257506	AF257506 Bos tauru
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18	662.5	52.2	1934	5	S59519	S59519 stanniocalc
19	654	51.6	2807	5	AB060558	AB060558 Osteoglos
20	617	48.7	555	5	S80134	S80134 Oncorhynchu
21	515	40.6	177104	10	AC091237	AC091237 Mus muscu
22	510	40.2	4479	9	AF098463	AF098463 Homo sapi
23	508	40.1	420	6	AX156284	AX156284 Sequence
24	480	37.9	18216	9	AF242179	AF242179 Homo sapi
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26	354.5	28.0	888	6	AR123908	AR123908 Sequence
27	354.5	28.0	1004	10	AF056244	AF056244 Mus muscu
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31	354	27.9	882	6	E58738	E58738 Osteogenesi
32	354	27.9	906	6	AR123898	AR123898 Sequence
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37	354	27.9	1778	9	AB012664	AB012664 Homo sapi
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ALIGNMENTS

RESULT 1

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E37712
LOCUS       E37712                    741 bp    DNA     linear   PAT 31-JAN-2002
DEFINITION  Osteogenesis promoter.
ACCESSION   E37712
VERSION     E37712.1  GI:18626798
KEYWORDS    JP 2000229880-A/3.
SOURCE      Homo sapiens.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 741)
  AUTHORS   Kinozaki,M., Goto,M., Yamaguchi,K., Morita,S. and Nakagawa,N.
  TITLE     Osteogenesis promoter
  JOURNAL   Patent: JP 2000229880-A 3 22-AUG-2000;
            SNOW BRAND MILK PROD CO LTD
COMMENT     OS   Homo sapiens (human)
            PN   JP 2000229880-A/3
            PD   22-AUG-2000
            PF   10-FEB-1999 JP 1999033262
            PR
            PI   MASAHIKO KINOZAKI,MASAAKI GOTO,KYOJI YAMAGUCHI,SHUJI MORITA,
            PI   NOBUAKI NAKAGAWA
            PC   A61K38/00,A61K31/00,A61K31/00,A61K31/00,C07K14/47 CC
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            FT                   /organism='Homo sapiens (human)'.
FEATURES             Location/Qualifiers
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Percent Similarity:     100.00%         Conservative:   0
Best Local Similarity:  100.00%         Mismatches:     0
Query Match:            100.00%         Indels:         0
DB:                     6               Gaps:           0

US-09-705-500A-3 (1-247) x E37712 (1-741)

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Qy         21 AlaGluGlnAsnAspSerValSerProArgLysSerArgValAlaAlaGlnAsnSerAla 40
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Qy         41 GluValValArgCysLeuAsnSerAlaLeuGlnValGlyCysGlyAlaPheAlaCysLeu 60
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Db        121 GAAGTGGTTCGTTGCCTCAACAGTGCTCTACAGGTCGGCTGCGGGGCTTTTGCATGCCTG 180

Qy         61 GluAsnSerThrCysAspThrAspGlyMetTyrAspIleCysLysSerPheLeuTyrSer 80
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Db        181 GAAAACTCCACCTGTGACACAGATGGGATGTATGACATCTGTAAATCCTTCTTGTACAGC 240

Qy         81 AlaAlaLysPheAspThrGlnGlyLysAlaPheValLysGluSerLeuLysCysIleAla 100
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Db        241 GCTGCTAAATTTGACACTCAGGGAAAAGCATTCGTCAAAGAGAGCTTAAAATGCATCGCC 300

Qy        101 AsnGlyValThrSerLysValPheLeuAlaIleArgArgCysSerThrPheGlnArgMet 120
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Db        301 AACGGGGTCACCTCCAAGGTCTTCCTCGCCATTCGGAGGTGCTCCACTTTCCAAAGGATG 360

Qy        121 IleAlaGluValGlnGluGluCysTyrSerLysLeuAsnValCysSerIleAlaLysArg 140
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Db        361 ATTGCTGAGGTGCAGGAAGAGTGCTACAGCAAGCTGAATGTGTGCAGCATCGCCAAGCGG 420

Qy        141 AsnProGluAlaIleThrGluValValGlnLeuProAsnHisPheSerAsnArgTyrTyr 160
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Db        421 AACCCTGAAGCCATCACTGAGGTCGTCCAGCTGCCCAATCACTTCTCCAACAGATACTAT 480

Qy        161 AsnArgLeuValArgSerLeuLeuGluCysAspGluAspThrValSerThrIleArgAsp 180
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Qy        181 SerLeuMetGluLysIleGlyProAsnMetAlaSerLeuPheHisIleLeuGlnThrAsp 200
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Qy        201 HisCysAlaGlnThrHisProArgAlaAspPheAsnArgArgArgThrAsnGluProGln 220
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Qy        221 LysLeuLysValLeuLeuArgAsnLeuArgGlyGluGluAspSerProSerHisIleLys 240
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Db        661 AAGCTGAAAGTCCTCCTCAGGAACCTCCGAGGTGAGGAGGACTCTCCCTCCCACATCAAA 720

Qy        241 ArgThrSerHisGluSerAla 247
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Db        721 CGCACATCCCATGAGAGTGCA 741

RESULT 2
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LOCUS       E39295                    741 bp    DNA     linear   PAT 31-JAN-2002
DEFINITION  Novel protein and process for producing the same.
ACCESSION   E39295
VERSION     E39295.1  GI:18628926
KEYWORDS    JP 2000239299-A/12.
SOURCE      Homo sapiens.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 741)
  AUTHORS   Goto,M., Tomoyasu,M., Yamaguchi,K., Kinozaki,M., Shima,N.,
            Yasuda,N. and Nakagawa,N.
  TITLE     Novel protein and process for producing the same
  JOURNAL   Patent: JP 2000239299-A 12 05-SEP-2000;
            SNOW BRAND MILK PROD CO LTD
COMMENT     OS   Homo sapiens (human)
            PN   JP 2000239299-A/12
            PD   05-SEP-2000
            PF   15-FEB-1999 JP 1999036225
            PR
            PI   MASAAKI GOTO,MASAAKI TOMOYASU,KYOJI YAMAGUCHI, PI   MASAHIKO
            KINOZAKI,
            PI   NOBUYUKI SHIMA,NAOTAKA YASUDA,NOBUAKI NAKAGAWA PC
            C07K14/47,C12N5/10,C12N15/09,C12P21/02//A61K31/00,A61K31/00, PC
            A61K38/00,
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Score:                  1268.00         Matches:        247
Percent Similarity:     100.00%         Conservative:   0
Best Local Similarity:  100.00%         Mismatches:     0
Query Match:            100.00%         Indels:         0
DB:                     6               Gaps:           0

US-09-705-500A-3 (1-247) x E39295 (1-741)

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Qy         21 AlaGluGlnAsnAspSerValSerProArgLysSerArgValAlaAlaGlnAsnSerAla 40
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Qy         41 GluValValArgCysLeuAsnSerAlaLeuGlnValGlyCysGlyAlaPheAlaCysLeu 60
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Db        121 GAAGTGGTTCGTTGCCTCAACAGTGCTCTACAGGTCGGCTGCGGGGCTTTTGCATGCCTG 180

Qy         61 GluAsnSerThrCysAspThrAspGlyMetTyrAspIleCysLysSerPheLeuTyrSer 80
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Qy         81 AlaAlaLysPheAspThrGlnGlyLysAlaPheValLysGluSerLeuLysCysIleAla 100
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Db        241 GCTGCTAAATTTGACACTCAGGGAAAAGCATTCGTCAAAGAGAGCTTAAAATGCATCGCC 300

Qy        101 AsnGlyValThrSerLysValPheLeuAlaIleArgArgCysSerThrPheGlnArgMet 120
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Db        301 AACGGGGTCACCTCCAAGGTCTTCCTCGCCATTCGGAGGTGCTCCACTTTCCAAAGGATG 360

Qy        121 IleAlaGluValGlnGluGluCysTyrSerLysLeuAsnValCysSerIleAlaLysArg 140
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Db        361 ATTGCTGAGGTGCAGGAAGAGTGCTACAGCAAGCTGAATGTGTGCAGCATCGCCAAGCGG 420

Qy        141 AsnProGluAlaIleThrGluValValGlnLeuProAsnHisPheSerAsnArgTyrTyr 160
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Qy        161 AsnArgLeuValArgSerLeuLeuGluCysAspGluAspThrValSerThrIleArgAsp 180
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Qy        201 HisCysAlaGlnThrHisProArgAlaAspPheAsnArgArgArgThrAsnGluProGln 220
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Db        601 CACTGTGCCCAAACACACCCACGAGCTGACTTCAACAGGAGACGCACCAATGAGCCGCAG 660

Qy        221 LysLeuLysValLeuLeuArgAsnLeuArgGlyGluGluAspSerProSerHisIleLys 240
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Db        661 AAGCTGAAAGTCCTCCTCAGGAACCTCCGAGGTGAGGAGGACTCTCCCTCCCACATCAAA 720

Qy        241 ArgThrSerHisGluSerAla 247
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Db        721 CGCACATCCCATGAGAGTGCA 741

RESULT 3
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LOCUS       AR055558                771 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 1 from patent US 5837498.
ACCESSION   AR055558
VERSION     AR055558.1  GI:5981135
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 771)
  AUTHORS   Olsen,H.S. and Adams,M.D.
  TITLE     Corpuscles of stannius protein, stanniocalcin
  JOURNAL   Patent: US 5837498-A 1 17-NOV-1998;
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ORIGIN

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Pred. No.:              1.78e-123       Length:         771
Score:                  1268.00         Matches:        247
Percent Similarity:     100.00%         Conservative:   0
Best Local Similarity:  100.00%         Mismatches:     0
Query Match:            100.00%         Indels:         0
DB:                     6               Gaps:           0

US-09-705-500A-3 (1-247) x AR055558 (1-771)

Qy          1 MetLeuGlnAsnSerAlaValLeuLeuValLeuValIleSerAlaSerAlaThrHisGlu 20
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Qy         21 AlaGluGlnAsnAspSerValSerProArgLysSerArgValAlaAlaGlnAsnSerAla 40
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Db         76 GCGGAGCAGAATGACTCTGTGAGCCCCAGGAAATCCCGAGTGGCGGCCCAAAACTCAGCT 135

Qy         41 GluValValArgCysLeuAsnSerAlaLeuGlnValGlyCysGlyAlaPheAlaCysLeu 60
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Db        136 GAAGTGGTTCGTTGCCTCAACAGTGCTCTACAGGTCGGCTGCGGGGCTTTTGCATGCCTG 195

Qy         61 GluAsnSerThrCysAspThrAspGlyMetTyrAspIleCysLysSerPheLeuTyrSer 80
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Qy         81 AlaAlaLysPheAspThrGlnGlyLysAlaPheValLysGluSerLeuLysCysIleAla 100
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Qy        121 IleAlaGluValGlnGluGluCysTyrSerLysLeuAsnValCysSerIleAlaLysArg 140
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Qy        141 AsnProGluAlaIleThrGluValValGlnLeuProAsnHisPheSerAsnArgTyrTyr 160
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Qy        221 LysLeuLysValLeuLeuArgAsnLeuArgGlyGluGluAspSerProSerHisIleLys 240
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Qy        241 ArgThrSerHisGluSerAla 247
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Db        736 CGCACATCCCATGAGAGTGCA 756

RESULT 4
AR091578
LOCUS       AR091578                771 bp    DNA     linear   PAT 07-SEP-2000
DEFINITION  Sequence 1 from patent US 5994301.
ACCESSION   AR091578
VERSION     AR091578.1  GI:10018333
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 771)
  AUTHORS   Olsen,H.S. and Adams,M.D.
  TITLE     Corpuscles of stannius protein, stanniocalcin
  JOURNAL   Patent: US 5994301-A 1 30-NOV-1999;
FEATURES             Location/Qualifiers
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     source          1. .771
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BASE COUNT      212 a    214 c    192 g    153 t
ORIGIN

Alignment Scores:
Pred. No.:              1.78e-123      Length:         771
Score:                  1268.00        Matches:        247
Percent Similarity:     100.00%        Conservative:   0
Best Local Similarity:  100.00%        Mismatches:     0
Query Match:            100.00%        Indels:         0
DB:                     6              Gaps:           0

US-09-705-500A-3 (1-247) x AR091578 (1-771)

Qy          1 MetLeuGlnAsnSerAlaValLeuLeuValLeuValIleSerAlaSerAlaThrHisGlu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         16 ATGCTCCAAAACTCAGCAGTGCTTCTGGTGCTGGTGATCAGTGCTTCTGCAACCCATGAG 75

Qy         21 AlaGluGlnAsnAspSerValSerProArgLysSerArgValAlaAlaGlnAsnSerAla 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         76 GCGGAGCAGAATGACTCTGTGAGCCCCAGGAAATCCCGAGTGGCGGCCCAAAACTCAGCT 135

Qy         41 GluValValArgCysLeuAsnSerAlaLeuGlnValGlyCysGlyAlaPheAlaCysLeu 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        136 GAAGTGGTTCGTTGCCTCAACAGTGCTCTACAGGTCGGCTGCGGGGCTTTTGCATGCCTG 195

Qy         61 GluAsnSerThrCysAspThrAspGlyMetTyrAspIleCysLysSerPheLeuTyrSer 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        196 GAAAACTCCACCTGTGACACAGATGGGATGTATGACATCTGTAAATCCTTCTTGTACAGC 255

Qy         81 AlaAlaLysPheAspThrGlnGlyLysAlaPheValLysGluSerLeuLysCysIleAla 100
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Db        256 GCTGCTAAATTTGACACTCAGGGAAAAGCATTCGTCAAAGAGAGCTTAAAATGCATCGCC 315

Qy        101 AsnGlyValThrSerLysValPheLeuAlaIleArgArgCysSerThrPheGlnArgMet 120
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Db        316 AACGGGGTCACCTCCAAGGTCTTCCTCGCCATTCGGAGGTGCTCCACTTTCCAAAGGATG 375

Qy        121 IleAlaGluValGlnGluGluCysTyrSerLysLeuAsnValCysSerIleAlaLysArg 140
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Db        376 ATTGCTGAGGTGCAGGAAGAGTGCTACAGCAAGCTGAATGTGTGCAGCATCGCCAAGCGG 435

Qy        141 AsnProGluAlaIleThrGluValValGlnLeuProAsnHisPheSerAsnArgTyrTyr 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        436 AACCCTGAAGCCATCACTGAGGTCGTCCAGCTGCCCAATCACTTCTCCAACAGATACTAT 495

Qy        161 AsnArgLeuValArgSerLeuLeuGluCysAspGluAspThrValSerThrIleArgAsp 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        496 AACAGACTTGTCCGAAGCCTGCTGGAATGTGATGAAGACACAGTCAGCACAATCAGAGAC 555

Qy        181 SerLeuMetGluLysIleGlyProAsnMetAlaSerLeuPheHisIleLeuGlnThrAsp 200
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Db        556 AGCCTGATGGAGAAAATTGGGCCTAACATGGCCAGCCTCTTCCACATCCTGCAGACAGAC 615

Qy        201 HisCysAlaGlnThrHisProArgAlaAspPheAsnArgArgArgThrAsnGluProGln 220
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Db        616 CACTGTGCCCAAACACACCCACGAGCTGACTTCAACAGGAGACGCACCAATGAGCCGCAG 675

Qy        221 LysLeuLysValLeuLeuArgAsnLeuArgGlyGluGluAspSerProSerHisIleLys 240
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Db        676 AAGCTGAAAGTCCTCCTCAGGAACCTCCGAGGTGAGGAGGACTCTCCCTCCCACATCAAA 735

Qy        241 ArgThrSerHisGluSerAla 247
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Db        736 CGCACATCCCATGAGAGTGCA 756

RESULT 5
HSU46768
LOCUS       HSU46768                840 bp    mRNA    linear   PRI 22-FEB-1996
DEFINITION  Human stanniocalcin mRNA, complete cds.
ACCESSION   U46768
VERSION     U46768.1  GI:1199619
KEYWORDS    .
SOURCE      Homo sapiens.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 840)
  AUTHORS   Olsen,H.S., Cepeda,M.A., Zhang,Q.-Q., Rosen,C.A., Vozzolo,B.L. and
            Wagner,G.F.
  TITLE     Human stanniocalcin: a hormonal regulator of mineral metabolism
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. (1996) In press
REFERENCE   2  (bases 1 to 840)
  AUTHORS   Olsen,H.S.
  TITLE     Direct Submission
  JOURNAL   Submitted (22-JAN-1996) Henrik S. Olsen, Human Genome Sciences,
            9410 Key West Avenue, Rockville, MD 20850, USA
FEATURES             Location/Qualifiers
     source          1. .840
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
     CDS             35. .778
                     /codon_start=1
                     /product="stanniocalcin"
                     /protein_id="AAA88903.1"
                     /db_xref="GI:1199620"
                     /translation="MLQNSAVLLVLVISASATHEAEQNDSVSPRKSRVAAQNSAEVVR
                     CLNSALQVGCGAFACLENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANG
                     VTSKVFLAIRRCSTFQRMIAEVQEECYSKLNVCSIAKRNPEAITEVVQLPNHFSNRYY
                     NRLVRSLLECDEDTVSTIRDSLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRRTNE
                     PQKLKVLLRNLRGEEDSPSHIKRTSHESA"
BASE COUNT      237 a    233 c    201 g    169 t
ORIGIN

Alignment Scores:
Pred. No.:              1.99e-123      Length:         840
Score:                  1268.00        Matches:        247
Percent Similarity:     100.00%        Conservative:   0
Best Local Similarity:  100.00%        Mismatches:     0
Query Match:            100.00%        Indels:         0
DB:                     9              Gaps:           0

US-09-705-500A-3 (1-247) x HSU46768 (1-840)

Qy          1 MetLeuGlnAsnSerAlaValLeuLeuValLeuValIleSerAlaSerAlaThrHisGlu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         35 ATGCTCCAAAACTCAGCAGTGCTTCTGGTGCTGGTGATCAGTGCTTCTGCAACCCATGAG 94

Qy         21 AlaGluGlnAsnAspSerValSerProArgLysSerArgValAlaAlaGlnAsnSerAla 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         95 GCGGAGCAGAATGACTCTGTGAGCCCCAGGAAATCCCGAGTGGCGGCCCAAAACTCAGCT 154

Qy         41 GluValValArgCysLeuAsnSerAlaLeuGlnValGlyCysGlyAlaPheAlaCysLeu 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        155 GAAGTGGTTCGTTGCCTCAACAGTGCTCTACAGGTCGGCTGCGGGGCTTTTGCATGCCTG 214

Qy         61 GluAsnSerThrCysAspThrAspGlyMetTyrAspIleCysLysSerPheLeuTyrSer 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        215 GAAAACTCCACCTGTGACACAGATGGGATGTATGACATCTGTAAATCCTTCTTGTACAGC 274

Qy         81 AlaAlaLysPheAspThrGlnGlyLysAlaPheValLysGluSerLeuLysCysIleAla 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        275 GCTGCTAAATTTGACACTCAGGGAAAAGCATTCGTCAAAGAGAGCTTAAAATGCATCGCC 334

Qy        101 AsnGlyValThrSerLysValPheLeuAlaIleArgArgCysSerThrPheGlnArgMet 120
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Db        335 AACGGGGTCACCTCCAAGGTCTTCCTCGCCATTCGGAGGTGCTCCACTTTCCAAAGGATG 394

Qy        121 IleAlaGluValGlnGluGluCysTyrSerLysLeuAsnValCysSerIleAlaLysArg 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        395 ATTGCTGAGGTGCAGGAAGAGTGCTACAGCAAGCTGAATGTGTGCAGCATCGCCAAGCGG 454

Qy        141 AsnProGluAlaIleThrGluValValGlnLeuProAsnHisPheSerAsnArgTyrTyr 160
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Db        455 AACCCTGAAGCCATCACTGAGGTCGTCCAGCTGCCCAATCACTTCTCCAACAGATACTAT 514
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Qy        161 AsnArgLeuValArgSerLeuLeuGluCysAspGluAspThrValSerThrIleArgAsp 180
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Db        515 AACAGACTTGTCCGAAGCCTGCTGGAATGTGATGAAGACACAGTCAGCACAATCAGAGAC 574

Qy        181 SerLeuMetGluLysIleGlyProAsnMetAlaSerLeuPheHisIleLeuGlnThrAsp 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        575 AGCCTGATGGAGAAAATTGGGCCTAACATGGCCAGCCTCTTCCACATCCTGCAGACAGAC 634

Qy        201 HisCysAlaGlnThrHisProArgAlaAspPheAsnArgArgArgThrAsnGluProGln 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        635 CACTGTGCCCAAACACACCCACGAGCTGACTTCAACAGGAGACGCACCAATGAGCCGCAG 694

Qy        221 LysLeuLysValLeuLeuArgAsnLeuArgGlyGluGluAspSerProSerHisIleLys 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        695 AAGCTGAAAGTCCTCCTCAGGAACCTCCGAGGTGAGGAGGACTCTCCCTCCCACATCAAA 754

Qy        241 ArgThrSerHisGluSerAla 247
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Db        755 CGCACATCCCATGAGAGTGCA 775

RESULT 6
BC029044
LOCUS       BC029044                2481 bp    mRNA    linear   PRI 16-MAY-2002
DEFINITION  Homo sapiens, stanniocalcin 1, clone MGC:34539 IMAGE:5191420, mRNA,
            complete cds.
ACCESSION   BC029044
VERSION     BC029044.1  GI:20810067
KEYWORDS    MGC.
SOURCE      Homo sapiens.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 2481)
  AUTHORS   Strausberg,R.
  TITLE     Direct Submission
  JOURNAL   Submitted (01-MAY-2002) National Institutes of Health, Mammalian
            Gene Collection (MGC), Cancer Genomics Office, National Cancer
            Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
            USA
  REMARK    NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT     Contact: MGC help desk
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Life Technologies, Inc.
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Baylor College of Medicine Human Genome
            Sequencing Center
            Center code: BCM-HGSC
            Web site: http://www.hgsc.bcm.tmc.edu/cdna/
            Contact: amg@bcm.tmc.edu
            Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Hale, S.M.,
            Yoon, V.S., Kowis, C.R., Lawrence, S., Martin, R.G., Muzny, D.M.,
            Richards, S., Gibbs, R.A.

            Clone distribution: MGC clone distribution information can be found
            through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
            Series: IRAK Plate: 50 Row: k Column: 5
            This clone was selected for full length sequencing because it
            passed the following selection criteria: matched mRNA gi: 4507264.
FEATURES             Location/Qualifiers
     source          1. .2481
                     /organism="Homo sapiens"
                     /db_xref="LocusID:6781"
                     /db_xref="taxon:9606"
                     /clone="MGC:34539 IMAGE:5191420"
                     /tissue_type="Colon, Kidney, Stomach, adult, whole pooled"
                     /clone_lib="NIH_MGC_116"
                     /lab_host="DH10B"
                     /note="Vector: pCMV-SPORT6"
     CDS             263. .1006
                     /codon_start=1
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                     /protein_id="AAH29044.1"
                     /db_xref="GI:20810068"
                     /translation="MLQNSAVLLVLVISASATHEAEQNDSVSPRKSRVAAQNSAEVVR
                     CLNSALQVGCGAFACLENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANG
                     VTSKVFLAIRRCSTFQRMIAEVQEECYSKLNVCSIAKRNPEAITEVVQLPNHFSNRYY
                     NRLVRSLLECDEDTVSTIRDSLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRRTNE
                     PQKLKVLLRNLRGEEDSPSHIKRTSHESA"
BASE COUNT      745 a    599 c    520 g    617 t
ORIGIN

Alignment Scores:
Pred. No.:              7.94e-123       Length:         2481
Score:                  1268.00         Matches:        247
Percent Similarity:     100.00%         Conservative:   0
Best Local Similarity:  100.00%         Mismatches:     0
Query Match:            100.00%         Indels:         0
DB:                     9               Gaps:           0

US-09-705-500A-3 (1-247) x BC029044 (1-2481)

Qy          1 MetLeuGlnAsnSerAlaValLeuLeuValLeuValIleSerAlaSerAlaThrHisGlu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        263 ATGCTCCAAAACTCAGCAGTGCTTCTGGTGCTGGTGATCAGTGCTTCTGCAACCCATGAG 322

Qy         21 AlaGluGlnAsnAspSerValSerProArgLysSerArgValAlaAlaGlnAsnSerAla 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        323 GCGGAGCAGAATGACTCTGTGAGCCCCAGGAAATCCCGAGTGGCGGCTCAAAACTCAGCT 382

Qy         41 GluValValArgCysLeuAsnSerAlaLeuGlnValGlyCysGlyAlaPheAlaCysLeu 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        383 GAAGTGGTTCGTTGCCTCAACAGTGCTCTACAGGTCGGCTGCGGGGCTTTTGCATGCCTG 442

Qy         61 GluAsnSerThrCysAspThrAspGlyMetTyrAspIleCysLysSerPheLeuTyrSer 80
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Db        443 GAAAACTCCACCTGTGACACAGATGGGATGTATGACATCTGTAAATCCTTCTTGTACAGC 502

Qy         81 AlaAlaLysPheAspThrGlnGlyLysAlaPheValLysGluSerLeuLysCysIleAla 100
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Db        503 GCTGCTAAATTTGACACTCAGGGAAAAGCATTCGTCAAAGAGAGCTTAAAATGCATCGCC 562

Qy        101 AsnGlyValThrSerLysValPheLeuAlaIleArgArgCysSerThrPheGlnArgMet 120
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Db        563 AACGGGGTCACCTCCAAGGTCTTCCTCGCCATTCGGAGGTGCTCCACTTTCCAAAGGATG 622

Qy        121 IleAlaGluValGlnGluGluCysTyrSerLysLeuAsnValCysSerIleAlaLysArg 140
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Db        623 ATTGCTGAGGTGCAGGAAGAGTGCTACAGCAAGCTGAATGTGTGCAGCATCGCCAAGCGG 682

Qy        141 AsnProGluAlaIleThrGluValValGlnLeuProAsnHisPheSerAsnArgTyrTyr 160
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Db        683 AACCCTGAAGCCATCACTGAGGTCGTCCAGCTGCCCAATCACTTCTCCAACAGATACTAT 742

Qy        161 AsnArgLeuValArgSerLeuLeuGluCysAspGluAspThrValSerThrIleArgAsp 180
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Db        743 AACAGACTTGTCCGAAGCCTGCTGGAATGTGATGAAGACACAGTCAGCACAATCAGAGAC 802

Qy        181 SerLeuMetGluLysIleGlyProAsnMetAlaSerLeuPheHisIleLeuGlnThrAsp 200
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Db        803 AGCCTGATGGAGAAAATTGGGCCTAACATGGCCAGCCTCTTCCACATCCTGCAGACAGAC 862

Qy        201 HisCysAlaGlnThrHisProArgAlaAspPheAsnArgArgArgThrAsnGluProGln 220
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Db        863 CACTGTGCCCAAACACACCCACGAGCTGACTTCAACAGGAGACGCACCAATGAGCCGCAG 922

Qy        221 LysLeuLysValLeuLeuArgAsnLeuArgGlyGluGluAspSerProSerHisIleLys 240
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Db        923 AAGCTGAAAGTCCTCCTCAGGAACCTCCGAGGTGAGGAGGACTCTCCCTCCCACATCAAA 982

Qy        241 ArgThrSerHisGluSerAla 247
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Db        983 CGCACATCCCATGAGAGTGCA 1003

RESULT 7
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HSU25997
LOCUS       HSU25997                3901 bp    mRNA    linear   PRI 02-APR-1998
DEFINITION  Homo sapiens stanniocalcin precursor (STC) mRNA, complete cds.
ACCESSION   U25997
VERSION     U25997.1  GI:3006202
KEYWORDS    .
SOURCE      Homo sapiens.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 3901)
  AUTHORS   Chang,A.C., Janosi,J., Hulsbeek,M., de Jong,D., Jeffrey,K.J.,
            Noble,J.R. and Reddel,R.R.
  TITLE     A novel human cDNA highly homologous to the fish hormone
            stanniocalcin
  JOURNAL   Mol. Cell. Endocrinol. 112 (2), 241-247 (1995)
  MEDLINE   96077825
   PUBMED   7489828
REFERENCE   2  (bases 1 to 3901)
  AUTHORS   Chang,A.C., Jeffrey,K.J., Tokutake,Y., Shimamoto,A., Neumann,A.A.,
            Dunham,M.A., Cha,J., Sugawara,M., Furuichi,Y. and Reddel,R.R.
  TITLE     Human stanniocalcin (STC): genomic structure, chromosomal
            localization, and the presence of CAG trinucleotide repeats
  JOURNAL   Genomics 47 (3), 393-398 (1998)
  MEDLINE   98149987
   PUBMED   9480753
REFERENCE   3  (bases 1 to 3901)
  AUTHORS   Chang,A.C.-M.
  TITLE     Direct Submission
  JOURNAL   Submitted (02-MAY-1995) Childrens Medical Research Institute, 214
            Hawkesbury Road, Westmead, NSW 2145, Australia
REFERENCE   4  (bases 1 to 3901)
  AUTHORS   Chang,A.C.-M.
  TITLE     Direct Submission
  JOURNAL   Submitted (02-APR-1998) Childrens Medical Research Institute, 214
            Hawkesbury Road, Westmead, NSW 2145, Australia
  REMARK    Sequence update by submitter
COMMENT     On Apr 2, 1998 this sequence version replaced gi:975297.
FEATURES             Location/Qualifiers
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     gene            1. .3901
                     /gene="STC"
     repeat_region   30. .125
                     /rpt_type=tandem
                     /rpt_unit=cag
     CDS             285. .1028
                     /gene="STC"
                     /function="putative calcium responsive hormone"
                     /note="similar to SwissProt Accession Number Q08264"
                     /codon_start=1
                     /product="stanniocalcin precursor"
                     /protein_id="AAC09472.1"
                     /db_xref="GI:975298"
                     /translation="MLQNSAVLLVLVISASATHEAEQNDSVSPRKSRVAAQNSAEVVR
                     CLNSALQVGCGAFACLENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANG
                     VTSKVFLAIRRCSTFQRMIAEVQEECYSKLNVCSIAKRNPEAITEVVQLPNHFSNRYY
                     NRLVRSLLECDEDTVSTIRDSLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRRTNE
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     sig_peptide     285. .383
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                     /note="pre-pro-peptide"
     mat_peptide     384. .1025
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                     /product="stanniocalcin"
                     /function="putative calcium responsive hormone"
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                     /gene="STC"
                     /note="19 A nucleotides"
BASE COUNT     1152 a    910 c    784 g   1055 t
ORIGIN

Alignment Scores:
Pred. No.:              1.41e-122      Length:          3901
Score:                  1268.00        Matches:         247
Percent Similarity:     100.00%        Conservative:    0
Best Local Similarity:  100.00%        Mismatches:      0
Query Match:            100.00%        Indels:          0
DB:                     9              Gaps:            0

US-09-705-500A-3 (1-247) x HSU25997 (1-3901)

Qy          1 MetLeuGlnAsnSerAlaValLeuLeuValLeuValIleSerAlaSerAlaThrHisGlu 20
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Db        285 ATGCTCCAAAACTCAGCAGTGCTTCTGGTGCTGGTGATCAGTGCTTCTGCAACCCATGAG 344

Qy         21 AlaGluGlnAsnAspSerValSerProArgLysSerArgValAlaAlaGlnAsnSerAla 40
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Db        345 GCGGAGCAGAATGACTCTGTGAGCCCCAGGAAATCCCGAGTGGCGGCTCAAAACTCAGCT 404

Qy         41 GluValValArgCysLeuAsnSerAlaLeuGlnValGlyCysGlyAlaPheAlaCysLeu 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        405 GAAGTGGTTCGTTGCCTCAACAGTGCTCTACAGGTCGGCTGCGGGGCTTTTGCATGCCTG 464

Qy         61 GluAsnSerThrCysAspThrAspGlyMetTyrAspIleCysLysSerPheLeuTyrSer 80
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Db        465 GAAAACTCCACCTGTGACACAGATGGGATGTATGACATCTGTAAATCCTTCTTGTACAGC 524

Qy         81 AlaAlaLysPheAspThrGlnGlyLysAlaPheValLysGluSerLeuLysCysIleAla 100
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Db        525 GCTGCTAAATTTGACACTCAGGGAAAAGCATTCGTCAAAGAGAGCTTAAAATGCATCGCC 584

Qy        101 AsnGlyValThrSerLysValPheLeuAlaIleArgArgCysSerThrPheGlnArgMet 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        585 AACGGGGTCACCTCCAAGGTCTTCCTCGCCATTCGGAGGTGCTCCACTTTCCAAAGGATG 644

Qy        121 IleAlaGluValGlnGluGluCysTyrSerLysLeuAsnValCysSerIleAlaLysArg 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        645 ATTGCTGAGGTGCAGGAAGAGTGCTACAGCAAGCTGAATGTGTGCAGCATCGCCAAGCGG 704

Qy        141 AsnProGluAlaIleThrGluValValGlnLeuProAsnHisPheSerAsnArgTyrTyr 160
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Db        705 AACCCTGAAGCCATCACTGAGGTCGTCCAGCTGCCCAATCACTTCTCCAACAGATACTAT 764

Qy        161 AsnArgLeuValArgSerLeuLeuGluCysAspGluAspThrValSerThrIleArgAsp 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        765 AACAGACTTGTCCGAAGCCTGCTGGAATGTGATGAAGACACAGTCAGCACAATCAGAGAC 824

Qy        181 SerLeuMetGluLysIleGlyProAsnMetAlaSerLeuPheHisIleLeuGlnThrAsp 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        825 AGCCTGATGGAGAAAATTGGGCCTAACATGGCCAGCCTCTTCCACATCCTGCAGACAGAC 884

Qy        201 HisCysAlaGlnThrHisProArgAlaAspPheAsnArgArgArgThrAsnGluProGln 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        885 CACTGTGCCCAAACACACCCACGAGCTGACTTCAACAGGAGACGCACCAATGAGCCGCAG 944

Qy        221 LysLeuLysValLeuLeuArgAsnLeuArgGlyGluGluAspSerProSerHisIleLys 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        945 AAGCTGAAAGTCCTCCTCAGGAACCTCCGAGGTGAGGAGGACTCTCCCTCCCACATCAAA 1004

Qy        241 ArgThrSerHisGluSerAla 247
              |||||||||||||||||||||
Db       1005 CGCACATCCCATGAGAGTGCA 1025

RESULT 8
MMU47815
LOCUS       MMU47815                1232 bp    DNA     linear   ROD 03-FEB-1998
DEFINITION  Mus musculus stanniocalcin gene, complete cds.
ACCESSION   U47815
VERSION     U47815.1  GI:2828524
KEYWORDS    .
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```
SOURCE      house mouse strain=BALB/c.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 1232)
  AUTHORS   Chang,A.C., Dunham,M.A., Jeffrey,K.J. and Reddel,R.R.
  TITLE     Molecular cloning and characterization of mouse stanniocalcin cDNA
  JOURNAL   Mol. Cell. Endocrinol. 124 (1-2), 185-187 (1996)
  MEDLINE   97179050
   PUBMED   9027337
REFERENCE   2  (bases 1 to 1232)
  AUTHORS   Chang,A.C.M. and Reddel,R.R.
  TITLE     Direct Submission
  JOURNAL   Submitted (30-JAN-1996) Andy C.M. Chang, Cancer Research Group,
            Children's Medical Research Institute, 214 Hawkesbury Road,
            Westmead, Sydney, NSW 2145, Australia
FEATURES             Location/Qualifiers
     source          1. .1232
                     /organism="Mus musculus"
                     /strain="BALB/c"
                     /db_xref="taxon:10090"
     CDS             228. .971
                     /codon_start=1
                     /product="stanniocalcin"
                     /protein_id="AAC00050.1"
                     /db_xref="GI:2828525"
                     /translation="MLQNSAVILALVISAAAAHEAEQNDSVSPRKSRVAAQNSAEVVR
                     CLNSALQVGCGAFACLENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANG
                     ITSKVFLAIRRCSTFQRMIAEVQEDCYSKLNVCSIAKRNPEAITEVIQLPNHFSNRYY
                     NRLVRSLLECDEDTVSTIRDSLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRRTNE
                     PQKLKVLLRNLRGEGDSPSHIKRTSQESA"
BASE COUNT      356 a    338 c    274 g    264 t
ORIGIN

Alignment Scores:
Pred. No.:                1.17e-119      Length:          1232
Score:                    1234.00        Matches:         238
Percent Similarity:       98.38%         Conservative:    5
Best Local Similarity:    96.36%         Mismatches:      4
Query Match:              97.32%         Indels:          0
DB:                       10             Gaps:            0

US-09-705-500A-3 (1-247) x MMU47815 (1-1232)

Qy          1 MetLeuGlnAsnSerAlaValLeuLeuValLeuValIleSerAlaSerAlaThrHisGlu 20
              ||||||||||||||||||||:::|||   ||||||||||||||:::|||   ||||||
Db        228 ATGCTCCAAAACTCAGCAGTGATTCTGGCGCTGGTCATCAGTGCAGCTGCAGCGCACGAG 287

Qy         21 AlaGluGlnAsnAspSerValSerProArgLysSerArgValAlaAlaGlnAsnSerAla 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        288 GCGGAACAAAATGATTCTGTGAGCCCCAGAAAATCCCGGGTGGCGGCTCAAAATTCAGCT 347

Qy         41 GluValValArgCysLeuAsnSerAlaLeuGlnValGlyCysGlyAlaPheAlaCysLeu 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        348 GAAGTGGTTCGCTGCCTCAACAGTGCCCTGCAGGTTGGCTGCGGGGCTTTTGCATGCCTG 407

Qy         61 GluAsnSerThrCysAspThrAspGlyMetTyrAspIleCysLysSerPheLeuTyrSer 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        408 GAAAACTCCACATGTGACACAGATGGGATGTACGACATTTGTAAATCCTTCTTGTACAGT 467

Qy         81 AlaAlaLysPheAspThrGlnGlyLysAlaPheValLysGluSerLeuLysCysIleAla 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        468 GCTGCTAAATTTGACACTCAGGGAAAAGCATTTGTCAAAGAGAGCTTAAAGTGCATCGCC 527

Qy        101 AsnGlyValThrSerLysValPheLeuAlaIleArgArgCysSerThrPheGlnArgMet 120
              ||||||:::||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        528 AATGGGATCACCTCCAAGGTGTTCCTTGCCATTCGGAGGTGTTCGACTTTCCAGAGGATG 587

Qy        121 IleAlaGluValGlnGluGluCysTyrSerLysLeuAsnValCysSerIleAlaLysArg 140
              ||||||||||||||||||:::||||||||||||||||||||||||||||||||||||||||
Db        588 ATCGCCGAGGTGCAGGAGGACTGCTACAGCAAGCTTAACGTTTGCAGCATCGCCAAGCGC 647

Qy        141 AsnProGluAlaIleThrGluValValGlnLeuProAsnHisPheSerAsnArgTyrTyr 160
              ||||||||||||||||||||||:::||||||||||||||||||||||||||||||||||||
Db        648 AACCCGGAAGCCATCACTGAAGTCATACAGCTGCCCAATCACTTCTCCAACAGATACTAC 707

Qy        161 AsnArgLeuValArgSerLeuLeuGluCysAspGluAspThrValSerThrIleArgAsp 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        708 AACAGACTTGTCCGAAGCCTTCTGGAATGTGATGAAGACACGGTCAGTACAATCAGAGAC 767

Qy        181 SerLeuMetGluLysIleGlyProAsnMetAlaSerLeuPheHisIleLeuGlnThrAsp 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        768 AGCCTGATGGAGAAGATCGGGCCCAACATGGCCAGCCTCTTCCACATCCTGCAGACAGAC 827

Qy        201 HisCysAlaGlnThrHisProArgAlaAspPheAsnArgArgArgThrAsnGluProGln 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        828 CACTGTGCCCAGACACACCCCAGAGCTGACTTCAATAGGAGGCGCACAAATGAGCCACAG 887

Qy        221 LysLeuLysValLeuLeuArgAsnLeuArgGlyGluGluAspSerProSerHisIleLys 240
              ||||||||||||||||||||||||||||||||   ||||||||||||||||||||
Db        888 AAGCTGAAAGTCCTCCTCAGGAACCTCCGAGGTGAGGGGGACTCTCCCTCACACATCAAA 947

Qy        241 ArgThrSerHisGluSerAla 247
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Db        948 CGCACCTCCCAAGAGAGTGCG 968

RESULT 9
BC021425
LOCUS       BC021425                2341 bp    mRNA    linear   ROD 07-AUG-2002
DEFINITION  Mus musculus, stanniocalcin, clone MGC:29066 IMAGE:5010981, mRNA,
            complete cds.
ACCESSION   BC021425
VERSION     BC021425.1  GI:18203894
KEYWORDS    MGC.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 2341)
  AUTHORS   Strausberg,R.
  TITLE     Direct Submission
  JOURNAL   Submitted (14-JAN-2002) National Institutes of Health, Mammalian
            Gene Collection (MGC), Cancer Genomics Office, National Cancer
            Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
            USA
  REMARK    NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT     Contact: MGC help desk
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Gilbert Smith, Ph.D.
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: National Institutes of Health Intramural
            Sequencing Center (NISC),
            Gaithersburg, Maryland;
            Web site: http://www.nisc.nih.gov/
            Contact: nisc_mgc@nhgri.nih.gov
            Akhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
            Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,
            Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P.,
            Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Laric,P., Legaspi,R.,
            Maduro,Q.L., Masiello,C., Maskeri,B., Mastrian,S.D.,McCloskey,J.C.,
            McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W.,
            Tsurgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L.,
            Young,A., Zhang,L.-H. and Green,E.D.

            Clone distribution: MGC clone distribution information can be found
            through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
            Series: IRAK Plate: 39 Row: f Column: 22.
FEATURES             Location/Qualifiers
     source          1. .2341
                     /organism="Mus musculus"
                     /db_xref="taxon:10090"
                     /map="FVB/N-3"
                     /clone="MGC:29066 IMAGE:5010981"
                     /tissue_type="Mammary tumor. MMTV-LTR/INT3 model. 5 month
                     old mouse. Taken by biopsy."
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                     /clone_lib="NCI_CGAP_Mam2"
                     /lab_host="DH10B"
                     /note="Vector: pCMV-SPORT6"
     CDS             123. .866
                     /codon_start=1
                     /product="stanniocalcin"
                     /protein_id="AAH21425.1"
                     /db_xref="GI:18203895"
                     /db_xref="LocusID:20855"
                     /translation="MLQNSAVILALVISAAAAHEAEQNDSVSPRKSRVAAQNSAEVVR
                     CLNSALQVGCGAFACLENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANG
                     ITSKVFLAIRRCSTFQRMIAEVQEDCYSKLNVCSIAKRNPEAITEVIQLPNHFSNRYY
                     NRLVRSLLECDEDTVSTIRDSLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRRTNE
                     PQKLKVLLRNLRGEGDSPSHIKRTSQESA"
BASE COUNT      694 a    559 c    478 g    610 t
ORIGIN

Alignment Scores:
Pred. No.:              2.67e-119      Length:         2341
Score:                  1234.00        Matches:        238
Percent Similarity:     98.38%         Conservative:   5
Best Local Similarity:  96.36%         Mismatches:     4
Query Match:            97.32%         Indels:         0
DB:                     10             Gaps:           0

US-09-705-500A-3 (1-247) x BC021425 (1-2341)

Qy          1 MetLeuGlnAsnSerAlaValLeuLeuValLeuValIleSerAlaSerAlaThrHisGlu 20
              ||||||||||||||||||||:::|||  ||||||||||||||||:::|||  ||||||
Db        123 ATGCTCCAAAACTCAGCAGTGATTCTGGCGCTGGTCATCAGTGCAGCTGCAGCGCACGAG 182

Qy         21 AlaGluGlnAsnAspSerValSerProArgLysSerArgValAlaAlaGlnAsnSerAla 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        183 GCGGAACAAAATGATTCTGTGAGCCCCAGAAAATCCCGGGTGGCGGCTCAAAATTCAGCT 242

Qy         41 GluValValArgCysLeuAsnSerAlaLeuGlnValGlyCysGlyAlaPheAlaCysLeu 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        243 GAAGTGGTTCGCTGCCTCAACAGTGCCCTGCAGGTTGGCTGCGGGGCTTTTGCATGCCTG 302

Qy         61 GluAsnSerThrCysAspThrAspGlyMetTyrAspIleCysLysSerPheLeuTyrSer 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        303 GAAAACTCCACATGTGACACAGATGGGATGTACGACATTTGTAAATCCTTCTTGTACAGT 362

Qy         81 AlaAlaLysPheAspThrGlnGlyLysAlaPheValLysGluSerLeuLysCysIleAla 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        363 GCTGCTAAATTTGACACTCAGGGAAAAGCATTTGTCAAAGAGAGCTTAAAGTGCATCGCC 422

Qy        101 AsnGlyValThrSerLysValPheLeuAlaIleArgArgCysSerThrPheGlnArgMet 120
              ||||||:::||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        423 AATGGGATCACCTCCAAGGTATTCCTTGCCATTCGGAGGTGTTCGACTTTCCAGAGGATG 482

Qy        121 IleAlaGluValGlnGluGluCysTyrSerLysLeuAsnValCysSerIleAlaLysArg 140
              ||||||||||||||||||:::||||||||||||||||||||||||||||||||||||||||
Db        483 ATCGCCGAGGTGCAGGAGGACTGCTACAGCAAGCTTAACGTTTGCAGCATCGCCAAGCGC 542

Qy        141 AsnProGluAlaIleThrGluValValGlnLeuProAsnHisPheSerAsnArgTyrTyr 160
              ||||||||||||||||||||||:::||||||||||||||||||||||||||||||||||||
Db        543 AACCCGGAAGCCATCACTGAAGTCATACAGCTGCCCAATCACTTCTCCAACAGATACTAC 602

Qy        161 AsnArgLeuValArgSerLeuLeuGluCysAspGluAspThrValSerThrIleArgAsp 180
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Db        603 AACAGACTTGTCCGAAGCCTTCTGGAATGTGATGAAGACACGGTCAGTACAATCAGAGAC 662

Qy        181 SerLeuMetGluLysIleGlyProAsnMetAlaSerLeuPheHisIleLeuGlnThrAsp 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        663 AGCCTGATGGAGAAGATCGGGCCCAACATGGCCAGCCTCTTCCACATCCTGCAGACAGAC 722

Qy        201 HisCysAlaGlnThrHisProArgAlaAspPheAsnArgArgArgThrAsnGluProGln 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        723 CACTGTGCCCAGACACACCCCAGAGCTGACTTCAATAGGAGGCGCACAAATGAGCCACAG 782

Qy        221 LysLeuLysValLeuLeuArgAsnLeuArgGlyGluGluAspSerProSerHisIleLys 240
              ||||||||||||||||||||||||||||||||||  ||||||||||||||||||||
Db        783 AAGCTGAAAGTCCTCCTCAGGAACCTCCGAGGTGAGGGGGACTCTCCCTCACACATCAAA 842

Qy        241 ArgThrSerHisGluSerAla 247
              |||||||||  |||||||||
Db        843 CGCACCTCCCAAGAGAGTGCG 863

RESULT 10
RNU62667
LOCUS       RNU62667                1004 bp    mRNA    linear   ROD 02-JAN-1997
DEFINITION  Rattus norvegicus stanniocalcin (rSTC) mRNA, complete cds.
ACCESSION   U62667
VERSION     U62667.1  GI:1762530
KEYWORDS    .
SOURCE      Rattus norvegicus.
  ORGANISM  Rattus norvegicus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
            Rattus.
REFERENCE   1  (bases 1 to 1004)
  AUTHORS   Abe,T., Tanemoto,M., Hall,A.E., Brown,E.M. and Hebert,S.C.
  TITLE     Molecular cloning and characterization of rat stanniocalcin peptide
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 1004)
  AUTHORS   Abe,T., Tanemoto,M., Hall,A.E., Brown,E.M. and Hebert,S.C.
  TITLE     Direct Submission
  JOURNAL   Submitted (01-JUL-1996) Renal Division, Brigham and Women's
            Hospital, 75 Francis Street, Boston, MA 02115, USA
FEATURES             Location/Qualifiers
     source          1. .1004
                     /organism="Rattus norvegicus"
                     /strain="Sprague-Dawley"
                     /db_xref="taxon:10116"
                     /tissue_type="kidney"
     gene            1. .1004
                     /gene="rSTC"
     CDS             110. .853
                     /gene="rSTC"
                     /codon_start=1
                     /product="stanniocalcin"
                     /protein_id="AAB39541.1"
                     /db_xref="GI:1762531"
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                     CLNSALQVGCGAFACLENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANG
                     ITSKVFLAIRRCSTFQRMIAEVQEDCYSKLNVCSIAKRNPEAITEVIQLPNHFSNRYY
                     NRLVRSLLECDEDTVSTIRDSLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRRTNE
                     PQKLKVLLRNLRGEGDSPSHIKRTSQENA"
BASE COUNT      288 a    253 c    241 g    222 t
ORIGIN

Alignment Scores:
Pred. No.:              1.86e-119      Length:         1004
Score:                  1231.00        Matches:        237
Percent Similarity:     98.38%         Conservative:   6
Best Local Similarity:  95.95%         Mismatches:     4
Query Match:            97.08%         Indels:         0
DB:                     10             Gaps:           0

US-09-705-500A-3 (1-247) x RNU62667 (1-1004)

Qy          1 MetLeuGlnAsnSerAlaValLeuLeuValLeuValIleSerAlaSerAlaThrHisGlu 20
              ||||||||||||||||||||:::|||  ||||||||||||||||:::|||  ||||||
Db        110 ATGCTCCAAAACTCAGCAGTGATTCTGGCGCTGGTCATCAGTGCTGCTGCAGCTCACGAG 169

Qy         21 AlaGluGlnAsnAspSerValSerProArgLysSerArgValAlaAlaGlnAsnSerAla 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        170 GCGGAACAGAATGATTCTGTGAGCCCCAGAAAATCCCGGGTGGCGGCTCAAAATTCAGCT 229

Qy         41 GluValValArgCysLeuAsnSerAlaLeuGlnValGlyCysGlyAlaPheAlaCysLeu 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        230 GAAGTGGTCCGCTGCCTCAACAGTGCCCTACAGGTTGGCTGTGGGGCTTTTGCATGCCTG 289

Qy         61 GluAsnSerThrCysAspThrAspGlyMetTyrAspIleCysLysSerPheLeuTyrSer 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        290 GAAAACTCCACATGTGACACAGATGGGATGTACGACATTTGTAAATCCTTCTTGTACAGT 349

Qy         81 AlaAlaLysPheAspThrGlnGlyLysAlaPheValLysGluSerLeuLysCysIleAla 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        350 GCTGCTAAATTTGACACTCAGGGAAAAGCATTTGTCAAAGAGAGCTTAAAGTGCATCGCC 409

Qy        101 AsnGlyValThrSerLysValPheLeuAlaIleArgArgCysSerThrPheGlnArgMet 120
              ||||||:::||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        410 AATGGGATCACCTCCAAGGTCTTCCTTGCCATTCGGAGGTGTTCTACTTTCCAGAGGATG 469

Qy        121 IleAlaGluValGlnGluGluCysTyrSerLysLeuAsnValCysSerIleAlaLysArg 140
              ||||||||||||||||||:::||||||||||||||||||||||||||||||||||||||||
Db        470 ATCGCCGAGGTGCAGGAGGACTGCTACAGCAAGCTCAATGTTTGCAGCATTGCCAAGCGC 529

Qy        141 AsnProGluAlaIleThrGluValValGlnLeuProAsnHisPheSerAsnArgTyrTyr 160
              ||||||||||||||||||||||:::||||||||||||||||||||||||||||||||||||
Db        530 AACCCGGAAGCCATCACTGAAGTCATACAGCTGCCCAATCACTTCTCCAACAGATACTAC 589

Qy        161 AsnArgLeuValArgSerLeuLeuGluCysAspGluAspThrValSerThrIleArgAsp 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        590 AACAGACTTGTCCGAAGCCTTCTGGAATGTGATGAAGATACGGTCAGCACAATCAGAGAC 649

Qy        181 SerLeuMetGluLysIleGlyProAsnMetAlaSerLeuPheHisIleLeuGlnThrAsp 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        650 AGCCTGATGGAGAAGATCGGGCCCAACATGGCCAGCCTCTTCCATATCCTGCAGACAGAC 709

Qy        201 HisCysAlaGlnThrHisProArgAlaAspPheAsnArgArgArgThrAsnGluProGln 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        710 CACTGTGCCCAGACACATCCCAGAGCTGACTTCAATAGGAGGCGCACAAATGAGCCACAG 769

Qy        221 LysLeuLysValLeuLeuArgAsnLeuArgGlyGluGluAspSerProSerHisIleLys 240
              ||||||||||||||||||||||||||||||||||   ||||||||||||||||||||||
Db        770 AAGCTGAAAGTCCTCCTCAGGAACCTCCGAGGTGAGGGGGATTCTCCCTCACACATCAAA 829

Qy        241 ArgThrSerHisGluSerAla 247
              |||||||||   |||:::|||
Db        830 CGCACCTCCCAAGAGAATGCG 850

RESULT 11
AF099098
LOCUS       AF099098               4183 bp    mRNA    linear   ROD 10-NOV-1998
DEFINITION  Mus musculus stanniocalcin precursor, mRNA, complete cds.
ACCESSION   AF099098
VERSION     AF099098.1  GI:3851659
KEYWORDS    .
SOURCE      Mus musculus.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 4183)
  AUTHORS   Varghese,R., Wong,C.K.C., Doel,H., Wagner,G.F. and DiMattia,G.E.
  TITLE     Comparative Analysis of Mammalian Stanniocalcin Genes
  JOURNAL   Endocrinology 139, 4717-4725 (1998)
REFERENCE   2  (bases 1 to 4183)
  AUTHORS   DiMattia,G.E., Varghese,R. and Wagner,G.F.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-OCT-1998) Oncology, London Regional Cancer Centre,
            790 Commissioners Rd., London, ONT N6C 4L6, Canada
FEATURES             Location/Qualifiers
     source          1. .4183
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                     /db_xref="taxon:10090"
     5'UTR           1. .153
     CDS             154. .897
                     /note="hormone"
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                     /product="stanniocalcin precursor"
                     /protein_id="AAC72394.1"
                     /db_xref="GI:3851660"
                     /translation="MLQNSAVILALVISAAAAHEAEQNDSVSPRKSRVAAQNSAEVVR
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                     ITSKVFLAIRRCSTFQRMIAEVQEDCYSKLNVCSIAKRNPEAITEVIQQPNHFSNRYY
                     NRLVRSLLECDEDTVSTIRDSLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRRTNE
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     3'UTR           898. .4183
BASE COUNT     1215 a    979 c    798 g   1191 t
ORIGIN

Alignment Scores:
Pred. No.:                2.38e-118      Length:          4183
Score:                    1228.00        Matches:         237
Percent Similarity:       97.98%         Conservative:    5
Best Local Similarity:    95.95%         Mismatches:      5
Query Match:              96.85%         Indels:          0
DB:                       10             Gaps:            0

US-09-705-500A-3 (1-247) x AF099098 (1-4183)

Qy          1 MetLeuGlnAsnSerAlaValLeuLeuValLeuValIleSerAlaSerAlaThrHisGlu 20
              ||||||||||||||||||||||:::|||   |||||||||||||||:::|||   ||||||
Db        154 ATGCTCCAAAACTCAGCAGTGATTCTGGCGCTGGTCATCAGTGCAGCTGCAGCGCACGAG 213

Qy         21 AlaGluGlnAsnAspSerValSerProArgLysSerArgValAlaAlaGlnAsnSerAla 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        214 GCGGAACAAAATGATTCTGTGAGCCCCAGAAAATCCCGGGTGGCGGCTCAAAATTCAGCT 273

Qy         41 GluValValArgCysLeuAsnSerAlaLeuGlnValGlyCysGlyAlaPheAlaCysLeu 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        274 GAAGTGGTTCGCTGCCTCAACAGTGCCCTGCAGGTTGGCTGCGGGGCTTTTGCATGCCTG 333

Qy         61 GluAsnSerThrCysAspThrAspGlyMetTyrAspIleCysLysSerPheLeuTyrSer 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        334 GAAAACTCCACATGTGACACAGATGGGATGTACGACATTTGTAAATCCTTCTTGTACAGT 393

Qy         81 AlaAlaLysPheAspThrGlnGlyLysAlaPheValLysGluSerLeuLysCysIleAla 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        394 GCTGCTAAATTTGACACTCAGGGAAAAGCATTTGTCAAAGAGAGCTTAAAGTGCATCGCC 453

Qy        101 AsnGlyValThrSerLysValPheLeuAlaIleArgArgCysSerThrPheGlnArgMet 120
              ||||||:::||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        454 AATGGGATCACCTCCAAGGTATTCCTTGCCATTCGGAGGTGTTCGACTTTCCAGAGGATG 513

Qy        121 IleAlaGluValGlnGluGluCysTyrSerLysLeuAsnValCysSerIleAlaLysArg 140
              ||||||||||||||||||:::||||||||||||||||||||||||||||||||||||||||
Db        514 ATCGCCGAGGTGCAGGAGGACTGCTACAGCAAGCTTAACGTTTGCAGCATCGCCAAGCGC 573

Qy        141 AsnProGluAlaIleThrGluValValGlnLeuProAsnHisPheSerAsnArgTyrTyr 160
              ||||||||||||||||||||||:::|||   ||||||||||||||||||||||||||||
Db        574 AACCCGGAAGCCATCACTGAAGTCATACAGCAGCCCAATCACTTCTCCAACAGATACTAC 633

Qy        161 AsnArgLeuValArgSerLeuLeuGluCysAspGluAspThrValSerThrIleArgAsp 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        634 AACAGACTTGTCCGAAGCCTTCTGGAATGTGATGAAGACACGGTCAGCACAATCAGAGAC 693

Qy        181 SerLeuMetGluLysIleGlyProAsnMetAlaSerLeuPheHisIleLeuGlnThrAsp 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        694 AGCCTGATGGAGAAGATCGGGCCCAACATGGCCAGCCTCTTCCACATCCTGCAGACAGAC 753

Qy        201 HisCysAlaGlnThrHisProArgAlaAspPheAsnArgArgArgThrAsnGluProGln 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        754 CACTGTGCCCAGACACACCCCAGAGCTGACTTCAATAGGAGGCGTACAAATGAGCCACAG 813

Qy        221 LysLeuLysValLeuLeuArgAsnLeuArgGlyGluGluAspSerProSerHisIleLys 240
              ||||||||||||||||||||||||||||||||||   ||||||||||||||||||||||
Db        814 AAGCTGAAAGTCCTCCTCAGGAACCTCCGAGGTGAGGGGGACTCTCCCTCACACATCAAA 873

Qy        241 ArgThrSerHisGluSerAla 247
              |||||||||   |||||||||
Db        874 CGCACCTCCCAAGAGAGTGCG 894

RESULT 12
AF257506
LOCUS       AF257506               834 bp    mRNA    linear   MAM 09-MAY-2000
DEFINITION  Bos taurus stanniocalcin mRNA, complete cds.
ACCESSION   AF257506
VERSION     AF257506.1  GI:7739750
```

```
KEYWORDS
SOURCE      Bos taurus.
  ORGANISM  Bos taurus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
            Bovidae; Bovinae; Bos.
REFERENCE   1  (bases 1 to 834)
  AUTHORS   DiMattia,G.E.
  TITLE     bovine stanniocalcin cDNA sequence
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 834)
  AUTHORS   DiMattia,G.E.
  TITLE     Direct Submission
  JOURNAL   Submitted (18-APR-2000) Oncology, London Regional Cancer centre,
            790 Commissioners Rd., London, ON N6A 4L6, Canada
FEATURES             Location/Qualifiers
     source          1. .834
                     /organism="Bos taurus"
                     /db_xref="taxon:9913"
                     /tissue_type="ovary"
     CDS             1. .744
                     /codon_start=1
                     /product="stanniocalcin"
                     /protein_id="AAF68996.1"
                     /db_xref="GI:7739751"
                     /translation="MLQNSAVILVLVISASATHEAEQNDSVSLRKSRVAAQNSAEVIR
                     CLNSALQVGCGAFACLENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANG
                     VTSKVFLAIRRCSTFQRMIAEVQEECYTKLNVCSVAKRNPEAITEVVQLPNHFSNRYY
                     NRLVRSLLDCDEDTVSTIRDSLMEKIGPNMASLFHILQTDHCAHTQQRADFNRRRANE
                     PQKLKVLLRNLRGEVASPSHIKRTSQESA"
     3'UTR           745. .834
BASE COUNT      218 a    227 c    215 g    174 t
ORIGIN

Alignment Scores:
Pred. No.:              3.28e-116      Length:          834
Score:                  1199.00        Matches:         234
Percent Similarity:     96.76%         Conservative:    5
Best Local Similarity:  94.74%         Mismatches:      8
Query Match:            94.56%         Indels:          0
DB:                     4              Gaps:            0

US-09-705-500A-3 (1-247) x AF257506 (1-834)

Qy          1 MetLeuGlnAsnSerAlaValLeuLeuValLeuValIleSerAlaSerAlaThrHisGlu 20
              |||||||||||||||||||:::|||||||||||||||||||||||||||||||||||||
Db          1 ATGCTCCAAAACTCAGCAGTGATTCTGGTGCTGGTGATCAGTGCTTCTGCAACCCATGAG 60

Qy         21 AlaGluGlnAsnAspSerValSerProArgLysSerArgValAlaAlaGlnAsnSerAla 40
              ||||||||||||||||||||    ||||||||||||||||||||||||||||||||||||
Db         61 GCGGAGCAGAATGATTCTGTGAGCCTCAGGAAATCCCGGGTGGCAGCTCAGAACTCAGCT 120

Qy         41 GluValValArgCysLeuAsnSerAlaLeuGlnValGlyCysGlyAlaPheAlaCysLeu 60
              ||||||:::||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GAAGTGATTCGCTGCCTCAACAGCGCGCTGCAGGTTGGCTGTGGAGCTTTTGCATGCCTG 180

Qy         61 GluAsnSerThrCysAspThrAspGlyMetTyrAspIleCysLysSerPheLeuTyrSer 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GAGAACTCCACCTGTGACACAGATGGGATGTACGACATCTGTAAATCCTTCTTGTACAGC 240

Qy         81 AlaAlaLysPheAspThrGlnGlyLysAlaPheValLysGluSerLeuLysCysIleAla 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GCTGCTAAATTTGACACTCAGGGAAAAGCATTTGTCAAAGAGAGCTTAAAGTGCATCGCC 300

Qy        101 AsnGlyValThrSerLysValPheLeuAlaIleArgArgCysSerThrPheGlnArgMet 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 AACGGGGTCACCTCCAAGGTCTTCCTGGCCATTCGGAGGTGCTCTACTTTTCAGAGGATG 360

Qy        121 IleAlaGluValGlnGluGluCysTyrSerLysLeuAsnValCysSerIleAlaLysArg 140
              |||||||||||||||||||||||||:::||||||||||||||||:::|||||||||||
Db        361 ATTGCCGAAGTCCAGGAGGAGTGCTACACCAAGCTGAACGTGTGCAGTGTCGCCAAGCGG 420

Qy        141 AsnProGluAlaIleThrGluValValGlnLeuProAsnHisPheSerAsnArgTyrTyr 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 AACCCGGAAGCCATCACGGAAGTCGTCCAGCTCCCTAATCATTTCTCCAACAGATACTAT 480

Qy        161 AsnArgLeuValArgSerLeuLeuGluCysAspGluAspThrValSerThrIleArgAsp 180
              ||||||||||||||||||||||||:::||||||||||||||||||||||||||||||||
Db        481 AACAGACTTGTCCGAAGCCTACTGGACTGTGACGAAGACACAGTGAGCACCATTAGAGAC 540

Qy        181 SerLeuMetGluLysIleGlyProAsnMetAlaSerLeuPheHisIleLeuGlnThrAsp 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 AGCCTGATGGAGAAAATCGGCCCCAACATGGCCAGCCTCTTTCACATCCTGCAGACGGAT 600

Qy        201 HisCysAlaGlnThrHisProArgAlaAspPheAsnArgArgArgThrAsnGluProGln 220
              |||||||||   |||      ||||||||||||||||||||||   ||||||||||||
Db        601 CACTGTGCCCATACACAGCAGCGAGCTGACTTCAACAGGAGGCGTGCCAATGAGCCACAG 660

Qy        221 LysLeuLysValLeuLeuArgAsnLeuArgGlyGluGluAspSerProSerHisIleLys 240
              ||||||||||||||||||||||||||||||||||||||      ||||||||||||||||
Db        661 AAGCTGAAAGTCCTCCTCAGGAACCTCCGAGGTGAGGTGGCCTCTCCCTCCCACATCAAA 720

Qy        241 ArgThrSerHisGluSerAla 247
              |||||||||   |||||||||
Db        721 CGCACCTCCCAGGAGAGTGCC 741

RESULT 13
AX156292
LOCUS       AX156292                585 bp    DNA     linear   PAT 22-JUN-2001
DEFINITION  Sequence 149 from Patent WO0140269.
ACCESSION   AX156292
VERSION     AX156292.1  GI:14537293
KEYWORDS
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 585)
  AUTHORS   Dillon,D.C., Day,C.H., Jiang,Y., Houghton,R.L., Mitcham,J.L. and
            Wang,A.
  TITLE     Compositions and methods for therapy and diagnosis of breast cancer
  JOURNAL   Patent: WO 0140269-A 149 07-JUN-2001;
            CORIXA CORPORATION (US)
FEATURES             Location/Qualifiers
     source          1. .585
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
BASE COUNT      171 a    163 c    136 g    110 t      5 others
ORIGIN

Alignment Scores:
Pred. No.:              4.94e-81       Length:          585
Score:                  861.00         Matches:         166
Percent Similarity:     98.22%         Conservative:    0
Best Local Similarity:  98.22%         Mismatches:      3
Query Match:            67.90%         Indels:          0
DB:                     6              Gaps:            0

US-09-705-500A-3 (1-247) x AX156292 (1-585)

Qy         79 TyrSerAlaAlaLysPheAspThrGlnGlyLysAlaPheValLysGluSerLeuLysCys 98
              |||       ||||||||||||||    ||||||||||||||||||||||||||||||||
Db          6 TACANCACTGCTAAATTTGACACTNANGGAAAAGCATTCGTCAAAGAGAGCTTAAAATGC 65

Qy         99 IleAlaAsnGlyValThrSerLysValPheLeuAlaIleArgArgCysSerThrPheGln 118
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         66 ATCGCCAACGGGGTCACCTCCAAGGTCTTCCTCGCCATTCGGAGGTGCTCCACTTTCCAA 125

Qy        119 ArgMetIleAlaGluValGlnGluGluCysTyrSerLysLeuAsnValCysSerIleAla 138
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        126 AGGATGATTGCTGAGGTGCAGGAAGAGTGCTACAGCAAGCTGAATGTGTGCAGCATCGCC 185

Qy        139 LysArgAsnProGluAlaIleThrGluValValGlnLeuProAsnHisPheSerAsnArg 158
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        186 AAGCGGAACCCTGAAGCCATCACTGAGGTCGTCCAGCTGCCCAATCACTTCTCCAACAGA 245
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Qy        159 TyrTyrAsnArgLeuValArgSerLeuLeuGluCysAspGluAspThrValSerThrIle 178
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        246 TACTATAACAGACTTGTCCGAAGCCTGCTGGAATGTGATGAAGACACAGTCAGCACAATC 305

Qy        179 ArgAspSerLeuMetGluLysIleGlyProAsnMetAlaSerLeuPheHisIleLeuGln 198
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        306 AGAGACAGCCTGATGGAGAAAATTGGGCCTAACATGGCCAGCCTCTTCCACATCCTGCAG 365

Qy        199 ThrAspHisCysAlaGlnThrHisProArgAlaAspPheAsnArgArgArgThrAsnGlu 218
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        366 ACAGACCACTGTGCCCAAACACACCCACGAGCTGACTTCAACAGGAGACGCACCAATGAG 425

Qy        219 ProGlnLysLeuLysValLeuLeuArgAsnLeuArgGlyGluGluAspSerProSerHis 238
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        426 CCGCAGAAGCTGAAAGTCCTCCTCAGGAACCTCCGAGGTGAGGAGGACTCTCCCTCCCAC 485

Qy        239 IleLysArgThrSerHisGluSerAla 247
              ||||||||||||||||||||||||||
Db        486 ATCAAACGCACATCCCATGAGAGTGCA 512

RESULT 14
ANGCSPA
LOCUS       ANGCSPA                 2192 bp    mRNA    linear   VRT 18-DEC-1997
DEFINITION  Anguilla australis corpuscles of Stannius protein (CS) mRNA,
            complete cds.
ACCESSION   M36967
VERSION     M36967.1  GI:2689882
KEYWORDS    corpuscles of Stannius protein.
SOURCE      Anguilla australis.
  ORGANISM  Anguilla australis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Actinopterygii; Neopterygii; Teleostei; Anguilliformes;
            Anguillidae; Anguilla.
REFERENCE   1  (bases 1 to 2192)
  AUTHORS   Butkus,A., Roche,P.J., Fernley,R.T., Haralambidis,J.,
            Penschow,J.D., Ryan,G.B., Trahair,J.F., Tregear,G.W. and
            Coghlan,J.P.
  TITLE     Purification and cloning of a corpuscles of Stannius protein from
            Anguilla australis
  JOURNAL   Mol. Cell. Endocrinol. 54 (2-3), 123-133 (1987)
  MEDLINE   88083961
   PUBMED   3319739
REFERENCE   2  (bases 1 to 2192)
  AUTHORS   Roche,P.J.
  TITLE     Direct Submission
  JOURNAL   Submitted (05-SEP-1990) Medical Lab Science, RMIT, Melbourne 3001,
            Australia
REFERENCE   3  (bases 1 to 2192)
  AUTHORS   Roche,P.J.
  TITLE     Direct Submission
  JOURNAL   Submitted (17-DEC-1997) Medical Lab Science, RMIT, Melbourne 3001,
            Australia
  REMARK    Sequence update by submitter
COMMENT     On Dec 17, 1997 this sequence version replaced gi:210954.
FEATURES             Location/Qualifiers
     source          1. .2192
                     /organism="Anguilla australis"
                     /db_xref="taxon:7940"
     gene            1. .2192
                     /gene="CS"
     CDS             122. .874
                     /gene="CS"
                     /note="corpuscles of Stannius protein"
                     /codon_start=1
                     /product="Stannius protein"
                     /protein_id="AAB91483.1"
                     /db_xref="GI:2689883"
                     /translation="MLRMSGLILTLVLVTAAYEQDESEPLSPRTARFSASSPSDVARC
                     LNGALQVGCSAFACLDNSTCNTDGMHEICRSFLHGAAKFDTQGKTFVKESLKCIANGI
                     TSKVFLTIRRCSSFQKMISEVQEECYSKLDLCSVAQSNPEAMGEVAQVPSQFPNRYYS
                     TLLQSLLTCDEDTVEQVRAGLVSRLEPEMGVLFQLLQTKACPPSAAGGTGPVGAGGSW
                     RWPMGPPMFKIQPNLRSRDPTHLFAKKRSTSS"
     sig_peptide     122. .172
                     /gene="CS"
     mat_peptide     218. .871
                     /gene="CS"
                     /product="Stannius protein"
                     /note="corpuscles of Stannius protein"
BASE COUNT      590 a    515 c    483 g    604 t
ORIGIN

Alignment Scores:
Pred. No.:                1.45e-61        Length:          2192
Score:                    682.00          Matches:         138
Percent Similarity:       72.83%          Conservative:    47
Best Local Similarity:    54.33%          Mismatches:      57
Query Match:              53.79%          Indels:          12
DB:                       5               Gaps:            6

US-09-705-500A-3 (1-247) x ANGCSPA (1-2192)

Qy          1 MetLeuGlnAsnSerAlaValLeuLeuValLeuValIleSerAlaSerAlaThrHisGlu 20
              ||||||:::   |||   ::::::|||   ||||||:::      :::|||   :::|||
Db        122 ATGCTGCGAATGAGTGGGCTAATCCTCACGCTTGTGCTG---GTAACTGCTGCCTACGAG 178

Qy         21 AlaGluGlnAsnAspSerValSerProArgLysSerArgValAlaAlaGlnAsnSerAla 40
                 ::::::::::::   :::||||||||   :::|||   :::|||   :::   :::
Db        179 CAGGATGAGAGCGAGCCCTTATCTCCAAGGACAGCGCGCTTCTCCGCCAGCAGCCCATCT 238

Qy         41 GluValValArgCysLeuAsnSerAlaLeuGlnValGlyCysGlyAlaPheAlaCysLeu 60
              :::|||   |||||||||||   ||||||||||||||||   |||||||||||||||||
Db        239 GATGTTGCACGCTGTCTGAACGGGGCCCTGCAGGTGGGCTGCAGTGCATTTGCCTGTCTT 298

Qy         61 GluAsnSerThrCysAspThrAspGlyMetTyrAspIleCysLysSerPheLeuTyrSer 80
              :::|||||||||||||:::|||||||||||:::::|||||:::|||||||||:::
Db        299 GACAACTCCACCTGCAACACCGACGGCATGCATGAAATCTGCAGGTCCTTCCTCCACGGT 358

Qy         81 AlaAlaLysPheAspThrGlnGlyLysAlaPheValLysGluSerLeuLysCysIleAla 100
              ||||||||||||||||||||||||||   ||||||||||||||||||||||||||||||
Db        359 GCTGCCAAATTTGACACACAGGGCAAGACTTTTGTGAAGGAGAGCCTGAAGTGCATAGCC 418

Qy        101 AsnGlyValThrSerLysValPheLeuAlaIleArgArgCysSerThrPheGlnArgMet 120
              ||||||:::|||||||||||||||||   |||||||||||||||:::|||||||:::|||
Db        419 AATGGCATCACCTCCAAAGTGTTCCTTACCATCCGCCGCTGCTCATCCTTCCAGAAGATG 478

Qy        121 IleAlaGluValGlnGluGluCysTyrSerLysLeuAsnValCysSerIleAlaLysArg 140
              |||:::|||||||||||||||||||||||||||:::::||||||:::|||:::
Db        479 ATCTCAGAGGTTCAGGAGGAGTGCTATAGCAAACTAGACCTCTGCTCTGTTGCCCAGAGC 538

Qy        141 AsnProGluAlaIleThrGluValValGlnLeuProAsnHisPheSerAsnArgTyrTyr 160
              ||||||||||||:::   ||||||   |||:::|||:::   |||   ||||||||||||
Db        539 AACCCAGAGGCCATGGGGGAGGTGGCCCAGGTGCCCAGCCAGTTTCCCAACAGGTACTAC 598

Qy        161 AsnArgLeuValArgSerLeuLeuGluCysAspGluAspThrValSerThrIleArgAsp 180
              :::   |||::::::|||||||||   |||||||||||||||||      :::|||
Db        599 AGCACCCTGCTGCAGAGTCTTCTGACGTGTGATGAGGACACCGTGGAGCAGGTGAGGGCC 658

Qy        181 SerLeuMetGluLysIleGlyProAsnMetAlaSerLeuPheHisIleLeuGlnThrAsp 200
              |||:::   ::::::   |||   |||   ||||||   :::||||||||||
Db        659 GGGTTGGTGTCCCGCCTGGAGCCAGAGATGGGGGTGCTCTTCCAGCTCCTCCAGACCAAG 718

Qy        201 HisCys--------------AlaGlnThrHisPro---ArgAlaAspPheAsnArgArg 214
              |||                   |||   |||       |||       :::   |||
Db        719 GCCTGCCCCCCGAGCGCGGCCGGTGGCACTGGCCCAGTAGGGGCAGGAGGCAGCTGGCGC 778

Qy        215 ArgThrAsnGluProGlnLysLeuLysValLeuLeuArgAsnLeuArgGlyGluGluAsp 234
                    |||         |||:::         |||||||||      :::
Db        779 TGGCCCATGGGGCCCCCCATGTTCAAGATC---CAGCCCAACCTGCGCTCCCGGGAC--- 832

Qy        235 SerProSerHisIle------LysArgThrSerHisGluSer 246
              |||:::|||:::      |||:::   |||       |||
Db        833 ---CCCACCCACCTCTTTGCTAAGAAACGCTCGACCAGCTCC 871

RESULT 15
A05174
LOCUS       A05174                  2190 bp    DNA     linear   PAT 30-APR-1993
```

```
DEFINITION  Synthetic nucleotide sequence of eel CS protein precursor.
ACCESSION   A05174
VERSION     A05174.1  GI:345033
KEYWORDS    .
SOURCE      Anguilla anguilla.
  ORGANISM  Anguilla anguilla
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Actinopterygii; Neopterygii; Teleostei; Anguilliformes;
            Anguillidae; Anguilla.
FEATURES             Location/Qualifiers
     source          1. .2190
                     /organism="Anguilla anguilla"
                     /db_xref="taxon:7936"
     CDS             122. .913
                     /codon_start=1
                     /product="CS protein"
                     /protein_id="CAA00432.1"
                     /db_xref="GI:345034"
                     /translation="MLRMSGLILTLVLVTAAYEQDESEPLSPRTARFSASSPSDVARC
                     LNGALQVGCSAFACLDNSTCNTDGMHEICRSFLHGAAKFDTQGKTFVKESLKCIANGI
                     TSKVFLTIRRCSSFQKMISEVQEECYSKLDLCSVAQSNPEAMGEVAQVPSQFPNRYYS
                     TLLQSLLTCDEDTVEQVRAGLVSRLEPEMGVLFQLLQTKACPPSAAGGTGPVGAGGSW
                     RCPWGPPCSRSSPTCAPGTPPTSLLRNARPAPNYHPPRLALMDCP"
BASE COUNT      590 a    514 c    482 g    604 t
ORIGIN
```

Alignment Scores:

Pred. No.:	2.07e-61	Length:	2190
Score:	680.50	Matches:	124
Percent Similarity:	81.68%	Conservative:	41
Best Local Similarity:	61.39%	Mismatches:	36
Query Match:	53.67%	Indels:	1
DB:	6	Gaps:	1

US-09-705-500A-3 (1-247) x A05174 (1-2190)

```
Qy          1 MetLeuGlnAsnSerAlaValLeuLeuValLeuValIleSerAlaSerAlaThrHisGlu 20
              ||||||:::   |||   :::::::|||   ||||||:::      :::|||   :::|||
Db        122 ATGCTGCGAATGAGTGGGCTAATCCTCACGCTTGTGCTG---GTAACTGCTGCCTACGAG 178

Qy         21 AlaGluGlnAsnAspSerValSerProArgLysSerArgValAlaAlaGlnAsnSerAla 40
                 ::::::::::::   :::|||||||||   :::|||   :::|||   :::   :::
Db        179 CAGGATGAGAGCGAGCCCTTATCTCCAAGGACAGCGCGCTTCTCCGCCAGCAGCCCATCT 238

Qy         41 GluValValArgCysLeuAsnSerAlaLeuGlnValGlyCysGlyAlaPheAlaCysLeu 60
              :::|||   ||||||||||||   ||||||||||||||||||   ||||||||||||||
Db        239 GATGTTGCACGCTGTCTGAACGGGGCCCTGCAGGTGGGCTGCAGTGCATTTGCCTGTCTT 298

Qy         61 GluAsnSerThrCysAspThrAspGlyMetTyrAspIleCysLysSerPheLeuTyrSer 80
              :::|||||||||||||:::||||||||||||:::::::|||||:::|||||||||:::
Db        299 GACAACTCCACCTGCAACACCGACGGCATGCATGAAATCTGCAGGTCCTTCCTCCACGGT 358

Qy         81 AlaAlaLysPheAspThrGlnGlyLysAlaPheValLysGluSerLeuLysCysIleAla 100
              ||||||||||||||||||||||||||   ||||||||||||||||||||||||||||||
Db        359 GCTGCCAAATTTGACACACAGGGCAAGACTTTTGTGAAGGAGAGCCTGAAGTGCATAGCC 418

Qy        101 AsnGlyValThrSerLysValPheLeuAlaIleArgArgCysSerThrPheGlnArgMet 120
              ||||||:::||||||||||||||||||   ||||||||||||||:::|||||||:::|||
Db        419 AATGGCATCACCTCCAAAGTGTTCCTTACCATCCGCCGCTGCTCATCCTTCCAGAAGATG 478

Qy        121 IleAlaGluValGlnGluGluCysTyrSerLysLeuAsnValCysSerIleAlaLysArg 140
              |||:::||||||||||||||||||||||||||||||:::::::||||||:::|||:::
Db        479 ATCTCAGAGGTTCAGGAGGAGTGCTATAGCAAACTAGACCTCTGCTCTGTTGCCCAGAGC 538

Qy        141 AsnProGluAlaIleThrGluValValGlnLeuProAsnHisPheSerAsnArgTyrTyr 160
              ||||||||||||:::   ||||||   |||:::|||:::   |||   ||||||||||||
Db        539 AACCCAGAGGCCATGGGGGAGGTGGCCCAGGTGCCCAGCCAGTTTCCCAACAGGTACTAC 598

Qy        161 AsnArgLeuValArgSerLeuLeuGluCysAspGluAspThrValSerThrIleArgAsp 180
              :::   |||::::::|||||||||   ||||||||||||||||||      :::|||
Db        599 AGCACCCTGCTGCAGAGTCTTCTGACGTGTGATGAGGACACCGTGGAGCAGGTGAGGGCC 658

Qy        181 SerLeuMetGluLysIleGlyProAsnMetAlaSerLeuPheHisIleLeuGlnThrAsp 200
```

```
                  |||:::   ::::::   |||   |||       ||||||   :::|||||||||
Db        659 GGGTTGGTGTCCCGCCTGGAGCCAGAGATGGGGGTGCTCTTCCAGCTCCTCCAGACCAAG 718

Qy        201 HisCys 202
                 |||
Db        719 GCCTGC 724
```

Search completed: June 12, 2003, 20:50:12
Job time : 2003 secs

GenCore version 5.1.6

OM protein - nucleic search, using frame_plus_p2n model

Run on: June 12, 2003, 20:08:29 ; Search time 221 Seconds
(without alignments)
2516.939 Million cell updates/sec

Title: US-09-705-500A-3
Perfect score: 1268
Sequence: 1 MLQNSAVLLVLVISASATHE.....NLRGEEDSPSHIKRTSHESA 247

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlp
-Q=/cgn2_1/USPTO_spool/US09705500/runat_06062003_113612_7443/app_query.fasta_1.391
-DB=N_Geneseq_101002 -QFMT=fastap -SUFFIX=rng -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09705500_@CGN_1_1_208_@runat_06062003_113612_7443 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : N_Geneseq_101002:*
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2: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1981.DAT:*
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23: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA2001B.DAT:*
24: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	1268	100.0	741	21	AAA97594	Human stanniocalci
	2	1268	100.0	741	21	AAA11145	Human stanniocalci
	3	1268	100.0	744	24	ABL40225	Human staniocalcin
	4	1268	100.0	771	16	AAT02438	cDNA encoding stan
	5	1268	100.0	771	21	AAZ39520	Human corpuscles o
	6	1268	100.0	1283	22	AAF83297	Human stanniocalci
	7	1268	100.0	3762	22	AAF83823	DNA encoding Lng10
	8	1250	98.6	2572	21	AAF16051	Human prostate can
	9	861	67.9	585	22	AAH55624	Human breast tumou
	10	661.5	52.2	2191	9	AAN80655	Sequence encoding
	11	508	40.1	420	22	AAH55616	Human breast tumou
c	12	370	29.2	219	22	ABA51055	Human breast cell
c	13	370	29.2	219	22	ABA69045	Human foetal liver
c	14	370	29.2	219	22	ABA35989	Probe #14455 for g
c	15	370	29.2	219	22	AAK17358	Human brain expres
c	16	370	29.2	219	22	AAK43155	Human bone marrow
c	17	370	29.2	219	22	AAI23927	Probe #13860 for g
c	18	370	29.2	219	22	AAI49233	Probe #17919 used
c	19	370	29.2	219	22	AAI09526	Probe #9517 used t
c	20	370	29.2	219	24	ABS17231	Human genome-deriv
	21	354.5	28.0	888	21	AAZ57117	Mouse stanniocalci
	22	354.5	28.0	888	22	AAF31040	Murine stanniocalc
	23	354	27.9	882	20	AAZ28026	Adipogenesis inhib
	24	354	27.9	882	21	AAA09620	Human adipocytogen
	25	354	27.9	906	21	AAZ57116	Human stanniocalci
	26	354	27.9	906	22	AAF25370	Nucleotide sequenc
	27	354	27.9	906	22	AAF31030	Human stanniocalci
	28	354	27.9	909	22	AAH25831	Human adipogenesis
	29	354	27.9	1942	22	AAH15669	Human cDNA sequenc
	30	354	27.9	4298	22	AAH17879	Human cDNA sequenc
	31	352	27.8	892	17	AAT18979	Stanniocalcin alph
	32	352	27.8	892	21	AAZ39303	Human stanniocalci
	33	328	25.9	198	17	AAT28165	Senescence-related
	34	265	20.9	697	22	AAH04989	Human cDNA clone (
	35	253	20.0	774	22	AAH06665	Human cDNA clone (
c	36	214	16.9	362	22	ABA45937	Human breast cell
c	37	214	16.9	362	22	ABA56464	Human foetal liver
c	38	214	16.9	362	22	ABA26097	Probe #4563 for ge
c	39	214	16.9	362	22	AAK04623	Human brain expres
c	40	214	16.9	362	22	AAK30134	Human bone marrow
c	41	214	16.9	362	22	AAI14733	Probe #4666 for ge
c	42	214	16.9	362	22	AAI36098	Probe #4784 used t
c	43	214	16.9	362	22	AAI04536	Probe #4527 used t
c	44	214	16.9	362	24	ABS04715	Human genome-deriv
	45	95	7.5	4420	22	AAC90043	Human resistin gen

ALIGNMENTS

RESULT 1
AAA97594
ID AAA97594 standard; cDNA; 741 BP.
XX
AC AAA97594;
XX
DT 02-FEB-2001 (first entry)
XX
DE Human stanniocalcin cDNA.
XX
KW Human; stanniocalcin; STC; osteogenesis; bone disease; osteoporosis;
KW mineral metabolism regulator; prophylaxis; therapy; ss.
XX
OS Homo sapiens.
XX
PN JP2000229880-A.
XX
PD 22-AUG-2000.

```
XX
PF   10-FEB-1999;   99JP-0033262.
XX
PR   10-FEB-1999;   99JP-0033262.
XX
PA   (SNOW ) SNOW BRAND MILK PROD CO LTD.
XX
DR   WPI; 2000-605236/58.
DR   P-PSDB; AAB23264.
XX
PT   An osteogenesis promoter useful in the prevention and/or treatment of
PT   bone diseases such as osteoporosis -
XX
PS   Example 1; Page 4-5; 6pp; Japanese.
XX
CC   The invention relates to a novel osteogenesis-promoting composition
CC   which contains stanniocalcin (STC) as the active component.
CC   Stanniocalcin is a possible regulator of mineral metabolism. The
CC   composition is useful as a prophylactic and/or therapeutic agent for
CC   bone diseases such as osteoporosis. The present sequence represents
CC   cDNA encoding human stanniocalcin which was used in an exemplification
CC   of the invention.
XX
SQ   Sequence 741 BP; 201 A; 209 C; 183 G; 148 T; 0 other;

Alignment Scores:
Pred. No.:                1.23e-139      Length:          741
Score:                    1268.00        Matches:         247
Percent Similarity:       100.00%        Conservative:    0
Best Local Similarity:    100.00%        Mismatches:      0
Query Match:              100.00%        Indels:          0
DB:                       21             Gaps:            0

US-09-705-500A-3 (1-247) x AAA97594 (1-741)

Qy          1 MetLeuGlnAsnSerAlaValLeuLeuValLeuValIleSerAlaSerAlaThrHisGlu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGCTCCAAAACTCAGCAGTGCTTCTGGTGCTGGTGATCAGTGCTTCTGCAACCCATGAG 60

Qy         21 AlaGluGlnAsnAspSerValSerProArgLysSerArgValAlaAlaGlnAsnSerAla 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GCGGAGCAGAATGACTCTGTGAGCCCCAGGAAATCCCGAGTGGCGGCCCAAAACTCAGCT 120

Qy         41 GluValValArgCysLeuAsnSerAlaLeuGlnValGlyCysGlyAlaPheAlaCysLeu 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GAAGTGGTTCGTTGCCTCAACAGTGCTCTACAGGTCGGCTGCGGGGCTTTTGCATGCCTG 180

Qy         61 GluAsnSerThrCysAspThrAspGlyMetTyrAspIleCysLysSerPheLeuTyrSer 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GAAAACTCCACCTGTGACACAGATGGGATGTATGACATCTGTAAATCCTTCTTGTACAGC 240

Qy         81 AlaAlaLysPheAspThrGlnGlyLysAlaPheValLysGluSerLeuLysCysIleAla 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GCTGCTAAATTTGACACTCAGGGAAAAGCATTCGTCAAAGAGAGCTTAAAATGCATCGCC 300

Qy        101 AsnGlyValThrSerLysValPheLeuAlaIleArgArgCysSerThrPheGlnArgMet 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 AACGGGGTCACCTCCAAGGTCTTCCTCGCCATTCGGAGGTGCTCCACTTTCCAAAGGATG 360

Qy        121 IleAlaGluValGlnGluGluCysTyrSerLysLeuAsnValCysSerIleAlaLysArg 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 ATTGCTGAGGTGCAGGAAGAGTGCTACAGCAAGCTGAATGTGTGCAGCATCGCCAAGCGG 420

Qy        141 AsnProGluAlaIleThrGluValValGlnLeuProAsnHisPheSerAsnArgTyrTyr 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 AACCCTGAAGCCATCACTGAGGTCGTCCAGCTGCCCAATCACTTCTCCAACAGATACTAT 480

Qy        161 AsnArgLeuValArgSerLeuLeuGluCysAspGluAspThrValSerThrIleArgAsp 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 AACAGACTTGTCCGAAGCCTGCTGGAATGTGATGAAGACACAGTCAGCACAATCAGAGAC 540

Qy        181 SerLeuMetGluLysIleGlyProAsnMetAlaSerLeuPheHisIleLeuGlnThrAsp 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 AGCCTGATGGAGAAAATTGGGCCTAACATGGCCAGCCTCTTCCACATCCTGCAGACAGAC 600

Qy        201 HisCysAlaGlnThrHisProArgAlaAspPheAsnArgArgArgThrAsnGluProGln 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CACTGTGCCCAAACACACCCACGAGCTGACTTCAACAGGAGACGCACCAATGAGCCGCAG 660

Qy        221 LysLeuLysValLeuLeuArgAsnLeuArgGlyGluGluAspSerProSerHisIleLys 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 AAGCTGAAAGTCCTCCTCAGGAACCTCCGAGGTGAGGAGGACTCTCCCTCCCACATCAAA 720

Qy        241 ArgThrSerHisGluSerAla 247
              ||||||||||||||||||||||
Db        721 CGCACATCCCATGAGAGTGCA 741

RESULT 2
AAA11145
ID   AAA11145 standard; cDNA; 741 BP.
XX
AC   AAA11145;
XX
DT   26-SEP-2000  (first entry)
XX
DE   Human stanniocalcin coding sequence.
XX
KW   PCR primer; human; stanniocalcin; inhibitor; differentiation; maturation;
KW   adipocyte; obesity; diabetes; hypertension; heart disease; ss.
XX
OS   Homo sapiens.
XX
PN   WO200016795-A1.
XX
PD   30-MAR-2000.
XX
PF   17-SEP-1999;   99WO-JP05080.
XX
PR   17-SEP-1998;   98JP-0263004.
XX
PA   (SNOW ) SNOW BRAND MILK PROD CO LTD.
XX
PI   Goto M,  Tomoyasu A,  Yamaguchi K,  Kinosaki M,  Nakagawa N;
XX
DR   WPI; 2000-283445/24.
DR   P-PSDB; AAY92901.
XX
PT   Treating or preventing obesity, which is a risk factor for diabetes,
PT   hypertension and heart disease, comprises administering an agent
PT   containing stanniocalcin  -
XX
PS   Example 1; Page 14-15; 19pp; Japanese.
XX
CC   This sequence represents the coding sequence for the human stanniocalcin
CC   protein. The stanniocalcin gene was isolated from IMR-90 cells.
CC   Stanniocalcin is an inhibitor of the differentiation and maturation of
CC   adipocytes. The protein is used for preventing and treating obesity which
CC   is a risk factor for diabetes, hypertension, and heart disease.
XX
SQ   Sequence 741 BP; 201 A; 209 C; 183 G; 148 T; 0 other;

Alignment Scores:
Pred. No.:                1.23e-139      Length:          741
Score:                    1268.00        Matches:         247
Percent Similarity:       100.00%        Conservative:    0
Best Local Similarity:    100.00%        Mismatches:      0
Query Match:              100.00%        Indels:          0
DB:                       21             Gaps:            0

US-09-705-500A-3 (1-247) x AAA11145 (1-741)

Qy          1 MetLeuGlnAsnSerAlaValLeuLeuValLeuValIleSerAlaSerAlaThrHisGlu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGCTCCAAAACTCAGCAGTGCTTCTGGTGCTGGTGATCAGTGCTTCTGCAACCCATGAG 60

Qy         21 AlaGluGlnAsnAspSerValSerProArgLysSerArgValAlaAlaGlnAsnSerAla 40
```

```
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          61 GCGGAGCAGAATGACTCTGTGAGCCCCAGGAAATCCCGAGTGGCGGCCCAAAACTCAGCT 120

Qy          41 GluValValArgCysLeuAsnSerAlaLeuGlnValGlyCysGlyAlaPheAlaCysLeu 60
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         121 GAAGTGGTTCGTTGCCTCAACAGTGCTCTACAGGTCGGCTGCGGGGCTTTTGCATGCCTG 180

Qy          61 GluAsnSerThrCysAspThrAspGlyMetTyrAspIleCysLysSerPheLeuTyrSer 80
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         181 GAAAACTCCACCTGTGACACAGATGGGATGTATGACATCTGTAAATCCTTCTTGTACAGC 240

Qy          81 AlaAlaLysPheAspThrGlnGlyLysAlaPheValLysGluSerLeuLysCysIleAla 100
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         241 GCTGCTAAATTTGACACTCAGGGAAAAGCATTCGTCAAAGAGAGCTTAAAATGCATCGCC 300

Qy         101 AsnGlyValThrSerLysValPheLeuAlaIleArgArgCysSerThrPheGlnArgMet 120
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         301 AACGGGGTCACCTCCAAGGTCTTCCTCGCCATTCGGAGGTGCTCCACTTTCCAAAGGATG 360

Qy         121 IleAlaGluValGlnGluGluCysTyrSerLysLeuAsnValCysSerIleAlaLysArg 140
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         361 ATTGCTGAGGTGCAGGAAGAGTGCTACAGCAAGCTGAATGTGTGCAGCATCGCCAAGCGG 420

Qy         141 AsnProGluAlaIleThrGluValValGlnLeuProAsnHisPheSerAsnArgTyrTyr 160
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         421 AACCCTGAAGCCATCACTGAGGTCGTCCAGCTGCCCAATCACTTCTCCAACAGATACTAT 480

Qy         161 AsnArgLeuValArgSerLeuLeuGluCysAspGluAspThrValSerThrIleArgAsp 180
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         481 AACAGACTTGTCCGAAGCCTGCTGGAATGTGATGAAGACACAGTCAGCACAATCAGAGAC 540

Qy         181 SerLeuMetGluLysIleGlyProAsnMetAlaSerLeuPheHisIleLeuGlnThrAsp 200
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         541 AGCCTGATGGAGAAAATTGGGCCTAACATGGCCAGCCTCTTCCACATCCTGCAGACAGAC 600

Qy         201 HisCysAlaGlnThrHisProArgAlaAspPheAsnArgArgArgThrAsnGluProGln 220
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         601 CACTGTGCCCAAACACACCCACGAGCTGACTTCAACAGGAGACGCACCAATGAGCCGCAG 660

Qy         221 LysLeuLysValLeuLeuArgAsnLeuArgGlyGluGluAspSerProSerHisIleLys 240
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         661 AAGCTGAAAGTCCTCCTCAGGAACCTCCGAGGTGAGGAGGACTCTCCCTCCCACATCAAA 720

Qy         241 ArgThrSerHisGluSerAla 247
                |||||||||||||||||||
Db         721 CGCACATCCCATGAGAGTGCA 741
```

RESULT 3
ABL40225
ID ABL40225 standard; cDNA; 744 BP.
XX
AC ABL40225;
XX
DT 23-MAY-2002 (first entry)
XX
DE Human staniocalcin 1 encoding cDNA.
XX
KW Human; staniocalcin 1; osteopathic; osteogenesis failure; osteoporosis;
KW bone mass reduction; traumatic bone injury; osteomalacia; bone disease;
KW rheumatic bone disease; cancer associated bone disease; rachitis;
KW arthritis deformans; gene; ss.
XX
OS Homo sapiens.
XX
FH Key   Location/Qualifiers
FT CDS   1..744
FT   /*tag= a
FT   /product= "staniocalcin 1"
XX
PN WO200204013-A1.
XX
PD 17-JAN-2002.
XX
PF 10-JUL-2001; 2001WO-JP05962.
XX
PR 11-JUL-2000; 2000JP-0209926.
XX
PA (BMLB-) BML INC.
XX
PI Yoshiko Y, Koide Y, Igarashi A, Takano S, Maeda N, Aubin JE;
XX
DR WPI; 2002-164600/21.
DR P-PSDB; ABB06259.
XX
PT Agent used for treating bone diseases e.g. osteoporosis, traumatic bone
PT injury, osteomalacia, rheumatic bone diseases, bone diseases associated
PT with cancer and arthritis deformans containing staniocalcin I -
XX
PS Claim 2; Fig 1; 24pp; Japanese.
XX
CC The present invention describes an agent containing staniocalcin 1,
CC particularly of human origin. Staniocalcin 1 has osteopathic activity.
CC The agent can be used for treating diseases relating to osteogenesis
CC failure or reduction in bone mass e.g. osteoporosis, traumatic bone
CC injury, osteomalacia, rheumatic bone diseases, bone diseases associated
CC with cancer, bone diseases due to phosphorus or calcium metabolic error,
CC rachitis and arthritis deformans. The agent increases bone mass. The
CC present sequence encodes human staniocalcin 1.
XX
SQ Sequence 744 BP; 203 A; 209 C; 183 G; 149 T; 0 other;

Alignment Scores:

Pred. No.:	1.24e-139	Length:	744
Score:	1268.00	Matches:	247
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	24	Gaps:	0

US-09-705-500A-3 (1-247) x ABL40225 (1-744)

```
Qy           1 MetLeuGlnAsnSerAlaValLeuLeuValLeuValIleSerAlaSerAlaThrHisGlu 20
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db           1 ATGCTCCAAAACTCAGCAGTGCTTCTGGTGCTGGTGATCAGTGCTTCTGCAACCCATGAG 60

Qy          21 AlaGluGlnAsnAspSerValSerProArgLysSerArgValAlaAlaGlnAsnSerAla 40
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          61 GCGGAGCAGAATGACTCTGTGAGCCCCAGGAAATCCCGAGTGGCGGCCCAAAACTCAGCT 120

Qy          41 GluValValArgCysLeuAsnSerAlaLeuGlnValGlyCysGlyAlaPheAlaCysLeu 60
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         121 GAAGTGGTTCGTTGCCTCAACAGTGCTCTACAGGTCGGCTGCGGGGCTTTTGCATGCCTG 180

Qy          61 GluAsnSerThrCysAspThrAspGlyMetTyrAspIleCysLysSerPheLeuTyrSer 80
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         181 GAAAACTCCACCTGTGACACAGATGGGATGTATGACATCTGTAAATCCTTCTTGTACAGC 240

Qy          81 AlaAlaLysPheAspThrGlnGlyLysAlaPheValLysGluSerLeuLysCysIleAla 100
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         241 GCTGCTAAATTTGACACTCAGGGAAAAGCATTCGTCAAAGAGAGCTTAAAATGCATCGCC 300

Qy         101 AsnGlyValThrSerLysValPheLeuAlaIleArgArgCysSerThrPheGlnArgMet 120
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         301 AACGGGGTCACCTCCAAGGTCTTCCTCGCCATTCGGAGGTGCTCCACTTTCCAAAGGATG 360

Qy         121 IleAlaGluValGlnGluGluCysTyrSerLysLeuAsnValCysSerIleAlaLysArg 140
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         361 ATTGCTGAGGTGCAGGAAGAGTGCTACAGCAAGCTGAATGTGTGCAGCATCGCCAAGCGG 420

Qy         141 AsnProGluAlaIleThrGluValValGlnLeuProAsnHisPheSerAsnArgTyrTyr 160
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         421 AACCCTGAAGCCATCACTGAGGTCGTCCAGCTGCCCAATCACTTCTCCAACAGATACTAT 480

Qy         161 AsnArgLeuValArgSerLeuLeuGluCysAspGluAspThrValSerThrIleArgAsp 180
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         481 AACAGACTTGTCCGAAGCCTGCTGGAATGTGATGAAGACACAGTCAGCACAATCAGAGAC 540
```

```
Qy        181 SerLeuMetGluLysIleGlyProAsnMetAlaSerLeuPheHisIleLeuGlnThrAsp 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 AGCCTGATGGAGAAAATTGGGCCTAACATGGCCAGCCTCTTCCACATCCTGCAGACAGAC 600

Qy        201 HisCysAlaGlnThrHisProArgAlaAspPheAsnArgArgArgThrAsnGluProGln 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CACTGTGCCCAAACACACCCACGAGCTGACTTCAACAGGAGACGCACCAATGAGCCGCAG 660

Qy        221 LysLeuLysValLeuLeuArgAsnLeuArgGlyGluGluAspSerProSerHisIleLys 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 AAGCTGAAAGTCCTCCTCAGGAACCTCCGAGGTGAGGAGGACTCTCCCTCCCACATCAAA 720

Qy        241 ArgThrSerHisGluSerAla 247
              |||||||||||||||||||||
Db        721 CGCACATCCCATGAGAGTGCA 741
```

RESULT 4
AAT02438
ID AAT02438 standard; cDNA; 771 BP.
XX
AC AAT02438;
XX
DT 19-APR-1996 (first entry)
XX
DE cDNA encoding stanniocalcin from Corpuscles of Stannius.
XX
KW stanniocalcin; Corpuscles of Stannius; hypocalcaemia; hypercalcaemia;
KW electrolyte disorder; osteoporosis; Paget's disease; treatment; ss.
XX
OS Homo sapiens.
XX

FH	Key	Location/Qualifiers
FT	CDS	16..759
FT		/*tag= a
FT		/product= prepro-stanniocalcin
FT	mat_peptide	115..757
FT		/*tag= b
FT		/product= mature stannicalcin
FT	misc_feature	16..114
FT		/*tag= c
FT		/note= "encodes prepro region"

XX
PN WO9524411-A1.
XX
PD 14-SEP-1995.
XX
PF 09-MAY-1994; 94WO-US05136.
XX
PR 08-MAR-1994; 94US-0208005.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Adams MD, Olsen H;
XX
DR WPI; 1995-328227/42.
DR P-PSDB; AAR84522.
XX
PT Human corpuscles of Stannius polypeptide(s) - used to treat
PT hypercalcaemia, hypocalcaemia and other electrolyte disorders
XX
PS Claim 1; Fig 1; 41pp; English.
XX
CC The cDNA encodes a stanniocalcin, a Corpuscles of Stannius polypeptide.
CC Stanniocalcin functions as a hypocalcaemic agent, and can be used for
CC the treatment of e.g. electrolyte disorders which lead to renal, bone
CC and heart diseases, hypertension, hypercalcaemia and disorders due to
CC elevated bone resorption, e.g. osteoporosis and Paget's disease.
XX
SQ Sequence 771 BP; 212 A; 214 C; 192 G; 153 T; 0 other;

Alignment Scores:
Pred. No.: 1.31e-139 Length: 771

Score:	1268.00		Matches:	247	
Percent Similarity:	100.00%		Conservative:	0	
Best Local Similarity:	100.00%		Mismatches:	0	
Query Match:	100.00%		Indels:	0	
DB:	16		Gaps:	0	

US-09-705-500A-3 (1-247) x AAT02438 (1-771)

```
Qy          1 MetLeuGlnAsnSerAlaValLeuLeuValLeuValIleSerAlaSerAlaThrHisGlu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         16 ATGCTCCAAAACTCAGCAGTGCTTCTGGTGCTGGTGATCAGTGCTTCTGCAACCCATGAG 75

Qy         21 AlaGluGlnAsnAspSerValSerProArgLysSerArgValAlaAlaGlnAsnSerAla 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         76 GCGGAGCAGAATGACTCTGTGAGCCCCAGGAAATCCCGAGTGGCGGCCCAAAACTCAGCT 135

Qy         41 GluValValArgCysLeuAsnSerAlaLeuGlnValGlyCysGlyAlaPheAlaCysLeu 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        136 GAAGTGGTTCGTTGCCTCAACAGTGCTCTACAGGTCGGCTGCGGGGCTTTTGCATGCCTG 195

Qy         61 GluAsnSerThrCysAspThrAspGlyMetTyrAspIleCysLysSerPheLeuTyrSer 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        196 GAAAACTCCACCTGTGACACAGATGGGATGTATGACATCTGTAAATCCTTCTTGTACAGC 255

Qy         81 AlaAlaLysPheAspThrGlnGlyLysAlaPheValLysGluSerLeuLysCysIleAla 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        256 GCTGCTAAATTTGACACTCAGGGAAAAGCATTCGTCAAAGAGAGCTTAAAATGCATCGCC 315

Qy        101 AsnGlyValThrSerLysValPheLeuAlaIleArgArgCysSerThrPheGlnArgMet 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        316 AACGGGGTCACCTCCAAGGTCTTCCTCGCCATTCGGAGGTGCTCCACTTTCCAAAGGATG 375

Qy        121 IleAlaGluValGlnGluGluCysTyrSerLysLeuAsnValCysSerIleAlaLysArg 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        376 ATTGCTGAGGTGCAGGAAGAGTGCTACAGCAAGCTGAATGTGTGCAGCATCGCCAAGCGG 435

Qy        141 AsnProGluAlaIleThrGluValValGlnLeuProAsnHisPheSerAsnArgTyrTyr 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        436 AACCCTGAAGCCATCACTGAGGTCGTCCAGCTGCCCAATCACTTCTCCAACAGATACTAT 495

Qy        161 AsnArgLeuValArgSerLeuLeuGluCysAspGluAspThrValSerThrIleArgAsp 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        496 AACAGACTTGTCCGAAGCCTGCTGGAATGTGATGAAGACACAGTCAGCACAATCAGAGAC 555

Qy        181 SerLeuMetGluLysIleGlyProAsnMetAlaSerLeuPheHisIleLeuGlnThrAsp 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        556 AGCCTGATGGAGAAAATTGGGCCTAACATGGCCAGCCTCTTCCACATCCTGCAGACAGAC 615

Qy        201 HisCysAlaGlnThrHisProArgAlaAspPheAsnArgArgArgThrAsnGluProGln 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        616 CACTGTGCCCAAACACACCCACGAGCTGACTTCAACAGGAGACGCACCAATGAGCCGCAG 675

Qy        221 LysLeuLysValLeuLeuArgAsnLeuArgGlyGluGluAspSerProSerHisIleLys 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        676 AAGCTGAAAGTCCTCCTCAGGAACCTCCGAGGTGAGGAGGACTCTCCCTCCCACATCAAA 735

Qy        241 ArgThrSerHisGluSerAla 247
              |||||||||||||||||||||
Db        736 CGCACATCCCATGAGAGTGCA 756
```

RESULT 5
AAZ39520
ID AAZ39520 standard; cDNA; 771 BP.
XX
AC AAZ39520;
XX
DT 11-FEB-2000 (first entry)
XX
DE Human corpuscles of stanius polypeptide encoding cDNA.
XX
KW Corpuscles of stanius polypeptide; calcium; inhibition; human; renal;
KW therapeutic; bone; heart disease; hypocalcemia; osteoperosis; ss.
XX

```
OS   Homo sapiens.
XX
PN   US5994301-A.
XX
PD   30-NOV-1999.
XX
PF   28-APR-1995;   95US-0431117.
XX
PR   08-MAR-1994;   94US-0208005.
XX
PA   (HUMA-) HUMAN GENOME SCI INC.
XX
PI   Adams MD,  Olsen HS;
XX
DR   WPI; 2000-038269/03.
DR   P-PSDB; AAY57166.
XX
PT   Human corpuscles of stanius polypeptides used to inhibit calcium uptake
PT   -
XX
PS   Disclosure; Fig 1A-B; 23pp; English.
XX
CC   This cDNA encodes a human corpuscles of stanius polypeptide, having a
CC   calcium uptake inhibitory activity. The cDNA is deposited under the
CC   accession number ATCC Deposit No. 75652. The polypeptide can be used in a
CC   method for the treatment of a patient having need to inhibit uptake of
CC   calcium. The method is also used for the therapeutic treatment of renal,
CC   bone, and heart diseases, and the antagonist (may be an antibody) may be
CC   used for treating hypocalcemia., and osteoperosis.
XX
SQ   Sequence 771 BP; 212 A; 214 C; 192 G; 153 T; 0 other;

Alignment Scores:
Pred. No.:              1.31e-139      Length:         771
Score:                  1268.00        Matches:        247
Percent Similarity:     100.00%        Conservative:   0
Best Local Similarity:  100.00%        Mismatches:     0
Query Match:            100.00%        Indels:         0
DB:                     21             Gaps:           0

US-09-705-500A-3 (1-247) x AAZ39520 (1-771)

Qy          1 MetLeuGlnAsnSerAlaValLeuLeuValLeuValIleSerAlaSerAlaThrHisGlu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         16 ATGCTCCAAAACTCAGCAGTGCTTCTGGTGCTGGTGATCAGTGCTTCTGCAACCCATGAG 75

Qy         21 AlaGluGlnAsnAspSerValSerProArgLysSerArgValAlaAlaGlnAsnSerAla 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         76 GCGGAGCAGAATGACTCTGTGAGCCCCAGGAAATCCCGAGTGGCGGCCCAAAACTCAGCT 135

Qy         41 GluValValArgCysLeuAsnSerAlaLeuGlnValGlyCysGlyAlaPheAlaCysLeu 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        136 GAAGTGGTTCGTTGCCTCAACAGTGCTCTACAGGTCGGCTGCGGGGCTTTTGCATGCCTG 195

Qy         61 GluAsnSerThrCysAspThrAspGlyMetTyrAspIleCysLysSerPheLeuTyrSer 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        196 GAAAACTCCACCTGTGACACAGATGGGATGTATGACATCTGTAAATCCTTCTTGTACAGC 255

Qy         81 AlaAlaLysPheAspThrGlnGlyLysAlaPheValLysGluSerLeuLysCysIleAla 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        256 GCTGCTAAATTTGACACTCAGGGAAAAGCATTCGTCAAAGAGAGCTTAAAATGCATCGCC 315

Qy        101 AsnGlyValThrSerLysValPheLeuAlaIleArgArgCysSerThrPheGlnArgMet 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        316 AACGGGGTCACCTCCAAGGTCTTCCTCGCCATTCGGAGGTGCTCCACTTTCCAAAGGATG 375

Qy        121 IleAlaGluValGlnGluGluCysTyrSerLysLeuAsnValCysSerIleAlaLysArg 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        376 ATTGCTGAGGTGCAGGAAGAGTGCTACAGCAAGCTGAATGTGTGCAGCATCGCCAAGCGG 435

Qy        141 AsnProGluAlaIleThrGluValValGlnLeuProAsnHisPheSerAsnArgTyrTyr 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        436 AACCCTGAAGCCATCACTGAGGTCGTCCAGCTGCCCAATCACTTCTCCAACAGATACTAT 495

Qy        161 AsnArgLeuValArgSerLeuLeuGluCysAspGluAspThrValSerThrIleArgAsp 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        496 AACAGACTTGTCCGAAGCCTGCTGGAATGTGATGAAGACACAGTCAGCACAATCAGAGAC 555

Qy        181 SerLeuMetGluLysIleGlyProAsnMetAlaSerLeuPheHisIleLeuGlnThrAsp 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        556 AGCCTGATGGAGAAAATTGGGCCTAACATGGCCAGCCTCTTCCACATCCTGCAGACAGAC 615

Qy        201 HisCysAlaGlnThrHisProArgAlaAspPheAsnArgArgArgThrAsnGluProGln 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        616 CACTGTGCCCAAACACACCCACGAGCTGACTTCAACAGGAGACGCACCAATGAGCCGCAG 675

Qy        221 LysLeuLysValLeuLeuArgAsnLeuArgGlyGluGluAspSerProSerHisIleLys 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        676 AAGCTGAAAGTCCTCCTCAGGAACCTCCGAGGTGAGGAGGACTCTCCCTCCCACATCAAA 735

Qy        241 ArgThrSerHisGluSerAla 247
              |||||||||||||||||||||
Db        736 CGCACATCCCATGAGAGTGCA 756

RESULT 6
AAF83297
ID   AAF83297 standard; cDNA; 1283 BP.
XX
AC   AAF83297;
XX
DT   09-JUL-2001  (first entry)
XX
DE   Human stanniocalcin (STC) protein encoding cDNA.
XX
KW   Stanniocalcin; STC; neuroprotective; antiinflammatory; antianemic;
KW   antirheumatic; antiarthritic; dermatological; antiallergic; human;
KW   nephrotropic; antithyroid; immunosuppressive; antidiabetic; vulnerary;
KW   antiasthmatic; hemostatic; antiarrhythmic; vasotropic; antipsoriatic;
KW   antitumor; anti HIV; antiparkinsonian; nootropic; cell proliferation;
KW   hemostatic; thrombolytic; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             45..788
FT                   /*tag=  a
FT                   /product= "stanniocalcin"
XX
PN   WO200130969-A2.
XX
PD   03-MAY-2001.
XX
PF   20-OCT-2000; 2000WO-US29432.
XX
PR   27-OCT-1999;   99US-0161740.
XX
PA   (HUMA-) HUMAN GENOME SCI INC.
PA   (UYHE-) UNIV HELSINKI.
XX
PI   Olsen HS,  Zhang K,  Lindsberg P,  Tatlisumak T,  Kaste M;
PI   Andersson LC;
XX
DR   WPI; 2001-308626/32.
DR   P-PSDB; AAB62473.
XX
PT   Novel composition useful for treating or protecting neural cells, for
PT   treating Addison's disease, organ rejection, hyperproliferative
PT   disorder, cancer, AIDS, multiple sclerosis, comprises stanniocalcin
PT   polypeptide  -
XX
PS   Example 2; Fig 1A-C; 253pp; English.
XX
CC   The invention relates to a human stanniocalcin (STC) polypeptide. A
CC   pharmaceutical composition comprising the STC is useful for treating a
CC   patient in need of increased levels of STC activity. STC and its
CC   modulators are useful for treating disorders or abnormalities of nervous
```

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CC   system, cerebrovascular diseases, dementia, encephalitis, central
CC   nervous system infections or neoplasms, demyelinating diseases,
CC   encephalomyelitis, spinal cord diseases, mental retardation such as
CC   Down's syndrome, Tay-Sachs disease, neuromuscular diseases such as
CC   muscular dystrophy, myasthenia gravis, deficiencies or disorders of
CC   immune system such as Addison's disease, hemolytic anemia, rheumatoid
CC   arthritis, dermatitis, glomerulonephritis, Goodpasture's Syndrome,
CC   Grave's disease, multiple sclerosis, autoimmune thyroiditis, systemic
CC   lupus erythematosus, insulin dependent diabetes mellitus, allergic
CC   reactions and conditions such as asthma, for treating and/or preventing
CC   organ rejection or graft-versus-host disease, hyperproliferative diseases
CC   such as purpura, Gaucher's disease, cardiovascular disorders such as
CC   arrhythmias, telangiectasia, vasculitis, and for treatment of disease or
CC   disorders with neovascularization. The composition can be used to treat
CC   hemangioma, psoriasis, angiofibroma, atherosclerotic plaques, delayed
CC   wound healing, granulations, Osler-Weber syndrome, solid tumors such as
CC   Kaposi's sarcoma, cancer, AIDS, neurodegenerative disorders such as
CC   Alzheimer's disease, Parkinson's disease, wound healing, and for treating
CC   or detecting infectious agents. The present sequence represents a cDNA
CC   encoding the human STC polypeptide.
XX
SQ   Sequence 1283 BP; 379 A; 327 C; 273 G; 301 T; 3 other;

Alignment Scores:
Pred. No.:              2.74e-139      Length:         1283
Score:                  1268.00        Matches:        247
Percent Similarity:     100.00%        Conservative:   0
Best Local Similarity:  100.00%        Mismatches:     0
Query Match:            100.00%        Indels:         0
DB:                     22             Gaps:           0

US-09-705-500A-3 (1-247) x AAF83297 (1-1283)

Qy          1 MetLeuGlnAsnSerAlaValLeuLeuValLeuValIleSerAlaSerAlaThrHisGlu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         45 ATGCTCCAAAACTCAGCAGTGCTTCTGGTGCTGGTGATCAGTGCTTCTGCAACCCATGAG 104

Qy         21 AlaGluGlnAsnAspSerValSerProArgLysSerArgValAlaAlaGlnAsnSerAla 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        105 GCGGAGCAGAATGACTCTGTGAGCCCCAGGAAATCCCGAGTGGCGGCCCAAAACTCAGCT 164

Qy         41 GluValValArgCysLeuAsnSerAlaLeuGlnValGlyCysGlyAlaPheAlaCysLeu 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        165 GAAGTGGTTCGTTGCCTCAACAGTGCTCTACAGGTCGGCTGCGGGGCTTTTGCATGCCTG 224

Qy         61 GluAsnSerThrCysAspThrAspGlyMetTyrAspIleCysLysSerPheLeuTyrSer 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        225 GAAAACTCCACCTGTGACACAGATGGGATGTATGACATCTGTAAATCCTTCTTGTACAGC 284

Qy         81 AlaAlaLysPheAspThrGlnGlyLysAlaPheValLysGluSerLeuLysCysIleAla 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        285 GCTGCTAAATTTGACACTCAGGGAAAAGCATTCGTCAAAGAGAGCTTAAAATGCATCGCC 344

Qy        101 AsnGlyValThrSerLysValPheLeuAlaIleArgArgCysSerThrPheGlnArgMet 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        345 AACGGGGTCACCTCCAAGGTCTTCCTCGCCATTCGGAGGTGCTCCACTTTCCAAAGGATG 404

Qy        121 IleAlaGluValGlnGluGluCysTyrSerLysLeuAsnValCysSerIleAlaLysArg 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        405 ATTGCTGAGGTGCAGGAAGAGTGCTACAGCAAGCTGAATGTGTGCAGCATCGCCAAGCGG 464

Qy        141 AsnProGluAlaIleThrGluValValGlnLeuProAsnHisPheSerAsnArgTyrTyr 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        465 AACCCTGAAGCCATCACTGAGGTCGTCCAGCTGCCCAATCACTTCTCCAACAGATACTAT 524

Qy        161 AsnArgLeuValArgSerLeuLeuGluCysAspGluAspThrValSerThrIleArgAsp 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        525 AACAGACTTGTCCGAAGCCTGCTGGAATGTGATGAAGACACAGTCAGCACAATCAGAGAC 584

Qy        181 SerLeuMetGluLysIleGlyProAsnMetAlaSerLeuPheHisIleLeuGlnThrAsp 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        585 AGCCTGATGGAGAAAATTGGGCCTAACATGGCCAGCCTCTTCCACATCCTGCAGACAGAC 644

Qy        201 HisCysAlaGlnThrHisProArgAlaAspPheAsnArgArgArgThrAsnGluProGln 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        645 CACTGTGCCCAAACACACCCACGAGCTGACTTCAACAGGAGACGCACCAATGAGCCGCAG 704

Qy        221 LysLeuLysValLeuLeuArgAsnLeuArgGlyGluGluAspSerProSerHisIleLys 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        705 AAGCTGAAAGTCCTCCTCAGGAACCTCCGAGGTGAGGAGGACTCTCCCTCCCACATCAAA 764

Qy        241 ArgThrSerHisGluSerAla 247
              |||||||||||||||||||||
Db        765 CGCACATCCCATGAGAGTGCA 785
```

RESULT 7
AAF83823
ID   AAF83823 standard; DNA; 3762 BP.
XX
AC   AAF83823;
XX
DT   06-AUG-2001 (first entry)
XX
DE   DNA encoding Lng108, a diagnostic marker for cancer.
XX
KW   Lng108; cancer; diagnostic marker; cytotoxic; immune response;
KW   imaging; ds.
XX
OS   Homo sapiens.
XX
FH   Key   Location/Qualifiers
FT   CDS   174..917
FT   /*tag= a
FT   /product= "Lng108"
XX
PN   WO200132209-A1.
XX
PD   10-MAY-2001.
XX
PF   03-NOV-2000; 2000WO-US30482.
XX
PR   04-NOV-1999;   99US-0163444.
XX
PA   (DIAD-) DIADEXUS INC.
XX
PI   Recipon H, Macina RA, Chen S, Sun Y;
XX
DR   WPI; 2001-316386/33.
DR   P-PSDB; AAB62690.
XX
PT   Novel assay for diagnosing and monitoring cancer, involves determining
PT   levels of Lng108 in cells, tissues or bodily fluids of the patient, and
PT   comparing with control -
XX
PS   Disclosure; Page 31-33; 36pp; English.
XX
CC   The invention relates to diagnosing the presence of cancer or diagnosing
CC   metastases of cancer in a patient that involves determining levels of
CC   Lng108 in a sample of cells, tissues or bodily fluids in a patient, and
CC   comparing the determined levels with levels of Lng108 a normal human
CC   control. The method is useful for diagnosing the presence of cancer,
CC   diagnosing metastases of cancer, staging cancer, monitoring cancer, and
CC   monitoring a change in stage of the cancer, in a patient. A therapeutic
CC   agent which is an antibody labeled with paramagnetic ions or a
CC   radioisotope, and conjugated with a cytotoxic agent is useful for imaging
CC   cancer in a patient. A molecule which downregulates the expression or
CC   activity of Lng108, is useful for treating cancer in a patient. Lng108
CC   protein is useful for inducing an immune response against a target cell
CC   expressing Lng108. The present sequence represents a DNA encoding the
CC   Lng108 polypeptide.
XX
SQ   Sequence 3762 BP; 1063 A; 865 C; 725 G; 1038 T; 71 other;

Alignment Scores:
Pred. No.:   1.31e-138   Length: 3762
Score: 1268.00   Matches: 247

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Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
DB:                     22             Gaps:          0

US-09-705-500A-3 (1-247) x AAF83823 (1-3762)

Qy          1 MetLeuGlnAsnSerAlaValLeuLeuValLeuValIleSerAlaSerAlaThrHisGlu 20
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        174 ATGCTCCAAAACTCAGCAGTGCTTCTGGTGCTGGTGATCAGTGCTTCTGCAACCCATGAG 233

Qy         21 AlaGluGlnAsnAspSerValSerProArgLysSerArgValAlaAlaGlnAsnSerAla 40
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        234 GCGGAGCAGAATGACTCTGTGAGCCCCAGGAAATCCCGAGTGGCGGCTCAAAACTCAGCT 293

Qy         41 GluValValArgCysLeuAsnSerAlaLeuGlnValGlyCysGlyAlaPheAlaCysLeu 60
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        294 GAAGTGGTTCGTTGCCTCAACAGTGCTCTACAGGTCGGCTGCGGGGCTTTTGCATGCCTG 353

Qy         61 GluAsnSerThrCysAspThrAspGlyMetTyrAspIleCysLysSerPheLeuTyrSer 80
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        354 GAAAACTCCACCTGTGACACAGATGGGATGTATGACATCTGTAAATCCTTCTTGTACAGC 413

Qy         81 AlaAlaLysPheAspThrGlnGlyLysAlaPheValLysGluSerLeuLysCysIleAla 100
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        414 GCTGCTAAATTTGACACTCAGGGAAAAGCATTCGTCAAAGAGAGCTTAAAATGCATCGCC 473

Qy        101 AsnGlyValThrSerLysValPheLeuAlaIleArgArgCysSerThrPheGlnArgMet 120
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        474 AACGGGGTCACCTCCAAGGTCTTCCTCGCCATTCGGAGGTGCTCCACTTTCCAAAGGATG 533

Qy        121 IleAlaGluValGlnGluGluCysTyrSerLysLeuAsnValCysSerIleAlaLysArg 140
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        534 ATTGCTGAGGTGCAGGAAGAGTGCTACAGCAAGCTGAATGTGTGCAGCATCGCCAAGCGG 593

Qy        141 AsnProGluAlaIleThrGluValValGlnLeuProAsnHisPheSerAsnArgTyrTyr 160
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        594 AACCCTGAAGCCATCACTGAGGTCGTCCAGCTGCCCAATCACTTCTCCAACAGATACTAT 653

Qy        161 AsnArgLeuValArgSerLeuLeuGluCysAspGluAspThrValSerThrIleArgAsp 180
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        654 AACAGACTTGTCCGAAGCCTGCTGGAATGTGATGAAGACACAGTCAGCACAATCAGAGAC 713

Qy        181 SerLeuMetGluLysIleGlyProAsnMetAlaSerLeuPheHisIleLeuGlnThrAsp 200
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        714 AGCCTGATGGAGAAAATTGGGCCTAACATGGCCAGCCTCTTCCACATCCTGCAGACAGAC 773

Qy        201 HisCysAlaGlnThrHisProArgAlaAspPheAsnArgArgArgThrAsnGluProGln 220
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        774 CACTGTGCCCAAACACACCCACGAGCTGACTTCAACAGGAGACGCACCAATGAGCCGCAG 833

Qy        221 LysLeuLysValLeuLeuArgAsnLeuArgGlyGluGluAspSerProSerHisIleLys 240
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        834 AAGCTGAAAGTCCTCCTCAGGAACCTCCGAGGTGAGGAGGACTCTCCCTCCCACATCAAA 893

Qy        241 ArgThrSerHisGluSerAla 247
              |||||||||||||||||||||
Db        894 CGCACATCCCATGAGAGTGCA 914

RESULT 8
AAF16051
ID   AAF16051 standard; cDNA; 2572 BP.
XX
AC   AAF16051;
XX
DT   13-MAR-2001  (first entry)
XX
DE   Human prostate cancer antigen nucleotide sequence SEQ ID NO:486.
XX
KW   Human; prostate cancer; prostate cancer antigen; detection; diagnosis;
KW   neuroprotective; cytostatic; cardioactive; immunomodulatory; muscular;
KW   vulnerary; gastrointestinal; nephrotropic; antiinfective; gynaecological;
KW   antibacterial; gene therapy; neural; immune; reproductive; renal;
KW   gastrointestinal; pulmonary; cardiovascular; proliferative disorder;
KW   wound; infectious disease; ss.
XX
OS   Homo sapiens.
XX
PN   WO200055174-A1.
XX
PD   21-SEP-2000.
XX
PF   08-MAR-2000; 2000WO-US05988.
XX
PR   12-MAR-1999;   99US-0124270.
XX
PA   (HUMA-) HUMAN GENOME SCI INC.
PA   (ROSE/) ROSEN C A.
XX
PI   Rosen CA,  Ruben SM;
XX
DR   WPI; 2000-587513/55.
DR   P-PSDB; AAB56848.
XX
PT   Prostate cancer associated gene sequences, referred to as prostate
PT   cancer antigens, useful for treatment, prevention, and diagnosis of
PT   disorders such as prostate cancer -
XX
PS   Claim 1; Page 956-957; 2338pp; English.
XX
CC   AAF15566 to AAF16505 encode the human prostate cancer associated
CC   proteins, called prostate cancer antigens, given in AAB56363 to AAB57302.
CC   The prostate cancer antigens can have neuroprotective, cytostatic,
CC   cardioactive, immunomodulatory, muscular, vulnerary, gastrointestinal,
CC   nephrotropic, antiinfective, gynaecological and antibacterial activities,
CC   and can be used in gene therapy. The prostate cancer antigen
CC   polynucleotides may be used for detection of prostate cancer, chromosome
CC   identification, as chromosome markers, and for numerous other diagnostic
CC   or research purposes. The prostate cancer antigens may be used to treat
CC   disorders such as neural, immune, muscular, reproductive,
CC   gastrointestinal, pulmonary, cardiovascular, renal, and proliferative
CC   disorders, wounds, and infectious diseases. AAF16506 to AAF16514 to
CC   AAB57303 represent sequences used in the exemplification of the present
CC   invention.
XX
SQ   Sequence 2572 BP; 746 A; 636 C; 539 G; 646 T; 5 other;

Alignment Scores:
Pred. No.:              9.93e-137      Length:        2572
Score:                  1250.00        Matches:       246
Percent Similarity:     99.19%         Conservative:  0
Best Local Similarity:  99.19%         Mismatches:    1
Query Match:            98.58%         Indels:        1
DB:                     21             Gaps:          0

US-09-705-500A-3 (1-247) x AAF16051 (1-2572)

Qy          1 MetLeuGlnAsnSerAlaValLeuLeuValLeuValIleSerAlaSerAlaThrHisGlu 20
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        265 ATGCTCCAAAACTCAGCAGTGCTTCTGGTGCTGGTGATCAGTGCTTCTGCAACCCATGAG 324

Qy         21 AlaGluGlnAsnAspSerValSerProArgLysSerArgValAlaAlaGlnAsnSerAla 40
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        325 GCGGAGCAGAATGACTCTGTGAGCCCCAGGAAATCCCGAGTGGCGGCTCAAAACTCAGCT 384

Qy         41 GluValValArgCysLeuAsnSerAlaLeuGlnValGlyCysGlyAlaPheAlaCysLeu 60
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        385 GAAGTGGTTCGTTGCCTCAACAGTGCTCTACAGGTCGGCTGCGGGGCTTTTGCATGCCTG 444

Qy         61 GluAsnSerThrCysAspThrAspGlyMetTyrAspIleCysLysSerPheLeuTyrSer 80
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        445 GAAAACTCCACCTGTGACACAGATGGGATGTATGACATCTGTAAATCCTTCTTGTACAGC 504

Qy         81 AlaAlaLysPheAspThrGlnGlyLysAlaPheValLysGluSerLeuLysCysIleAla 100
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        505 GCTGCTAAATTTGACACTCAGGGAAAAGCATTCGTCAAAGAGAGCTTAAAATGCATCGCC 564
```

```
Qy        101 AsnGlyValThrSerLysValPheLeuAlaIleArgArgCysSerThrPheGlnArgMet 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        565 AACGGGGTCACCTCCAAGGTCTTCCTCGCCATTCGGAGGTGCTCCACTTTCCAAAGGATG 624

Qy        121 IleAlaGluValGlnGluGluCysTyrSerLysLeuAsnValCysSerIleAlaLysArg 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        625 ATTGCTGAGGTGCAGGAAGAGTGCTACAGCAAGCTGAATGTGTGCAGCATCGCCAAGCGG 684

Qy        141 AsnProGluAlaIleThrGluValValGlnLeuProAsnHisPheSerAsnArgTyrTyr 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        685 AACCCTGAAGCCATCACTGAGGTCGTCCAGCTGCCCAATCACTTCTCCAACAGATACTAT 744

Qy        161 AsnArgLeuValArgSerLeuLeuGluCysAspGluAspThrValSerThrIleArgAsp 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        745 AACAGACTTGTCCGAAGCCTGCTGGAATGTGATGAAGACACAGTCAGCACAATCAGAGAC 804

Qy        181 SerLeuMetGlu-LysIleGlyProAsnMetAlaSerLeuPheHisIleLeuGlnThrAs 200
              |||||||||||| |||   ||||||||||||||||||||||||||||||||||||||||
Db        805 AGCCTGATGGAGRAAATTNGGGCCTAACATGGCCAGCCTCTTCCACATCCTGCAGACAGA 864

Qy        200 pHisCysAlaGlnThrHisProArgAlaAspPheAsnArgArgArgThrAsnGluProGl 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        865 CCACTGTGCCCAAACACACCCACGAGCTGACTTCAACAGGAGACGCACCAATGAGCCGCA 924

Qy        220 nLysLeuLysValLeuLeuArgAsnLeuArgGlyGluGluAspSerProSerHisIleLy 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        925 GAAGCTGAAAGTCCTCCTCAGGAACCTCCGAGGTGAGGAGGACTCTCCCTCCCACATCAA 984

Qy        240 sArgThrSerHisGluSerAla 247
              |||||||||||||||||||||
Db        985 ACGCACATCCCATGAGAGTGCA 1006
```

RESULT 9
AAH55624
ID AAH55624 standard; DNA; 585 BP.
XX
AC AAH55624;
XX
DT 04-SEP-2001 (first entry)
XX
DE Human breast tumour protein clone 48987 DNA sequence.
XX
KW Cytostatic; vaccine; human; breast tumour protein; breast cancer;
KW gene therapy; ds.
XX
OS Homo sapiens.
XX
PN WO200140269-A2.
XX
PD 07-JUN-2001.
XX
PF 29-NOV-2000; 2000WO-US32520.
XX
PR 30-NOV-1999; 99US-0451651.
PR 22-FEB-2000; 2000US-0510662.
PR 10-MAR-2000; 2000US-0523586.
PR 07-APR-2000; 2000US-0545068.
PR 15-MAY-2000; 2000US-0571025.
XX
PA (CORI-) CORIXA CORP.
XX
PI Dillon DC, Day CH, Jiang Y, Houghton RL, Mitcham JL, Wang A;
XX
DR WPI; 2001-356154/37.
XX
PT Breast tumor polypeptides and the nucleic acids that encode them,
PT useful for the prevention, diagnosis and treatment of breast cancer -
XX
PS Claim 24; Page 168; 221pp; English.
XX
CC The present sequence is a human breast tumour protein coding sequence.
CC This sequence may be used in the prevention, diagnosis and treatment of
CC diseases associated with inappropriate expression of the breast tumour
CC protein e.g. breast cancer. For example, this sequence may be used to
CC treat disorders associated with decreased expression by rectifying
CC mutations or deletions in a patient's genome that affect the activity of
CC breast tumour protein by expressing inactive proteins or to supplement
CC the patients own production of the breast tumour protein. Additionally,
CC the present sequence may be used to produce the breast tumour protein, by
CC inserting the nucleic acids into a host cell and culturing the cell to
CC express the protein. The present sequence and its complementary sequences
CC may also be used as DNA probes in diagnostic assays to detect and
CC quantitate the presence of similar nucleic acids in samples, and
CC therefore which patients may be in need of restorative therapy.
XX
SQ Sequence 585 BP; 171 A; 163 C; 136 G; 110 T; 5 other;

Alignment Scores:

Pred. No.:	7.64e-92	Length:	585
Score:	861.00	Matches:	166
Percent Similarity:	98.22%	Conservative:	0
Best Local Similarity:	98.22%	Mismatches:	3
Query Match:	67.90%	Indels:	0
DB:	22	Gaps:	0

US-09-705-500A-3 (1-247) x AAH55624 (1-585)

```
Qy         79 TyrSerAlaAlaLysPheAspThrGlnGlyLysAlaPheValLysGluSerLeuLysCys 98
              |||       |||||||||||||||   ||||||||||||||||||||||||||||||||
Db          6 TACANCACTGCTAAATTTGACACTNANGGAAAAGCATTCGTCAAAGAGAGCTTAAAATGC 65

Qy         99 IleAlaAsnGlyValThrSerLysValPheLeuAlaIleArgArgCysSerThrPheGln 118
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         66 ATCGCCAACGGGGTCACCTCCAAGGTCTTCCTCGCCATTCGGAGGTGCTCCACTTTCCAA 125

Qy        119 ArgMetIleAlaGluValGlnGluGluCysTyrSerLysLeuAsnValCysSerIleAla 138
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        126 AGGATGATTGCTGAGGTGCAGGAAGAGTGCTACAGCAAGCTGAATGTGTGCAGCATCGCC 185

Qy        139 LysArgAsnProGluAlaIleThrGluValValGlnLeuProAsnHisPheSerAsnArg 158
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        186 AAGCGGAACCCTGAAGCCATCACTGAGGTCGTCCAGCTGCCCAATCACTTCTCCAACAGA 245

Qy        159 TyrTyrAsnArgLeuValArgSerLeuLeuGluCysAspGluAspThrValSerThrIle 178
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        246 TACTATAACAGACTTGTCCGAAGCCTGCTGGAATGTGATGAAGACACAGTCAGCACAATC 305

Qy        179 ArgAspSerLeuMetGluLysIleGlyProAsnMetAlaSerLeuPheHisIleLeuGln 198
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        306 AGAGACAGCCTGATGGAGAAAATTGGGCCTAACATGGCCAGCCTCTTCCACATCCTGCAG 365

Qy        199 ThrAspHisCysAlaGlnThrHisProArgAlaAspPheAsnArgArgArgThrAsnGlu 218
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        366 ACAGACCACTGTGCCCAAACACACCCACGAGCTGACTTCAACAGGAGACGCACCAATGAG 425

Qy        219 ProGlnLysLeuLysValLeuLeuArgAsnLeuArgGlyGluGluAspSerProSerHis 238
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        426 CCGCAGAAGCTGAAAGTCCTCCTCAGGAACCTCCGAGGTGAGGAGGACTCTCCCTCCCAC 485

Qy        239 IleLysArgThrSerHisGluSerAla 247
              ||||||||||||||||||||||||||
Db        486 ATCAAACGCACATCCCATGAGAGTGCA 512
```

RESULT 10
AAN80655
ID AAN80655 standard; cDNA; 2191 BP.
XX
AC AAN80655;
XX
DT 30-NOV-1990 (first entry)
XX
DE Sequence encoding Corpuscles of Stannius CS protein precursor.
XX
KW Corpuscles of Stannius; CS protein; cardiovascular disease;
KW oedema; heart failure; high blood pressure; ss.

```
XX
OS   Anguilla australis.
XX
FH   Key             Location/Qualifiers
FT   CDS             122..914
FT                   /*tag=  a
FT                   /label=eel CS protein precursor
XX
PN   WO8803949-A.
XX
PD   02-JUN-1988.
XX
PF   19-NOV-1987;   87WO-AU00389.
XX
PR   22-MAY-1987;   87AU-0002086.
PR   22-MAY-1987;   87AU-0009107.
XX
PA   (FLOR-) FLOREY INST EXPER.
XX
PI   Butkus A,  Coghlan JP,  Roche PJ;
XX
DR   WPI; 1988-161619/23.
DR   P-PSDB; AAP82968.
XX
PT   CS protein of corpuscles of stannius - used for treating cardiovascular
PT   disease, renal disease and electrolyte disorders.
XX
PS   Disclosure; ; p; English.
XX
CC   This sequence includes the gene encoding the prepro-CS protein.
CC   Cleavage of the signal or pro-hormone fragment (amino acids -17
CC   to 1) results in the pro-CS protein which can be processed to
CC   yield the mature form.  Recombinant DNA methods are utilised in
CC   the prodn. of the CS protein.  The protein is useful as e.g. a
CC   therapeutic agent for the treatment of cardiovascular disease
CC   and oedema.  See also N8064.
XX
SQ   Sequence 2191 BP; 591 A; 516 C; 482 G; 602 T; 0 other;

Alignment Scores:
Pred. No.:              1.65e-67        Length:         2191
Score:                  661.50          Matches:        123
Percent Similarity:     80.79%          Conservative:   41
Best Local Similarity:  60.59%          Mismatches:     37
Query Match:            52.17%          Indels:         2
DB:                     9               Gaps:           1

US-09-705-500A-3 (1-247) x AAN80655 (1-2191)

Qy          1 MetLeuGlnAsnSerAlaValLeuLeuValLeuValIleSerAlaSerAlaThrHisGlu 20
              ||||||:::   |||   ::::::|||  ||||||:::     :::|||   :::|||
Db        122 ATGCTGCGAATGAGTGGGCTAATCCTCACGCTTGTGCTG---GTAACTGCTGCCTACGAG 178

Qy         21 AlaGluGlnAsnAspSerValSerProArgLysSerArgValAlaAlaGlnAsnSerAla 40
                ::::::::::::   :::|||||||||   :::|||   :::|||   :::   :::
Db        179 CAGGATGAGAGCGAGCCCTTATCTCCAAGGACAGCCCGCTTCTCCGCCAGCAGCCCATCT 238

Qy         41 GluValValArgCysLeuAsnSerAlaLeuGlnValGlyCysGlyAlaPheAlaCysLeu 60
              :::|||   ||||||||||   ||||||||||||||||||   ||||||||||||||||
Db        239 GATGTTGCACGCTGTCTGAACGGGGCCCTGCAGGTGGGCTGCAGTGCATTTGCCTGCCTT 298

Qy         61 GluAsnSerThrCysAspThrAspGlyMetTyrAspIleCysLysSerPheLeuTyrSer 80
              :::|||||||||||:::|||||||||||||:::::|||||:::|||||||||:::
Db        299 GACAACTCCACCTGCAACACCGACGGCATGCATGAAATCTGCAGGTCCTTCCTCCACGGT 358

Qy         81 AlaAlaLysPheAspThrGlnGlyLysAlaPheValLysGluSerLeuLysCysIleAla 100
              ||||||||||||||||||||||||   ||||||||||||||||||||||||||||||
Db        359 GCTGCCAAATTTGACACACAGGGCAAGACTTTTGTGAAGGAGAGCCTGAAGTGCATAGCC 418

Qy        101 AsnGlyValThrSerLysValPheLeuAlaIleArgArgCysSerThrPheGlnArgMet 120
              ||||||:::||||||||||||||||||   ||||||||||||||:::||||||:::|||
Db        419 AATGGCATCACCTCCAAAGTGTTCCTTACCATCCGCCGCTGCTCATCCTTCCAGAAGATG 478

Qy        121 IleAlaGluValGlnGluGluCysTyrSerLysLeuAsnValCysSerIleAlaLysArg 140
              |||:::||||||||||||||||||||||||||||||:::::|||||:::|||:::
Db        479 ATCTCAGAGGTTCAGGAGGAGTGCTATAGCAAACTAGACCTCTGCTCTGTTGCCCAGAGC 538

Qy        141 AsnProGluAlaIleThrGluValValGlnLeuProAsnHisPheSerAsnArgTyrTyr 160
              ||||||||||||:::   ||||||   |||:::|||:::   |||   ||||||||||||
Db        539 AACCCAGAGGCCATGGGGGAGGTGGCCCAGGTGCCCAGCCAGTTTCCCAACAGGTACTAC 598

Qy        161 AsnArgLeuValArgSer-LeuLeuGluCysAspGluAspThrValSerThrIleArgAs 180
              :::   |||:::::::||| ||||||   ||||||||||||||||||      :::|||
Db        599 AGCACCCTGCTGCAGAGTACTTCTGACGTGTGATGAGGACACCGTGGAGCAGGTGAGGGC 658

Qy        180 pSerLeuMetGluLysIleGlyProAsnMetAlaSerLeuPheHisIleLeuGlnThrAs 200
                    :::  ::::::  |||  |||      ||||||  :::|||||||||
Db        659 CGGGTGGGTGTCCCGCCTGGAGCCAGAGATGGGGGTGCTCTTCCAGCTCCTCCAGACCAA 718

Qy        200 pHisCys 202
                  |||
Db        719 GGCCTGC 725

RESULT 11
AAH55616
ID   AAH55616 standard; DNA; 420 BP.
XX
AC   AAH55616;
XX
DT   04-SEP-2001  (first entry)
XX
DE   Human breast tumour protein clone 47593 DNA sequence.
XX
KW   Cytostatic; vaccine; human; breast tumour protein; breast cancer;
KW   gene therapy; ds.
XX
OS   Homo sapiens.
XX
PN   WO200140269-A2.
XX
PD   07-JUN-2001.
XX
PF   29-NOV-2000; 2000WO-US32520.
XX
PR   30-NOV-1999;   99US-0451651.
PR   22-FEB-2000; 2000US-0510662.
PR   10-MAR-2000; 2000US-0523586.
PR   07-APR-2000; 2000US-0545068.
PR   15-MAY-2000; 2000US-0571025.
XX
PA   (CORI-) CORIXA CORP.
XX
PI   Dillon DC,  Day CH,  Jiang Y,  Houghton RL,  Mitcham JL,  Wang A;
XX
DR   WPI; 2001-356154/37.
XX
PT   Breast tumor polypeptides and the nucleic acids that encode them,
PT   useful for the prevention, diagnosis and treatment of breast cancer -
XX
PS   Claim 24; Page 165; 221pp; English.
XX
CC   The present sequence is a human breast tumour protein coding sequence.
CC   This sequence may be used in the prevention, diagnosis and treatment of
CC   diseases associated with inappropriate expression of the breast tumour
CC   protein e.g. breast cancer. For example, this sequence may be used to
CC   treat disorders associated with decreased expression by rectifying
CC   mutations or deletions in a patient's genome that affect the activity of
CC   breast tumour protein by expressing inactive proteins or to supplement
CC   the patients own production of the breast tumour protein. Additionally,
CC   the present sequence may be used to produce the breast tumour protein, by
CC   inserting the nucleic acids into a host cell and culturing the cell to
CC   express the protein. The present sequence and its complementary sequences
CC   may also be used as DNA probes in diagnostic assays to detect and
CC   quantitate the presence of similar nucleic acids in samples, and
CC   therefore which patients may be in need of restorative therapy.
XX
```

```
SQ   Sequence 420 BP; 118 A; 115 C; 101 G; 65 T; 21 other;

Alignment Scores:
Pred. No.:              1.8e-50       Length:         420
Score:                  508.00        Matches:        116
Percent Similarity:     82.27%        Conservative:   0
Best Local Similarity:  82.27%        Mismatches:     19
Query Match:            40.06%        Indels:         6
DB:                     22            Gaps:           0

US-09-705-500A-3 (1-247) x AAH55616 (1-420)

Qy         85 AspThrGlnGlyLysAlaPheValLysGluSerLeuLysCysIleAlaAsnGlyValThr 104
              ||||||||||||||||||      |||   ||||||||||||||||||||||||||||
Db          1 GACACTCAGGGAAAAGCATNNGNCAAANAGAGCTTAAAATGCATCGCCAACGGGGTCACC 60

Qy        105 SerLysValPheLeuAlaIleArgArgCysSerThrPheGlnArgMetIleAlaGluVal 124
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TCCAAGGTCTTCCTCGCCATTCGGAGGTGCTCCACTTTCCAAAGGATGATTGCTGAGGTG 120

Qy        125 GlnGluGluCysTyrSerLysLeuAsnValCysSerIleAlaLysArgAsnProGluAla 144
              ||||||||||||||||||||||||||||||      ||||||||||||||||||||||||
Db        121 CAGGAAGAGTGCTACAGCAAGCTGAATGTGCGCANCATCGCCAAGCGGAACCCNGAAGCC 180

Qy        145 IleThrGluValValGlnLeuProAsnHisPheSerAsnArgTyrTyrAsnArgLeuVal 164
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ATCACTGAGGTCGTGCAGCTGCCCAATCACTTCTCCAACANATACTATAACAGACTTGNN 240

Qy        165 ArgSerLeuLeuGluCysAspGluAspThr-ValSerThrIleArg-AspSerLeuMetG 184
              ||||||||||||||   ||||||  |||    ||||||||||| ||||||||||||
Db        241 CGAAGCCTGCTGGAATGNGATGAANACACAGGGCAGCACAATCAGGAGACAGCCTGATGG 300

Qy        184 luLysIleGlyProAsnMetAla-SerLeuPheHisIleLeu--GlnThrAspHisCysA 203
                 |||   ||||||   ||||||    ||||||||||||||     ||||||||||||
Db        301 ANAAAANTGGGCCTANCATGGCCAGGCCTCTTCCACATCCTNGCANGACAGACCACTGTG 360

Qy        203 laGlnThrHisProArg-AlaAspPheAsnArgArgArgThrAsnGluPro 219
              |||||||||||||    ||||||      ||||||||||||   ||||||
Db        361 CCCAAACACACCCNCTGAGCTGACTTNNACAGGAGACGCACNAAGGAGCCC 411

RESULT 12
ABA51055/c
ID   ABA51055 standard; DNA; 219 BP.
XX
AC   ABA51055;
XX
DT   01-FEB-2002  (first entry)
XX
DE   Human breast cell single exon nucleic acid probe #9750.
XX
KW   Human; microarray; single exon probe; gene expression; breast;
KW   disease; cancer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200157271-A2.
XX
PD   09-AUG-2001.
XX
PF   30-JAN-2001; 2001WO-US00662.
XX
PR   04-FEB-2000; 2000US-0180312.
PR   26-MAY-2000; 2000US-0207456.
PR   30-JUN-2000; 2000US-0608408.
PR   03-AUG-2000; 2000US-0632366.
PR   21-SEP-2000; 2000US-0234687.
PR   27-SEP-2000; 2000US-0236359.
PR   04-OCT-2000; 2000GB-0024263.
XX
PA   (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI   Penn SG,  Hanzel DK,  Chen W,  Rank DR;
XX
DR   WPI; 2001-496933/54.
XX
PT   New spatially-addressable set of single exon nucleic acid probes,
PT   useful for measuring gene expression in sample derived from human
PT   breast, comprises number of single exon nucleic acid probes  -
XX
PS   Claim 4; SEQ ID NO 9750; 327pp + sequence listing; English.
XX
CC   The invention relates to a spatially-addressable set of single exon
CC   nucleic acid probes for measuring gene expression in a sample derived
CC   from human breast and BT 474 cells. The method involves contacting
CC   the probes with a collection of detectably labelled nucleic acids
CC   derived from mRNA of human breast, and then measuring the label
CC   bound to each probe of the microarray. The probes are useful for
CC   verifying the expression of regions of genomic DNA predicted to
CC   encode proteins. They are useful for gene discovery, and for
CC   determining predisposition and/or prognosing breast disease. Gene
CC   expression analysis is useful for assessing the toxicity of chemical
CC   agents on cells. The microarray of this invention presents a far greater
CC   diversity of probes for measuring gene expression, with far less bias
CC   than expressed sequence tag microarrays. The method is suitable for
CC   rapid production of functional information from genomic sequence. The
CC   present sequence is a single exon nucleic acid probe of the invention.
CC   Note: The sequence data for this patent did not form part of the
CC   printed specification, but was obtained in electronic format directly
CC   from WIPO at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence 219 BP; 43 A; 55 C; 60 G; 61 T; 0 other;

Alignment Scores:
Pred. No.:              1.25e-34      Length:         219
Score:                  370.00        Matches:        72
Percent Similarity:     100.00%       Conservative:   0
Best Local Similarity:  100.00%       Mismatches:     0
Query Match:            29.18%        Indels:         0
DB:                     22            Gaps:           0

US-09-705-500A-3 (1-247) x ABA51055 (1-219)

Qy         88 GlyLysAlaPheValLysGluSerLeuLysCysIleAlaAsnGlyValThrSerLysVal 107
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        219 GGAAAAGCATTCGTCAAAGAGAGCTTAAAATGCATCGCCAACGGGGTCACCTCCAAGGTC 160

Qy        108 PheLeuAlaIleArgArgCysSerThrPheGlnArgMetIleAlaGluValGlnGluGlu 127
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        159 TTCCTCGCCATTCGGAGGTGCTCCACTTTCCAAAGGATGATTGCTGAGGTGCAGGAAGAG 100

Qy        128 CysTyrSerLysLeuAsnValCysSerIleAlaLysArgAsnProGluAlaIleThrGlu 147
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         99 TGCTACAGCAAGCTGAATGTGTGCAGCATCGCCAAGCGGAACCCTGAAGCCATCACTGAG 40

Qy        148 ValValGlnLeuProAsnHisPheSerAsnArgTyr 159
              |||||||||||||||||||||||||||||||||||
Db         39 GTCGTCCAGCTGCCCAATCACTTCTCCAACAGGTAC 4

RESULT 13
ABA69045/c
ID   ABA69045 standard; DNA; 219 BP.
XX
AC   ABA69045;
XX
DT   01-FEB-2002  (first entry)
XX
DE   Human foetal liver single exon nucleic acid probe #17350.
XX
KW   Human; foetal liver; gene expression; single exon nucleic acid probe; ss.
XX
OS   Homo sapiens.
XX
PN   WO200157277-A2.
XX
PD   09-AUG-2001.
XX
```

PF 30-JAN-2001; 2001WO-US00669.
XX
PR 04-FEB-2000; 2000US-0180312.
PR 26-MAY-2000; 2000US-0207456.
PR 30-JUN-2000; 2000US-0608408.
PR 03-AUG-2000; 2000US-0632366.
PR 21-SEP-2000; 2000US-0234687.
PR 27-SEP-2000; 2000US-0236359.
PR 04-OCT-2000; 2000GB-0024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
DR WPI; 2001-483447/52.
XX
PT Human genome-derived single exon nucleic acid probes useful for
PT analyzing gene expression in human fetal liver -
XX
PS Claim 4; SEQ ID NO 17350; 639pp + sequence listing; English.
XX
CC The invention relates to a single exon nucleic acid probe for
CC measuring human gene expression in a sample derived from human foetal
CC liver. The single exon nucleic acid probes may be used for predicting,
CC measuring and displaying gene expression in samples derived from human
CC fetal liver. The present sequence is a single exon nucleic acid
CC probe of the invention.
CC Note: The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 219 BP; 43 A; 55 C; 60 G; 61 T; 0 other;

Alignment Scores:

Pred. No.:	1.25e-34	Length:	219
Score:	370.00	Matches:	72
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	29.18%	Indels:	0
DB:	22	Gaps:	0

US-09-705-500A-3 (1-247) x ABA69045 (1-219)

```
Qy         88 GlyLysAlaPheValLysGluSerLeuLysCysIleAlaAsnGlyValThrSerLysVal 107
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        219 GGAAAAGCATTCGTCAAAGAGAGCTTAAAATGCATCGCCAACGGGGTCACCTCCAAGGTC 160

Qy        108 PheLeuAlaIleArgArgCysSerThrPheGlnArgMetIleAlaGluValGlnGluGlu 127
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        159 TTCCTCGCCATTCGGAGGTGCTCCACTTTCCAAAGGATGATTGCTGAGGTGCAGGAAGAG 100

Qy        128 CysTyrSerLysLeuAsnValCysSerIleAlaLysArgAsnProGluAlaIleThrGlu 147
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         99 TGCTACAGCAAGCTGAATGTGTGCAGCATCGCCAAGCGGAACCCTGAAGCCATCACTGAG 40

Qy        148 ValValGlnLeuProAsnHisPheSerAsnArgTyr 159
              |||||||||||||||||||||||||||||||||||
Db         39 GTCGTCCAGCTGCCCAATCACTTCTCCAACAGGTAC 4
```

RESULT 14
ABA35989/c
ID ABA35989 standard; DNA; 219 BP.
XX
AC ABA35989;
XX
DT 23-JAN-2002 (first entry)
XX
DE Probe #14455 for gene expression analysis in human heart cell sample.
XX
KW Human; gene expression; heart; microarray; vascular system; probe;
KW cardiovascular disease; hypertension; cardiac arrhythmia;
KW congenital heart disease; ss.
XX
OS Homo sapiens.
XX
PN WO200157274-A2.
XX
PD 09-AUG-2001.
XX
PF 30-JAN-2001; 2001WO-US00666.
XX
PR 04-FEB-2000; 2000US-0180312.
PR 26-MAY-2000; 2000US-0207456.
PR 30-JUN-2000; 2000US-0608408.
PR 03-AUG-2000; 2000US-0632366.
PR 21-SEP-2000; 2000US-0234687.
PR 27-SEP-2000; 2000US-0236359.
PR 04-OCT-2000; 2000GB-0024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
DR WPI; 2001-488899/53.
XX
PT Single exon nucleic acid probes for analyzing gene expression in human
PT hearts -
XX
PS Claim 4; SEQ ID No 14455; 530pp; English.
XX
CC The present invention relates to single exon nucleic acid probes for
CC measuring human gene expression in a sample derived from human heart. The
CC present sequence is one such probe. The probes may be used for
CC predicting, measuring and displaying gene expression in samples derived
CC from the human heart via microarrays. By measuring gene expression, the
CC probes are useful for predicting, diagnosing, grading, staging,
CC monitoring and prognosing diseases of the human heart and vascular system
CC e.g. cardiovascular disease, hypertension, cardiac arrhythmias and
CC congenital heart disease.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 219 BP; 43 A; 55 C; 60 G; 61 T; 0 other;

Alignment Scores:

Pred. No.:	1.25e-34	Length:	219
Score:	370.00	Matches:	72
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	29.18%	Indels:	0
DB:	22	Gaps:	0

US-09-705-500A-3 (1-247) x ABA35989 (1-219)

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Qy         88 GlyLysAlaPheValLysGluSerLeuLysCysIleAlaAsnGlyValThrSerLysVal 107
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        219 GGAAAAGCATTCGTCAAAGAGAGCTTAAAATGCATCGCCAACGGGGTCACCTCCAAGGTC 160

Qy        108 PheLeuAlaIleArgArgCysSerThrPheGlnArgMetIleAlaGluValGlnGluGlu 127
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        159 TTCCTCGCCATTCGGAGGTGCTCCACTTTCCAAAGGATGATTGCTGAGGTGCAGGAAGAG 100

Qy        128 CysTyrSerLysLeuAsnValCysSerIleAlaLysArgAsnProGluAlaIleThrGlu 147
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         99 TGCTACAGCAAGCTGAATGTGTGCAGCATCGCCAAGCGGAACCCTGAAGCCATCACTGAG 40

Qy        148 ValValGlnLeuProAsnHisPheSerAsnArgTyr 159
              |||||||||||||||||||||||||||||||||||
Db         39 GTCGTCCAGCTGCCCAATCACTTCTCCAACAGGTAC 4
```

RESULT 15
AAK17358/c
ID AAK17358 standard; DNA; 219 BP.
XX
AC AAK17358;

XX
DT 05-NOV-2001 (first entry)
XX
DE Human brain expressed single exon probe SEQ ID NO: 17349.
XX
KW Human; brain expressed exon; gene expression analysis; probe;
KW microarray; Alzheimer's disease; multiple sclerosis; schizophrenia;
KW epilepsy; cancer; ss.
XX
OS Homo sapiens.
XX
PN WO200157275-A2.
XX
PD 09-AUG-2001.
XX
PF 30-JAN-2001; 2001WO-US00667.
XX
PR 04-FEB-2000; 2000US-0180312.
PR 26-MAY-2000; 2000US-0207456.
PR 30-JUN-2000; 2000US-0608408.
PR 03-AUG-2000; 2000US-0632366.
PR 21-SEP-2000; 2000US-0234687.
PR 27-SEP-2000; 2000US-0236359.
PR 04-OCT-2000; 2000GB-0024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
DR WPI; 2001-483446/52.
XX
PT Single exon nucleic acid probes for analyzing gene expression in human
PT brains -
XX
PS Example 4; SEQ ID NO: 17349; 650pp + Sequence Listing; English.
XX
CC The present invention provides a number of single exon nucleic acid
CC probes which are derived from genomic sequences expressed in the human
CC brain. They can be used to measure gene expression in brain cell samples,
CC which may enable the diagnosis and improved treatment of nervous system
CC diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia,
CC epilepsy and cancers. The present sequence is one of the probes of the
CC invention.
XX
SQ Sequence 219 BP; 43 A; 55 C; 60 G; 61 T; 0 other;

Alignment Scores:

Pred. No.:	1.25e-34	Length:	219
Score:	370.00	Matches:	72
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	29.18%	Indels:	0
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US-09-705-500A-3 (1-247) x AAK17358 (1-219)

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              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        219 GGAAAAGCATTCGTCAAAGAGAGCTTAAAATGCATCGCCAACGGGGTCACCTCCAAGGTC 160

Qy        108 PheLeuAlaIleArgArgCysSerThrPheGlnArgMetIleAlaGluValGlnGluGlu 127
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        159 TTCCTCGCCATTCGGAGGTGCTCCACTTTCCAAAGGATGATTGCTGAGGTGCAGGAAGAG 100

Qy        128 CysTyrSerLysLeuAsnValCysSerIleAlaLysArgAsnProGluAlaIleThrGlu 147
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         99 TGCTACAGCAAGCTGAATGTGTGCAGCATCGCCAAGCGGAACCCTGAAGCCATCACTGAG 40

Qy        148 ValValGlnLeuProAsnHisPheSerAsnArgTyr 159
              |||||||||||||||||||||||||||||||||||
Db         39 GTCGTCCAGCTGCCCAATCACTTCTCCAACAGGTAC 4
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Search completed: June 12, 2003, 20:16:40
Job time : 226 secs

GenCore version 5.1.6

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(without alignments)
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Title: US-09-705-500A-3
Perfect score: 1268
Sequence: 1 MLQNSAVLLVLVISASATHE.....NLRGEEDSPSHIKRTSHESA 247

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
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Delop 6.0 , Delext 7.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1268	100.0	771	2	US-08-208-005C-1	Sequence 1, Appli
2	1268	100.0	771	2	US-09-038-597A-1	Sequence 1, Appli
3	1268	100.0	771	2	US-08-431-117A-1	Sequence 1, Appli
4	354.5	28.0	888	3	US-08-831-132-13	Sequence 13, Appl
5	354.5	28.0	888	4	US-09-416-150-13	Sequence 13, Appl
6	354	27.9	906	3	US-08-831-132-1	Sequence 1, Appli
7	354	27.9	906	4	US-09-416-150-1	Sequence 1, Appli
8	352	27.8	892	2	US-08-460-529B-1	Sequence 1, Appli
9	93.5	7.4	30549	4	US-09-134-001C-322	Sequence 322, App
10	90	7.1	1384	4	US-09-227-357-142	Sequence 142, App
11	85.5	6.7	1971	4	US-09-134-001C-1485	Sequence 1485, Ap
12	84	6.6	10136	1	US-08-353-700-2	Sequence 2, Appli
13	84	6.6	10136	5	PCT-US95-16216-2	Sequence 2, Appli
14	83	6.5	1254	4	US-09-134-001C-973	Sequence 973, App
15	82	6.5	1089	4	US-09-134-001C-1833	Sequence 1833, Ap
c 16	82	6.5	4411529	4	US-09-103-840A-1	Sequence 1, Appli
17	81	6.4	2160	2	US-08-840-236-2	Sequence 2, Appli
18	81	6.4	2160	2	US-08-840-236-5	Sequence 5, Appli
19	81	6.4	2160	2	US-08-505-448A-2	Sequence 2, Appli
20	81	6.4	2160	2	US-08-505-448A-5	Sequence 5, Appli
21	81	6.4	3467	4	US-09-298-924-3	Sequence 3, Appli
c 22	80	6.3	4403765	4	US-09-103-840A-2	Sequence 2, Appli
23	79.5	6.3	2347	1	US-08-145-681-3	Sequence 3, Appli
24	79.5	6.3	2347	1	US-08-453-703-3	Sequence 3, Appli
25	79.5	6.3	2347	2	US-08-456-106-3	Sequence 3, Appli
26	79.5	6.3	2347	3	US-08-456-108-3	Sequence 3, Appli
27	79.5	6.3	2347	4	US-09-265-577-3	Sequence 3, Appli
c 28	78.5	6.2	1447	4	US-09-484-970B-121	Sequence 121, App
c 29	78	6.2	18475	4	US-08-961-527-38	Sequence 38, Appl
c 30	77	6.1	714	4	US-09-221-017B-1030	Sequence 1030, Ap
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32	76.5	6.0	3572	2	US-08-713-815A-2	Sequence 2, Appli
c 33	76	6.0	1461	2	US-08-578-516-1	Sequence 1, Appli
34	75.5	6.0	1479	2	US-08-686-599A-4	Sequence 4, Appli
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36	75	5.9	2840	5	PCT-US93-06251-64	Sequence 64, Appl
37	75	5.9	5816	4	US-09-220-641-4	Sequence 4, Appli
38	75	5.9	11091	4	US-09-134-001C-2243	Sequence 2243, Ap
c 39	75	5.9	12508	4	US-09-655-270A-1	Sequence 1, Appli
c 40	75	5.9	12523	4	US-09-651-941-1	Sequence 1, Appli
c 41	75	5.9	12523	4	US-09-955-597-1	Sequence 1, Appli
42	74.5	5.9	1602	2	US-08-770-544-3	Sequence 3, Appli
43	74.5	5.9	2259	6	5185254-3	Patent No. 5185254
44	74.5	5.9	3515	4	US-09-221-017B-824	Sequence 824, App
45	74	5.8	1026	4	US-09-134-001C-1431	Sequence 1431, Ap

ALIGNMENTS

RESULT 1
US-08-208-005C-1
; Sequence 1, Application US/08208005C
; Patent No. 5837498
; GENERAL INFORMATION:
; APPLICANT: OLSEN, ET AL.
; TITLE OF INVENTION: Corpuscles of Stannius Protein, Stanniocalcin
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
; ADDRESSEE: CECCHI, STEWART & OLSTEIN
; STREET: 6 BECKER FARM ROAD
; CITY: ROSELAND
; STATE: NEW JERSEY
; COUNTRY: USA
; ZIP: 07068
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 INCH DISKETTE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WORD PERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/208,005C
; FILING DATE: 8 MARCH 1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: FERRARO, GREGORY D.
; REGISTRATION NUMBER: 36,134
; REFERENCE/DOCKET NUMBER: 325800-78
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 1:

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;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  771 BASE PAIRS
;       TYPE:  NUCLEIC ACID
;       STRANDEDNESS:  SINGLE
;       TOPOLOGY:  LINEAR
;     MOLECULE TYPE:  cDNA
US-08-208-005C-1

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Score:                    1268.00         Matches:        247
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Best Local Similarity:    100.00%         Mismatches:     0
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US-09-705-500A-3 (1-247) x US-08-208-005C-1 (1-771)

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Qy         21 AlaGluGlnAsnAspSerValSerProArgLysSerArgValAlaAlaGlnAsnSerAla 40
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Qy         41 GluValValArgCysLeuAsnSerAlaLeuGlnValGlyCysGlyAlaPheAlaCysLeu 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        136 GAAGTGGTTCGTTGCCTCAACAGTGCTCTACAGGTCGGCTGCGGGGCTTTTGCATGCCTG 195

Qy         61 GluAsnSerThrCysAspThrAspGlyMetTyrAspIleCysLysSerPheLeuTyrSer 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        196 GAAAACTCCACCTGTGACACAGATGGGATGTATGACATCTGTAAATCCTTCTTGTACAGC 255

Qy         81 AlaAlaLysPheAspThrGlnGlyLysAlaPheValLysGluSerLeuLysCysIleAla 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        256 GCTGCTAAATTTGACACTCAGGGAAAAGCATTCGTCAAAGAGAGCTTAAAATGCATCGCC 315

Qy        101 AsnGlyValThrSerLysValPheLeuAlaIleArgArgCysSerThrPheGlnArgMet 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        316 AACGGGGTCACCTCCAAGGTCTTCCTCGCCATTCGGAGGTGCTCCACTTTCCAAAGGATG 375

Qy        121 IleAlaGluValGlnGluGluCysTyrSerLysLeuAsnValCysSerIleAlaLysArg 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        376 ATTGCTGAGGTGCAGGAAGAGTGCTACAGCAAGCTGAATGTGTGCAGCATCGCCAAGCGG 435

Qy        141 AsnProGluAlaIleThrGluValValGlnLeuProAsnHisPheSerAsnArgTyrTyr 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        436 AACCCTGAAGCCATCACTGAGGTCGTCCAGCTGCCCAATCACTTCTCCAACAGATACTAT 495

Qy        161 AsnArgLeuValArgSerLeuLeuGluCysAspGluAspThrValSerThrIleArgAsp 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        496 AACAGACTTGTCCGAAGCCTGCTGGAATGTGATGAAGACACAGTCAGCACAATCAGAGAC 555

Qy        181 SerLeuMetGluLysIleGlyProAsnMetAlaSerLeuPheHisIleLeuGlnThrAsp 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        556 AGCCTGATGGAGAAAATTGGGCCTAACATGGCCAGCCTCTTCCACATCCTGCAGACAGAC 615

Qy        201 HisCysAlaGlnThrHisProArgAlaAspPheAsnArgArgArgThrAsnGluProGln 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        616 CACTGTGCCCAAACACACCCACGAGCTGACTTCAACAGGAGACGCACCAATGAGCCGCAG 675

Qy        221 LysLeuLysValLeuLeuArgAsnLeuArgGlyGluGluAspSerProSerHisIleLys 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        676 AAGCTGAAAGTCCTCCTCAGGAACCTCCGAGGTGAGGAGGACTCTCCCTCCCACATCAAA 735

Qy        241 ArgThrSerHisGluSerAla 247
              ||||||||||||||||||||
Db        736 CGCACATCCCATGAGAGTGCA 756

RESULT 2
US-09-038-597A-1
;,Sequence 1, Application US/09038597A
; Patent No. 5877290
; GENERAL INFORMATION:
;   APPLICANT:  OLSEN, ET AL.
;   TITLE OF INVENTION:  Corpuscles of Stannius Protein,
;   TITLE OF INVENTION:  Stanniocalcin
;   NUMBER OF SEQUENCES:  5
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE:  CARELLA, BYRNE, BAIN, GILFILLAN,
;     ADDRESSEE:  CECCHI, STEWART & OLSTEIN
;     STREET:  6 BECKER FARM ROAD
;     CITY:  ROSELAND
;     STATE:  NEW JERSEY
;     COUNTRY:  USA
;     ZIP:  07068
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE:  3.5 INCH DISKETTE
;     COMPUTER:  IBM PS/2
;     OPERATING SYSTEM:  MS-DOS
;     SOFTWARE:  WORD PERFECT 5.1
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER:  US/09/038,597A
;     FILING DATE:
;     CLASSIFICATION:
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER:  08/208,005
;     FILING DATE:  8-MARCH-1994
;   ATTORNEY/AGENT INFORMATION:
;     NAME:  FERRARO, GREGORY D.
;     REGISTRATION NUMBER:  36,134
;     REFERENCE/DOCKET NUMBER:  325800-78
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE:  201-994-1700
;     TELEFAX:  201-994-1744
; INFORMATION FOR SEQ ID NO:  1:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH:  771 BASE PAIRS
;     TYPE:  NUCLEIC ACID
;     STRANDEDNESS:  SINGLE
;     TOPOLOGY:  LINEAR
;   MOLECULE TYPE:  cDNA
US-09-038-597A-1

Alignment Scores:
Pred. No.:                3.15e-152       Length:         771
Score:                    1268.00         Matches:        247
Percent Similarity:       100.00%         Conservative:   0
Best Local Similarity:    100.00%         Mismatches:     0
Query Match:              100.00%         Indels:         0
DB:                       2               Gaps:           0

US-09-705-500A-3 (1-247) x US-09-038-597A-1 (1-771)

Qy          1 MetLeuGlnAsnSerAlaValLeuLeuValLeuValIleSerAlaSerAlaThrHisGlu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         16 ATGCTCCAAAACTCAGCAGTGCTTCTGGTGCTGGTGATCAGTGCTTCTGCAACCCATGAG 75

Qy         21 AlaGluGlnAsnAspSerValSerProArgLysSerArgValAlaAlaGlnAsnSerAla 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         76 GCGGAGCAGAATGACTCTGTGAGCCCCAGGAAATCCCGAGTGGCGGCCCAAAACTCAGCT 135

Qy         41 GluValValArgCysLeuAsnSerAlaLeuGlnValGlyCysGlyAlaPheAlaCysLeu 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        136 GAAGTGGTTCGTTGCCTCAACAGTGCTCTACAGGTCGGCTGCGGGGCTTTTGCATGCCTG 195

Qy         61 GluAsnSerThrCysAspThrAspGlyMetTyrAspIleCysLysSerPheLeuTyrSer 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        196 GAAAACTCCACCTGTGACACAGATGGGATGTATGACATCTGTAAATCCTTCTTGTACAGC 255

Qy         81 AlaAlaLysPheAspThrGlnGlyLysAlaPheValLysGluSerLeuLysCysIleAla 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        256 GCTGCTAAATTTGACACTCAGGGAAAAGCATTCGTCAAAGAGAGCTTAAAATGCATCGCC 315

Qy        101 AsnGlyValThrSerLysValPheLeuAlaIleArgArgCysSerThrPheGlnArgMet 120
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                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        316 AACGGGGTCACCTCCAAGGTCTTCCTCGCCATTCGGAGGTGCTCCACTTTCCAAAGGATG 375

Qy        121 IleAlaGluValGlnGluGluCysTyrSerLysLeuAsnValCysSerIleAlaLysArg 140
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        376 ATTGCTGAGGTGCAGGAAGAGTGCTACAGCAAGCTGAATGTGTGCAGCATCGCCAAGCGG 435

Qy        141 AsnProGluAlaIleThrGluValValGlnLeuProAsnHisPheSerAsnArgTyrTyr 160
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        436 AACCCTGAAGCCATCACTGAGGTCGTCCAGCTGCCCAATCACTTCTCCAACAGATACTAT 495

Qy        161 AsnArgLeuValArgSerLeuLeuGluCysAspGluAspThrValSerThrIleArgAsp 180
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        496 AACAGACTTGTCCGAAGCCTGCTGGAATGTGATGAAGACACAGTCAGCACAATCAGAGAC 555

Qy        181 SerLeuMetGluLysIleGlyProAsnMetAlaSerLeuPheHisIleLeuGlnThrAsp 200
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        556 AGCCTGATGGAGAAAATTGGGCCTAACATGGCCAGCCTCTTCCACATCCTGCAGACAGAC 615

Qy        201 HisCysAlaGlnThrHisProArgAlaAspPheAsnArgArgArgThrAsnGluProGln 220
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        616 CACTGTGCCCAAACACACCCACGAGCTGACTTCAACAGGAGACGCACCAATGAGCCGCAG 675

Qy        221 LysLeuLysValLeuLeuArgAsnLeuArgGlyGluGluAspSerProSerHisIleLys 240
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        676 AAGCTGAAAGTCCTCCTCAGGAACCTCCGAGGTGAGGAGGACTCTCCCTCCCACATCAAA 735

Qy        241 ArgThrSerHisGluSerAla 247
                |||||||||||||||||||
Db        736 CGCACATCCCATGAGAGTGCA 756

RESULT 3
US-08-431-117A-1
; Sequence 1, Application US/08431117A
; Patent No. 5994301
;  GENERAL INFORMATION:
;    APPLICANT:  OLSEN, ET AL.
;    TITLE OF INVENTION:  Corpuscles of Stannius Protein, Stanniocalcin
;    NUMBER OF SEQUENCES:  8
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  CARELLA, BYRNE, BAIN, GILFILLAN,
;      ADDRESSEE:  CECCHI, STEWART & OLSTEIN
;      STREET:  6 BECKER FARM ROAD
;      CITY:  ROSELAND
;      STATE:  NEW JERSEY
;      COUNTRY:  USA
;      ZIP:  07068
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5 INCH DISKETTE
;      COMPUTER:  IBM PS/2
;      OPERATING SYSTEM:  MS-DOS
;      SOFTWARE:  WORD PERFECT 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/431,117A
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/208,005
;      FILING DATE:  8 MARCH 1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  FERRARO, GREGORY D.
;      REGISTRATION NUMBER:  36,134
;      REFERENCE/DOCKET NUMBER:  325800-296
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  201-994-1700
;      TELEFAX:  201-994-1744
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  771 BASE PAIRS
;      TYPE:  NUCLEIC ACID
;      STRANDEDNESS:  SINGLE
;      TOPOLOGY:  LINEAR
;    MOLECULE TYPE:  cDNA
```

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US-08-431-117A-1

Alignment Scores:
Pred. No.:                3.15e-152       Length:          771
Score:                    1268.00         Matches:         247
Percent Similarity:       100.00%         Conservative:    0
Best Local Similarity:    100.00%         Mismatches:      0
Query Match:              100.00%         Indels:          0
DB:                       2               Gaps:            0

US-09-705-500A-3 (1-247) x US-08-431-117A-1 (1-771)

Qy          1 MetLeuGlnAsnSerAlaValLeuLeuValLeuValIleSerAlaSerAlaThrHisGlu 20
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         16 ATGCTCCAAAACTCAGCAGTGCTTCTGGTGCTGGTGATCAGTGCTTCTGCAACCCATGAG 75

Qy         21 AlaGluGlnAsnAspSerValSerProArgLysSerArgValAlaAlaGlnAsnSerAla 40
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         76 GCGGAGCAGAATGACTCTGTGAGCCCCAGGAAATCCCGAGTGGCGGCCCAAAACTCAGCT 135

Qy         41 GluValValArgCysLeuAsnSerAlaLeuGlnValGlyCysGlyAlaPheAlaCysLeu 60
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        136 GAAGTGGTTCGTTGCCTCAACAGTGCTCTACAGGTCGGCTGCGGGGCTTTTGCATGCCTG 195

Qy         61 GluAsnSerThrCysAspThrAspGlyMetTyrAspIleCysLysSerPheLeuTyrSer 80
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        196 GAAAACTCCACCTGTGACACAGATGGGATGTATGACATCTGTAAATCCTTCTTGTACAGC 255

Qy         81 AlaAlaLysPheAspThrGlnGlyLysAlaPheValLysGluSerLeuLysCysIleAla 100
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        256 GCTGCTAAATTTGACACTCAGGGAAAAGCATTCGTCAAAGAGAGCTTAAAATGCATCGCC 315

Qy        101 AsnGlyValThrSerLysValPheLeuAlaIleArgArgCysSerThrPheGlnArgMet 120
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        316 AACGGGGTCACCTCCAAGGTCTTCCTCGCCATTCGGAGGTGCTCCACTTTCCAAAGGATG 375

Qy        121 IleAlaGluValGlnGluGluCysTyrSerLysLeuAsnValCysSerIleAlaLysArg 140
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        376 ATTGCTGAGGTGCAGGAAGAGTGCTACAGCAAGCTGAATGTGTGCAGCATCGCCAAGCGG 435

Qy        141 AsnProGluAlaIleThrGluValValGlnLeuProAsnHisPheSerAsnArgTyrTyr 160
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        436 AACCCTGAAGCCATCACTGAGGTCGTCCAGCTGCCCAATCACTTCTCCAACAGATACTAT 495

Qy        161 AsnArgLeuValArgSerLeuLeuGluCysAspGluAspThrValSerThrIleArgAsp 180
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        496 AACAGACTTGTCCGAAGCCTGCTGGAATGTGATGAAGACACAGTCAGCACAATCAGAGAC 555

Qy        181 SerLeuMetGluLysIleGlyProAsnMetAlaSerLeuPheHisIleLeuGlnThrAsp 200
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        556 AGCCTGATGGAGAAAATTGGGCCTAACATGGCCAGCCTCTTCCACATCCTGCAGACAGAC 615

Qy        201 HisCysAlaGlnThrHisProArgAlaAspPheAsnArgArgArgThrAsnGluProGln 220
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        616 CACTGTGCCCAAACACACCCACGAGCTGACTTCAACAGGAGACGCACCAATGAGCCGCAG 675

Qy        221 LysLeuLysValLeuLeuArgAsnLeuArgGlyGluGluAspSerProSerHisIleLys 240
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        676 AAGCTGAAAGTCCTCCTCAGGAACCTCCGAGGTGAGGAGGACTCTCCCTCCCACATCAAA 735

Qy        241 ArgThrSerHisGluSerAla 247
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Db        736 CGCACATCCCATGAGAGTGCA 756

RESULT 4
US-08-831-132-13
; Sequence 13, Application US/08831132
; Patent No. 6008322
;  GENERAL INFORMATION:
;    APPLICANT:  Kuestner, Rolf E.
;    APPLICANT:  Conklin, Darrell C.
;    APPLICANT:  Lok, Si
;    APPLICANT:  Buddle, Michele
```

```
;    APPLICANT:  Downey, William
;    TITLE OF INVENTION:  STANNIOCALCIN-2
;    NUMBER OF SEQUENCES:  22
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  ZymoGenetics, Inc.
;      STREET:  1201 Eastlake Avenue East
;      CITY:  Seattle
;      STATE:  WA
;      COUNTRY:  USA
;      ZIP:  98102
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/831,132
;      FILING DATE:
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Sawislak, Deborah A.
;      REGISTRATION NUMBER:  37,438
;      REFERENCE/DOCKET NUMBER:  96-01
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  206-442-6672
;      TELEFAX:  206-442-6678
;  INFORMATION FOR SEQ ID NO:  13:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  888 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  sig_peptide
;      LOCATION:  1..72
;    FEATURE:
;      NAME/KEY:  mat_peptide
;      LOCATION:  73..888
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  1..888
US-08-831-132-13

Alignment Scores:
Pred. No.:              9.86e-36        Length:         888
Score:                  354.50          Matches:        85
Percent Similarity:     48.51%          Conservative:   45
Best Local Similarity:  31.72%          Mismatches:     109
Query Match:            27.96%          Indels:         29
DB:                     3               Gaps:           5

US-09-705-500A-3 (1-247) x US-08-831-132-13 (1-888)

Qy          7 ValLeuLeuValLeuValIleSerAlaSerAlaThrHisGluAlaGluGlnAsnAspSer 26
              |||   |||   ||||||          :::             |||:::      ||||||
Db         28 GTGACCCTGGCTTTGGTGTTT------GCCACCTTGGACCCGGCGCAGGGGACGGACTCC 81

Qy         27 ValSerPro----------------------------ArgLysSerArgValAlaAla 36
                 :::|||                           :::|||   |||::::::
Db         82 ACGAACCCTCCGGAAGGTCCCCAAGACAGGAGCTCGCAGCAGAAAGGCCGTCTGTCCCTG 141

Qy         37 GlnAsnSerAlaGluValValArgCysLeuAsnSerAlaLeuGlnValGlyCysGlyAla 56
              ||||||:::||||||:::      ||||||   :::|||      ||||||||||||
Db        142 CAGAACACAGCGGAGATCCAGCACTGTTTGGTCAATGCCGGGGACGTGGGCTGTGGTGTG 201

Qy         57 PheAlaCysLeuGluAsnSerThrCysAspThrAspGlyMetTyrAspIleCysLysSer 76
              |||   |||   ||||||::::::|||:::      |||::::::   ||||||   :::
Db        202 TTTGAGTGTTTCGAGAACAACTCTTGTGAAATCCAGGGTTTACATGGGATTTGCATGACG 261

Qy         77 PheLeuTyrSerAlaAlaLysPheAspThrGlnGlyLysAlaPheValLysGluSerLeu 96
              ||||||::::::|||   |||||||||   ||||||||||:::|||:::|||::::::|||
Db        262 TTTCTGCACAACGCTGGAAAATTCGATGCCCAGGGAAAGTCATTCATCAAGGATGCCCTG 321

Qy         97 LysCysIleAlaAsnGlyValThrSerLysValPheLeuAlaIleArgArgCysSerThr 116
              :::|||   |||:::   :::       |||                 |||:::|||
Db        322 AGGTGCAAGGCCCATGCCCTGCGTCATAAATTTGGCTGCATCAGCAGGAAGTGTCCAGCA 381

Qy        117 PheGlnArgMetIleAlaGluValGlnGluGluCysTyrSerLysLeuAsnValCysSer 136
                 :::   |||:::   :::::::|||   |||||||||   |||   ::::::||||||
Db        382 ATTAGGGAAATGGTTTTCCAGTTGCAGAGGGAATGCTATCTGAAGCATGACCTGTGCTCC 441

Qy        137 IleAlaLysArgAsnProGluAlaIleThrGluValValGlnLeuProAsnHisPheSer 156
                 |||:::   |||         |||   |||::::::         :::
Db        442 GCAGCCCAGGAGAACGTCGGTGTGATTGTGGAGATGATTCATTTCAAGGATCTCCTGCTG 501

Qy        157 AsnArgTyrTyrAsnArgLeuValArgSerLeuLeuGluCysAspGluAspThrValSer 176
                 :::      |||      ||||||      ||||||   |||   ||||||
Db        502 CATGAGCCCTATGTGGACCTTGTGAACCTGCTGCTGACCTGCGGGGAAGATGTGAAGGAG 561

Qy        177 ThrIleArgAspSerLeuMetGluLysIleGlyProAsnMetAlaSerLeuPheHisIle 196
                 :::.     |||:::      :::         :::         |||      |||
Db        562 GCAGTCACCCGCAGCGTCCAGGCTCAGTGTGAACAGAGCTGGGGAGGCCTCTGCTCCATC 621

Qy        197 Leu----------------------GlnThrAspHisCysAlaGlnThrHis------ 206
                |||                          :::             |||      |||
Db        622 CTGAGTTTCTGCACCTCCAATATACAGAGACCTCCCACGGCAGCCCCAGAGCATCAGCCC 681

Qy        207 ------ProArgAlaAspPheAsnArgArgArgThrAsnGluProGlnLysLeuLysVal 224
                    ||||||      :::|||         :::
Db        682 CTGGCAGACAGGGCTCAGCTCTCCAGGCCTCACCACCGGGACACAGACCATCACCTAACA 741

Qy        225 LeuLeuArgAsnLeuArgGlyGluGluAspSerProSerHisIleLys------------ 240
                 |||      :::||||||      |||   ||||||
Db        742 GCCAACAGAGGTGCCAAGGGTGAGCGAGGGAGCAAAAGCCACCCGAATGCCCATGCTCGA 801

Qy        241 ---ArgThrSerHisGluSerAla 247
                 ||||||      :::||||||
Db        802 GGCAGAACCGGTGGCCAGAGCGCT 825

RESULT 5
US-09-416-150-13
; Sequence 13, Application US/09416150
; Patent No. 6171822
;   GENERAL INFORMATION:
;        APPLICANT: Kuestner, Rolf E.
;                   Conklin, Darrell C.
;                   Lok, Si
;                   Buddle, Michele
;                   Downey, William
;        TITLE OF INVENTION: STANNIOCALCIN-2
;        NUMBER OF SEQUENCES: 22
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: ZymoGenetics, Inc.
;             STREET: 1201 Eastlake Avenue East
;             CITY: Seattle
;             STATE: WA
;             COUNTRY: USA
;             ZIP: 98102
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.25
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/416,150
;             FILING DATE: 11-Oct-1999
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 08/831,132
;             FILING DATE: <Unknown>
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Sawislak, Deborah A.
;             REGISTRATION NUMBER: 37,438
;             REFERENCE/DOCKET NUMBER: 96-01
;        TELECOMMUNICATION INFORMATION:
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;             TELEPHONE: 206-442-6672
;             TELEFAX: 206-442-6678
;   INFORMATION FOR SEQ ID NO: 13:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 888 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: cDNA
;        FEATURE:
;             NAME/KEY:  sig_peptide
;             LOCATION:  1..72
;        FEATURE:
;             NAME/KEY:  mat_peptide
;             LOCATION:  73..888
;        FEATURE:
;             NAME/KEY:  CDS
;             LOCATION:  1..888
;        SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-09-416-150-13

Alignment Scores:
Pred. No.:              9.86e-36        Length:         888
Score:                  354.50          Matches:        85
Percent Similarity:     48.51%          Conservative:   45
Best Local Similarity:  31.72%          Mismatches:     109
Query Match:            27.96%          Indels:         29
DB:                     4               Gaps:           5

US-09-705-500A-3 (1-247) x US-09-416-150-13 (1-888)

Qy          7 ValLeuLeuValLeuValIleSerAlaSerAlaThrHisGluAlaGluGlnAsnAspSer 26
              |||   |||   ||||||         :::           |||:::      ||||||
Db         28 GTGACCCTGGCTTTGGTGTTT------GCCACCTTGGACCCGGCGCAGGGGACGGACTCC 81

Qy         27 ValSerPro----------------------------ArgLysSerArgValAlaAla 36
                 :::|||                          :::|||   |||::::::
Db         82 ACGAACCCTCCGGAAGGTCCCCAAGACAGGAGCTCGCAGCAGAAAGGCCGTCTGTCCCTG 141

Qy         37 GlnAsnSerAlaGluValValArgCysLeuAsnSerAlaLeuGlnValGlyCysGlyAla 56
              ||||||:::||||||:::      ||||||   :::|||       ||||||||||||
Db        142 CAGAACACAGCGGAGATCCAGCACTGTTTGGTCAATGCCGGGGACGTGGGCTGTGGTGTG 201

Qy         57 PheAlaCysLeuGluAsnSerThrCysAspThrAspGlyMetTyrAspIleCysLysSer 76
              |||   |||   ||||||::::::|||:::      |||::::::   ||||||   :::
Db        202 TTTGAGTGTTTCGAGAACAACTCTTGTGAAATCCAGGGTTTACATGGGATTTGCATGACG 261

Qy         77 PheLeuTyrSerAlaAlaLysPheAspThrGlnGlyLysAlaPheValLysGluSerLeu 96
              ||||||::::::|||   |||||||||   |||||||||:::|||:::|||:::::|||
Db        262 TTTCTGCACAACGCTGGAAAATTCGATGCCCAGGGAAAGTCATTCATCAAGGATGCCCTG 321

Qy         97 LysCysIleAlaAsnGlyValThrSerLysValPheLeuAlaIleArgArgCysSerThr 116
              :::|||   |||:::   :::      |||                |||:::|||
Db        322 AGGTGCAAGGCCCATGCCCTGCGTCATAAATTTGGCTGCATCAGCAGGAAGTGTCCAGCA 381

Qy        117 PheGlnArgMetIleAlaGluValGlnGluGluCysTyrSerLysLeuAsnValCysSer 136
                 :::   |||:::   ::::::|||   |||||||||   |||   ::::::||||||
Db        382 ATTAGGGAAATGGTTTTCCAGTTGCAGAGGGAATGCTATCTGAAGCATGACCTGTGCTCC 441

Qy        137 IleAlaLysArgAsnProGluAlaIleThrGluValValGlnLeuProAsnHisPheSer 156
              |||:::   |||         |||   |||::::::         :::
Db        442 GCAGCCCAGGAGAACGTCGGTGTGATTGTGGAGATGATTCATTTCAAGGATCTCCTGCTG 501

Qy        157 AsnArgTyrTyrAsnArgLeuValArgSerLeuLeuGluCysAspGluAspThrValSer 176
              :::      |||      ||||||      ||||||   |||   ||||||
Db        502 CATGAGCCCTATGTGGACCTTGTGAACCTGCTGCTGACCTGCGGGGAAGATGTGAAGGAG 561

Qy        177 ThrIleArgAspSerLeuMetGluLysIleGlyProAsnMetAlaSerLeuPheHisIle 196
                 :::      |||:::      :::          :::          |||      |||
Db        562 GCAGTCACCCGCAGCGTCCAGGCTCAGTGTGAACAGAGCTGGGGAGGCCTCTGCTCCATC 621

Qy        197 Leu-----------------------GlnThrAspHisCysAlaGlnThrHis------ 206
              |||                       :::           |||      |||
```

```
Db        622 CTGAGTTTCTGCACCTCCAATATACAGAGACCTCCCACGGCAGCCCCAGAGCATCAGCCC 681

Qy        207 ------ProArgAlaAspPheAsnArgArgArgThrAsnGluProGlnLysLeuLysVal 224
                       ||||||      :::|||           :::
Db        682 CTGGCAGACAGGGCTCAGCTCTCCAGGCCTCACCACCGGGACACAGACCATCACCTAACA 741

Qy        225 LeuLeuArgAsnLeuArgGlyGluGluAspSerProSerHisIleLys------------ 240
                    |||      :::||||||      |||   ||||||
Db        742 GCCAACAGAGGTGCCAAGGGTGAGCGAGGGAGCAAAAGCCACCCGAATGCCCATGCTCGA 801

Qy        241 ---ArgThrSerHisGluSerAla 247
                 ||||||      :::||||||
Db        802 GGCAGAACCGGTGGCCAGAGCGCT 825

RESULT 6
US-08-831-132-1
; Sequence 1, Application US/08831132
; Patent No. 6008322
;  GENERAL INFORMATION:
;    APPLICANT:  Kuestner, Rolf E.
;    APPLICANT:  Conklin, Darrell C.
;    APPLICANT:  Lok, Si
;    APPLICANT:  Buddle, Michele
;    APPLICANT:  Downey, William
;    TITLE OF INVENTION:  STANNIOCALCIN-2
;    NUMBER OF SEQUENCES:  22
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  ZymoGenetics, Inc.
;      STREET:  1201 Eastlake Avenue East
;      CITY:  Seattle
;      STATE:  WA
;      COUNTRY:  USA
;      ZIP:  98102
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/831,132
;      FILING DATE:
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Sawislak, Deborah A.
;      REGISTRATION NUMBER:  37,438
;      REFERENCE/DOCKET NUMBER:  96-01
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  206-442-6672
;      TELEFAX:  206-442-6678
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  906 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  sig_peptide
;      LOCATION:  1..72
;    FEATURE:
;      NAME/KEY:  mat_peptide
;      LOCATION:  73..906
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  1..906
US-08-831-132-1

Alignment Scores:
Pred. No.:              1.18e-35        Length:         906
Score:                  354.00          Matches:        82
Percent Similarity:     52.32%          Conservative:   42
Best Local Similarity:  34.60%          Mismatches:     102
Query Match:            27.92%          Indels:         12
```

```
DB:                    3              Gaps:          4

US-09-705-500A-3 (1-247) x US-08-831-132-1 (1-906)

Qy          9 LeuValLeuValIleSer--------------------AlaSerAlaThrHisGluAla 21
              |||   ||||||::::::                              ||||||:::
Db         34 CTGGCTTTGGTGTTGGCCACCTTTGACCCGGCGCGGGGGACCGACGCCACCAACCCACCC 93

Qy         22 Glu---GlnAsnAspSerValSerProArgLysSerArgValAlaAlaGlnAsnSerAla 40
              |||       |||      |||   :::|||   |||::::::   ||||||:::|||
Db         94 GAGGGTCCCCAAGACAGGAGCTCCCAGCAGAAAGGCCGCCTGTCCCTGCAGAATACAGCG 153

Qy         41 GluValValArgCysLeuAsnSerAlaLeuGlnValGlyCysGlyAlaPheAlaCysLeu 60
              |||:::     ||||||   :::|||      ||||||||||||   |||   |||
Db        154 GAGATCCAGCACTGTTTGGTCAACGCTGGCGATGTGGGGTGTGGCGTGTTTGAATGTTTC 213

Qy         61 GluAsnSerThrCysAspThrAspGlyMetTyrAspIleCysLysSerPheLeuTyrSer 80
              ||||||::::::|||:::      |||::::::   ||||||   :::||||||::::::
Db        214 GAGAACAACTCTTGTGAGATTCGGGGCTTACATGGGATTTGCATGACTTTTCTGCACAAC 273

Qy         81 AlaAlaLysPheAspThrGlnGlyLysAlaPheValLysGluSerLeuLysCysIleAla 100
              |||   |||||||||   |||||||||:::|||:::|||::::::|||||||||   |||
Db        274 GCTGGAAAATTTGATGCCCAGGGCAAGTCATTCATCAAAGACGCCTTGAAATGTAAGGCC 333

Qy        101 AsnGlyValThrSerLysValPheLeuAlaIleArgArgCysSerThrPheGlnArgMet 120
              :::   :::      :::                |||:::|||         :::   |||
Db        334 CACGCTCTGCGGCACAGGTTCGGCTGCATAAGCCGGAAGTGCCCGGCCATCAGGGAAATG 393

Qy        121 IleAlaGluValGlnGluGluCysTyrSerLysLeuAsnValCysSerIleAlaLysArg 140
              ::::::::::::|||   |||||||||   |||   ::::::|||:::   |||:::
Db        394 GTGTCCCAGTTGCAGCGGGAATGCTACCTCAAGCACGACCTGTGCGCGGCTGCCCAGGAG 453

Qy        141 AsnProGluAlaIleThrGluValValGlnLeuProAsnHisPheSerAsnArgTyrTyr 160
              |||       |||   |||::::::       :::         :::      |||
Db        454 AACACCCGGGTGATAGTGGAGATGATCCATTTCAAGGACTTGCTGCTGCACGAACCCTAC 513

Qy        161 AsnArgLeuValArgSerLeuLeuGluCysAspGluAspThrValSerThrIleArgAsp 180
              ||||||     ||||||   |||   |||:::             |||
Db        514 GTGGACCTCGTGAACTTGCTGCTGACCTGTGGGGAGGAGGTGAAGGAGGCCATCACCCAC 573

Qy        181 SerLeuMetGluLysIleGlyProAsnMetAlaSerLeuPheHisIleLeuGlnThrAsp 200
              |||:::     ::::      |||      ||||||      ||||||
Db        574 AGCGTGCAGGTTCAGTGTGAGCAGAACTGGGGAAGCCTGTGCTCCATCTTG------AGC 627

Qy        201 HisCysAlaGlnThrHisProArgAlaAspPheAsnArgArgArgThrAsnGluProGln 220
              |||       ||||||   |||          |||          |||
Db        628 TTCTGCACCTCGGC-CATCCAGAAGCCTCCCACGGCGCCCCCCGAGCGCCAGCCCCAGGT 686

Qy        221 LysLeuLysValLeuLeuArgAsn---LeuArgGlyGluGluAspSerPro 236
                          |||:::         ||||||         ||||||
Db        687 GGACAGAACCAAGCTCTCCAGGGCCCACCACGGGGAAGCAGGACATCACCT 737

RESULT 7
US-09-416-150-1
; Sequence 1, Application US/09416150
; Patent No. 6171822
;   GENERAL INFORMATION:
;        APPLICANT: Kuestner, Rolf E.
;                   Conklin, Darrell C.
;                   Lok, Si
;                   Buddle, Michele
;                   Downey, William
;        TITLE OF INVENTION: STANNIOCALCIN-2
;        NUMBER OF SEQUENCES: 22
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: ZymoGenetics, Inc.
;             STREET: 1201 Eastlake Avenue East
;             CITY: Seattle
;             STATE: WA
;             COUNTRY: USA
;             ZIP: 98102
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.25
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/416,150
;             FILING DATE: 11-Oct-1999
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 08/831,132
;             FILING DATE: <Unknown>
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Sawislak, Deborah A.
;             REGISTRATION NUMBER: 37,438
;             REFERENCE/DOCKET NUMBER: 96-01
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 206-442-6672
;             TELEFAX: 206-442-6678
;   INFORMATION FOR SEQ ID NO: 1:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 906 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: cDNA
;        FEATURE:
;             NAME/KEY:  sig_peptide
;             LOCATION:  1..72
;        FEATURE:
;             NAME/KEY:  mat_peptide
;             LOCATION:  73..906
;        FEATURE:
;             NAME/KEY:  CDS
;             LOCATION:  1..906
;        SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-416-150-1

Alignment Scores:
Pred. No.:                1.18e-35        Length:          906
Score:                    354.00          Matches:         82
Percent Similarity:       52.32%          Conservative:    42
Best Local Similarity:    34.60%          Mismatches:      102
Query Match:              27.92%          Indels:          12
DB:                       4               Gaps:            4

US-09-705-500A-3 (1-247) x US-09-416-150-1 (1-906)

Qy          9 LeuValLeuValIleSer--------------------AlaSerAlaThrHisGluAla 21
              |||   ||||||::::::                              ||||||:::
Db         34 CTGGCTTTGGTGTTGGCCACCTTTGACCCGGCGCGGGGGACCGACGCCACCAACCCACCC 93

Qy         22 Glu---GlnAsnAspSerValSerProArgLysSerArgValAlaAlaGlnAsnSerAla 40
              |||       |||      |||   :::|||   |||::::::   ||||||:::|||
Db         94 GAGGGTCCCCAAGACAGGAGCTCCCAGCAGAAAGGCCGCCTGTCCCTGCAGAATACAGCG 153

Qy         41 GluValValArgCysLeuAsnSerAlaLeuGlnValGlyCysGlyAlaPheAlaCysLeu 60
              |||:::     ||||||   :::|||      ||||||||||||   |||   |||
Db        154 GAGATCCAGCACTGTTTGGTCAACGCTGGCGATGTGGGGTGTGGCGTGTTTGAATGTTTC 213

Qy         61 GluAsnSerThrCysAspThrAspGlyMetTyrAspIleCysLysSerPheLeuTyrSer 80
              ||||||::::::|||:::      |||::::::   ||||||   :::||||||::::::
Db        214 GAGAACAACTCTTGTGAGATTCGGGGCTTACATGGGATTTGCATGACTTTTCTGCACAAC 273

Qy         81 AlaAlaLysPheAspThrGlnGlyLysAlaPheValLysGluSerLeuLysCysIleAla 100
              |||   |||||||||   |||||||||:::|||:::|||::::::|||||||||   |||
Db        274 GCTGGAAAATTTGATGCCCAGGGCAAGTCATTCATCAAAGACGCCTTGAAATGTAAGGCC 333

Qy        101 AsnGlyValThrSerLysValPheLeuAlaIleArgArgCysSerThrPheGlnArgMet 120
              :::   :::      :::                |||:::|||         :::   |||
Db        334 CACGCTCTGCGGCACAGGTTCGGCTGCATAAGCCGGAAGTGCCCGGCCATCAGGGAAATG 393

Qy        121 IleAlaGluValGlnGluGluCysTyrSerLysLeuAsnValCysSerIleAlaLysArg 140
              ::::::::::::|||   |||||||||   |||   ::::::|||:::   |||:::
Db        394 GTGTCCCAGTTGCAGCGGGAATGCTACCTCAAGCACGACCTGTGCGCGGCTGCCCAGGAG 453
```

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Qy        141 AsnProGluAlaIleThrGluValValGlnLeuProAsnHisPheSerAsnArgTyrTyr 160
              |||         |||  |||::::::        :::        :::     |||
Db        454 AACACCCGGGTGATAGTGGAGATGATCCATTTCAAGGACTTGCTGCTGCACGAACCCTAC 513

Qy        161 AsnArgLeuValArgSerLeuLeuGluCysAspGluAspThrValSerThrIleArgAsp 180
              ||||||     ||||||  |||  |||:::            |||
Db        514 GTGGACCTCGTGAACTTGCTGCTGACCTGTGGGGAGGAGGTGAAGGAGGCCATCACCCAC 573

Qy        181 SerLeuMetGluLysIleGlyProAsnMetAlaSerLeuPheHisIleLeuGlnThrAsp 200
              |||:::      :::       |||      ||||||      ||||||
Db        574 AGCGTGCAGGTTCAGTGTGAGCAGAACTGGGGAAGCCTGTGCTCCATCTTG------AGC 627

Qy        201 HisCysAlaGlnThrHisProArgAlaAspPheAsnArgArgArgThrAsnGluProGln 220
              |||         ||||||  |||               |||        |||
Db        628 TTCTGCACCTCGGC-CATCCAGAAGCCTCCCACGGCGCCCCCCGAGCGCCAGCCCCAGGT 686

Qy        221 LysLeuLysValLeuLeuArgAsn---LeuArgGlyGluGluAspSerPro 236
                          |||:::       ||||||       ||||||
Db        687 GGACAGAACCAAGCTCTCCAGGGCCCACCACGGGGAAGCAGGACATCACCT 737

RESULT 8
US-08-460-529B-1
; Sequence 1, Application US/08460529B
; Patent No. 5994103
;  GENERAL INFORMATION:
;    APPLICANT:  OLSEN, ET AL.
;    TITLE OF INVENTION:  Human Stanniocalcin-alpha
;    NUMBER OF SEQUENCES:  10
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  CARELLA, BYRNE, BAIN, GILFILLAN,
;      ADDRESSEE:  CECCHI, STEWART & OLSTEIN
;      STREET:  6 BECKER FARM ROAD
;      CITY:  ROSELAND
;      STATE:  NEW JERSEY
;      COUNTRY:  USA
;      ZIP:  07068
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5 INCH DISKETTE
;      COMPUTER:  IBM PS/2
;      OPERATING SYSTEM:  MS-DOS
;      SOFTWARE:  WORD PERFECT 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/460,529B
;      FILING DATE:  June 2, 1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US94/13206
;      FILING DATE:  10 NOV 1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  MULLINS, J.G.
;      REGISTRATION NUMBER:  33,073
;      REFERENCE/DOCKET NUMBER:  325800-334  (PF143)
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  201-994-1700
;      TELEFAX:  201-994-1744
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  892 BASE PAIRS
;      TYPE:  NUCLEIC ACID
;      STRANDEDNESS:  SINGLE
;      TOPOLOGY:  LINEAR
;    MOLECULE TYPE:  cDNA
US-08-460-529B-1

Alignment Scores:
Pred. No.:              2.07e-35        Length:         892
Score:                  352.00          Matches:        81
Percent Similarity:     52.94%          Conservative:   45
Best Local Similarity:  34.03%          Mismatches:     101
Query Match:            27.76%          Indels:         12
DB:                     2               Gaps:           4
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```
US-09-705-500A-3 (1-247) x US-08-460-529B-1 (1-892)

Qy          9 LeuValLeuValIleSer--------------------AlaSerAlaThrHisGluAla 21
              |||   |||||::::::                              ||||||:::
Db        115 CTGGCTTTGGTGTTGGCCACCTTTGACCCGGCGCGGGGGACCGACGCCACCAACCCACCC 174

Qy         22 Glu---GlnAsnAspSerValSerProArgLysSerArgValAlaAlaGlnAsnSerAla 40
              |||         |||       |||  :::|||   |||::::::   ||||||:::|||
Db        175 GAGGGTCCCCAAGACAGGAGCTCCCAGCAGAAAGGCCGCCTGTCCCTGCAGAATACAGCG 234

Qy         41 GluValValArgCysLeuAsnSerAlaLeuGlnValGlyCysGlyAlaPheAlaCysLeu 60
              |||:::      ||||||   :::|||      ||||||||||||   |||   |||
Db        235 GAGATCCAGCACTGTTTGGTCAACGCTGGCGATGTGGGGTGTGGCGTGTTTGAATGTTTC 294

Qy         61 GluAsnSerThrCysAspThrAspGlyMetTyrAspIleCysLysSerPheLeuTyrSer 80
              ||||||::::::|||:::      |||::::::   ||||||   :::||||||::::::
Db        295 GAGAACAACTCTTGTGAGATTCGGGGCTTACATGGGATTTGCATGACTTTTCTGCACAAC 354

Qy         81 AlaAlaLysPheAspThrGlnGlyLysAlaPheValLysGluSerLeuLysCysIleAla 100
              |||   |||||||||   |||||||||:::|||:::|||::::::|||||||||   |||
Db        355 GCTGGAAAATTTGATGCCCAGGGCAAGTCATTCATCAAAGACGCCTTGAAATGTAAGGCC 414

Qy        101 AsnGlyValThrSerLysValPheLeuAlaIleArgArgCysSerThrPheGlnArgMet 120
              :::   :::      :::                |||:::|||         :::   |||
Db        415 CACGCTCTGCGGCACAGGTTCGGCTGCATAAGCCGGAAGTGCCCGGCCATCAGGGAAATG 474

Qy        121 IleAlaGluValGlnGluGluCysTyrSerLysLeuAsnValCysSerIleAlaLysArg 140
              :::::::::::::::   |||||||||   |||   ::::::|||:::   |||:::
Db        475 GTGTCCCAGTTGGAGCGGGAATGCTACCTCAAGCACGACCTGTGCGCGGCTGCCCAGGAG 534

Qy        141 AsnProGluAlaIleThrGluValValGlnLeuProAsnHisPheSerAsnArgTyrTyr 160
              |||         |||  |||::::::        :::        :::     |||
Db        535 AACACCCGGGTGATAGTGGAGATGATCCATTTCAAGGACTTGCTGCTGCACGAACCCTAC 594

Qy        161 AsnArgLeuValArgSerLeuLeuGluCysAspGluAspThrValSerThrIleArgAsp 180
              ||||||     ||||||  |||  |||:::            |||
Db        595 GTGGACCTCGTGAACTTGCTGCTGACCTGTGGGGAGGAGGTGAAGGAGGCCATCACCCAC 654

Qy        181 SerLeuMetGluLysIleGlyProAsnMetAlaSerLeuPheHisIleLeuGlnThrAsp 200
              |||:::      :::       |||      ||||||      ||||||
Db        655 AGCGTGCAGGTTCAGTGTGAGCAGAACTGGGGAAGCCTGTGCTCCATCTTG------AGC 708

Qy        201 HisCysAlaGlnThrHisProArgAlaAspPheAsnArgArgArgThrAsnGluProGln 220
              |||         ||||||  |||               |||        |||
Db        709 TTCTGCACCTCGGA-CATCCAGAAGCCTCCCACGGCGCCCCCCGAGCGCCAGCCCCAGGT 767

Qy        221 LysLeuLysValLeuLeuArgAsn---LeuArgGlyGluGluAspSerProSer 237
                          |||:::       ||||||::::::|||      |||
Db        768 GGACAGAACCAAGCTCTCCAGGGCCCACCACGGGGGAAGAAGGACATCACCTCC 821

RESULT 9
US-09-134-001C-322
; Sequence 322, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
;  APPLICANT: Lynn Doucette-Stamm et al
;  TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
;  TITLE OF INVENTION:  EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
;  FILE REFERENCE: GTC-007
;  CURRENT APPLICATION NUMBER: US/09/134,001C
;  CURRENT FILING DATE:  1998-08-13
;  PRIOR APPLICATION NUMBER: US 60/064,964
;  PRIOR FILING DATE: 1997-11-08
;  PRIOR APPLICATION NUMBER: US 60/055,779
;  PRIOR FILING DATE: 1997-08-14
;  NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 322
;   LENGTH: 30549
;   TYPE: DNA
;   ORGANISM: Staphylococcus epidermidis
US-09-134-001C-322

Alignment Scores:
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Pred. No.:              4.34          Length:         30549
Score:                  93.50         Matches:        47
Percent Similarity:     40.28%        Conservative:   38
Best Local Similarity:  22.27%        Mismatches:     86
Query Match:            7.37%         Indels:         40
DB:                     4             Gaps:           9

US-09-705-500A-3 (1-247) x US-09-134-001C-322 (1-30549)

Qy         14 SerAlaSerAlaThrHisGluAlaGluGlnAsnAspSer-ValSerProArgLysSerAr 33
              |||   ::::::           |||||||||   ||| :::   |||:::   :::
Db       8904 AGTATCACAAGTAACTCAAGCATTGAACAAAATCAAAGCTATTCAACCAAAATTAACAGA 8963

Qy         33 gValAla---------------AlaGlnAsnSerAlaGluValValArgCysLeuAsnSe 48
                                    :::|||:::   |||:::|||          |||
Db       8964 AGCTATCAACATGCTTCAAAACAAAGAAAATAATACAGAATTAGTCAATGCTAAAAACAG 9023

Qy         48 rAlaLeuGlnValGlyCysGlyAlaPheAlaCysLeuGluAsnSerThrCysAspThrAs 68
                                          |||||||||:::     ||||||||
Db       9024 A--------------------------------CTTGAAAATGCAGTAAATGATACAGA 9050

Qy         68 pGlyMetTyrAspIleCysLysSerPheLeu------TyrSerAlaAlaLysPheAspTh 86
              |     :::   :::   :::      :::      |||:::|||   |||   :::
Db       9051 TCCAACACACGGTATGACTCAAGAAACAATTAATAATTACAACGCTAAAAAGCGAGAAGC 9110

Qy         86 rGlnGlyLysAlaPheValLysGluSerLeuLysCysIleAlaAsnGly---------- 102
               |||   :::      ::::::::::::         |||   ||||||
Db       9111 TCAAAATGAA------ATACAAAAAGCGAACATGATTATTAATAATGGAGATGCTACTGC 9164

Qy        103 ------------------------ValThrSerLysValPheLeuAlaIleArgArgCy 114
                                       :::|||      |||::::::
Db       9165 TCAAGATATTTCTTCTGAAAAATCTAAAGTAGAGCAAGTATTACAAGCATTACAAAATGC 9224

Qy        114 sSerThrPheGlnArgMetIleAlaGluValGlnGluGluCysTyrSerLysLeu----- 132
                  |||                  :::      |||:::||||||
Db       9225 TAAGAATGACTTAAGAGCTGATAAAAGAGAATTACAGACTGCATACAATAAACTTATACA 9284

Qy        133 -AsnValCysSerIleAlaLysArgAsnProGluAlaIleThrGluValValGlnLeuPr 152
              ||||||   :::      |||:::   |||   :::|||
Db       9285 AAATGTTAATACCAATGGTAAAAAA---CCATCTAGTATTCAAAACTATAAGTCTGCAAG 9341

Qy        152 oAsnHisPheSerAsnArgTyr------TyrAsnArgLeuValArgSerLeuLeuGluCy 170
                 :::      |||:::|||                  ::::::||||||
Db       9342 ACGAAATATCGAAAACCAATATAATACCGCTAAAAATGAAGCACATAATGTTCTTGAAAA 9401

Qy        170 sAspGluAspThrValSerThrIleArgAspSerLeu------MetGluLysIleGlyPr 188
                   ||||||:::   :::   |||:::|||      :::      |||   ||
Db       9402 TACAAACCCTACTGTAAATGCAGTAGAAGATGCTTTACGTAAGATAAATGCAATTCAACC 9461

Qy        188 oAsnMetAlaSerLeuPheHisIleLeuGln 198
              |   :::             :::|||||||||
Db       9462 AGAGGTTACAAAAGCTATTAATATACTTCAA 9492

RESULT 10
US-09-227-357-142
; Sequence 142, Application US/09227357
; Patent No. 6342581
; GENERAL INFORMATION:
;  APPLICANT: Fischer et al.
;  TITLE OF INVENTION: 123 Human Secreted Proteins
;  FILE REFERENCE: PZ010P1
;  CURRENT APPLICATION NUMBER: US/09/227,357
;  CURRENT FILING DATE: 1999-01-08
;  EARLIER APPLICATION NUMBER: PCT/US98/13684
;  EARLIER FILING DATE: 1998-07-07
;  EARLIER APPLICATION NUMBER: 60/051,926
;  EARLIER FILING DATE: 1997-07-08
;  EARLIER APPLICATION NUMBER: 60/052,793
;  EARLIER FILING DATE: 1997-07-08
;  EARLIER APPLICATION NUMBER: 60/051,925
;  EARLIER FILING DATE: 1997-07-08
;  EARLIER APPLICATION NUMBER: 60/051,929
;  EARLIER FILING DATE: 1997-07-08
;  EARLIER APPLICATION NUMBER: 60/052,803
;  EARLIER FILING DATE: 1997-07-08
;  EARLIER APPLICATION NUMBER: 60/052,732
;  EARLIER FILING DATE: 1997-07-08
;  EARLIER APPLICATION NUMBER: 60/051,931
;  EARLIER FILING DATE: 1997-07-08
;  EARLIER APPLICATION NUMBER: 60/051,932
;  EARLIER FILING DATE: 1997-07-08
;  EARLIER APPLICATION NUMBER: 60/051,916
;  EARLIER FILING DATE: 1997-07-08
;  EARLIER APPLICATION NUMBER: 60/051,930
;  EARLIER FILING DATE: 1997-07-08
;  EARLIER APPLICATION NUMBER: 60/051,918
;  EARLIER FILING DATE: 1997-07-08
;  EARLIER APPLICATION NUMBER: 60/051,920
;  EARLIER FILING DATE: 1997-07-08
;  EARLIER APPLICATION NUMBER: 60/052,733
;  EARLIER FILING DATE: 1997-07-08
;  EARLIER APPLICATION NUMBER: 60/052,795
;  EARLIER FILING DATE: 1997-07-08
;  EARLIER APPLICATION NUMBER: 60/051,919
;  EARLIER FILING DATE: 1997-07-08
;  EARLIER APPLICATION NUMBER: 60/051,928
;  EARLIER FILING DATE: 1997-07-08
;  EARLIER APPLICATION NUMBER: 60/055,722
;  EARLIER FILING DATE: 1997-08-18
;  EARLIER APPLICATION NUMBER: 60/055,723
;  EARLIER FILING DATE: 1997-08-18
;  EARLIER APPLICATION NUMBER: 60/055,948
;  EARLIER FILING DATE: 1997-08-18
;  EARLIER APPLICATION NUMBER: 60/055,949
;  EARLIER FILING DATE: 1997-08-18
;  EARLIER APPLICATION NUMBER: 60/055,953
;  EARLIER FILING DATE: 1997-08-18
;  EARLIER APPLICATION NUMBER: 60/055,950
;  EARLIER FILING DATE: 1997-08-18
;  EARLIER APPLICATION NUMBER: 60/055,947
;  EARLIER FILING DATE: 1997-08-18
;  EARLIER APPLICATION NUMBER: 60/055,964
;  EARLIER FILING DATE: 1997-08-18
;  EARLIER APPLICATION NUMBER: 60/056,360
;  EARLIER FILING DATE: 1997-08-18
;  EARLIER APPLICATION NUMBER: 60/055,684
;  EARLIER FILING DATE: 1997-08-18
;  EARLIER APPLICATION NUMBER: 60/055,984
;  EARLIER FILING DATE: 1997-08-18
;  EARLIER APPLICATION NUMBER: 60/055,954
;  EARLIER FILING DATE: 1997-08-18
;  EARLIER APPLICATION NUMBER: 60/058,785
;  EARLIER FILING DATE: 1997-09-12
;  EARLIER APPLICATION NUMBER: 60/058,664
;  EARLIER FILING DATE: 1997-09-12
;  EARLIER APPLICATION NUMBER: 60/058,660
;  EARLIER FILING DATE: 1997-09-12
;  EARLIER APPLICATION NUMBER: 60/058,661
;  EARLIER FILING DATE: 1997-09-12
;  NUMBER OF SEQ ID NOS: 672
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 142
;   LENGTH: 1384
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-227-357-142

Alignment Scores:
Pred. No.:              0.0992        Length:         1384
Score:                  90.00         Matches:        41
Percent Similarity:     38.46%        Conservative:   24
Best Local Similarity:  24.26%        Mismatches:     64
Query Match:            7.10%         Indels:         40
DB:                     4             Gaps:           8

US-09-705-500A-3 (1-247) x US-09-227-357-142 (1-1384)
```

```
Qy          84 PheAspThrGlnGlyLys-----------AlaPheValLysGluSerLeuLysCysIle 99
               :::|||   :::||||||              |||      |||      :::|||:::
Db         243 TGGGACCTAGAAGGGAAGGTCACAGCCACCACGTTCTCCCTGGAGCAGCCTCGCTGTGTC 302

Qy         100 AlaAsn---------GlyValThrSerLysValPheLeuAlaIleArgArgCysSerThr 116
                  :::         ||||||   |||   ::::::|||   :::
Db         303 CTGGACGGGCTTGMCGGCGTTGCCAGCACCATCTGGCTGGTGGTG-----------GCC 350

Qy         117 PheGlnArgMetIleAlaGluValGlnGluGluCysTyrSerLysLeuAsnValCysSer 136
               |||                  :::   |||
Db         351 TTCAGCAACGCCTCCAGAGACTTCCAG------------------------------- 377

Qy         137 IleAlaLysArgAsnProGluAlaIleThrGluValValGlnLeuProAsnHisPheSer 156
                        ||||||:::         |||:::         |||         :::
Db         378 -----------AACCCACAGACGCGAGCTGAGATCCCAGCCTTCCCACGGCTGCTGACG 425

Qy         157 AsnArgTyrTyrAsnArgLeuValArgSerLeu------LeuGluCysAspGluAspThr 174
                     :::|||      |||      ||||||      |||   |||   :::|||
Db         426 GAGGGGCACTATATGACACTGCCCCTGTCCCTGGACCAGCTGCCCTGT---CAGGACCCC 482

Qy         175 ValSerThrIleArgAspSerLeuMetGluLysIleGlyProAsnMetAlaSerLeuPhe 194
                        ||||||      :::   ::::::|||   :::      |||
Db         483 GCAGGCGGCGGCAGGGACGTCCCCTTGCTGCGGGTGGGCAATGACCCCGGCTGCCTTGCT 542

Qy         195 HisIleLeuGlnThrAspHisCysAlaGlnThrHisProArgAlaAspPheAsnArgArg 214
                  :::||||||      :::|||            |||
Db         543 GACCTCCTCCAGCCGCCCTACTGCAACAGCCCCCTCCCC--------------------- 581

Qy         215 ArgThrAsnGluProGlnLysLeuLysValLeuLeuArgAsnLeuArgGlyGluGluAsp 234
                  :::      |||   ::::::|||   ||||||   :::   ||||||
Db         582 ---AGCCCCGGACCTTACAGGGTGAAGTTCCTCCTGATGGACGCCAGGGGC--------- 629

Qy         235 SerProSerHisIleLysArgThrSer 243
               ||||||         |||   |||
Db         630 TCACCCCAGGCCGAGACCAGGTGGTCC 656

RESULT 11
US-09-134-001C-1485
; Sequence 1485, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
;  APPLICANT: Lynn Doucette-Stamm et al
;  TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
;  TITLE OF INVENTION:  EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
;  FILE REFERENCE: GTC-007
;  CURRENT APPLICATION NUMBER: US/09/134,001C
;  CURRENT FILING DATE:  1998-08-13
;  PRIOR APPLICATION NUMBER: US 60/064,964
;  PRIOR FILING DATE: 1997-11-08
;  PRIOR APPLICATION NUMBER: US 60/055,779
;  PRIOR FILING DATE: 1997-08-14
;  NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 1485
;   LENGTH: 1971
;   TYPE: DNA
;   ORGANISM: Staphylococcus epidermidis
US-09-134-001C-1485

Alignment Scores:
Pred. No.:              0.643          Length:          1971
Score:                  85.50          Matches:           42
Percent Similarity:     38.41%         Conservative:      21
Best Local Similarity:  25.61%         Mismatches:        70
Query Match:            6.74%          Indels:            31
DB:                     4              Gaps:               6

US-09-705-500A-3 (1-247) x US-09-134-001C-1485 (1-1971)

Qy          35 AlaAlaGlnAsnSerAlaGluValValArgCysLeuAsnSerAlaLeuGlnValGlyCys 54
               :::|||:::      |||      :::      |||   |||   |||::::::
Db          73 AGTGCAGAAAAACTTGCTACTGAAATTATTAACTTAGAGTCAATCTTAGAATTACCTAAA 132

Qy          55 GlyAlaPheAlaCysLeuGluAsnSerThrCysAspThrAspGlyMetTyr--------- 71
                  |||              |||:::         |||      |||   |||
Db         133 GGGACT-----------GAACATTTTGTTAGTGACCTTCATGGTGAATACGAATCTTTC 180

Qy          72 ----------------------------------------------AspIleCysLys 75
                                                             ||||||   |||
Db         181 CAACATGTTTTAAGAAACGGATCTGGAAATGTGCGTGCTAAAATTAATGATATCTTCAAA 240

Qy          76 SerPheLeuTyrSerAlaAlaLysPheAspThrGlnGlyLysAlaPheVal---LysGlu 94
                  |||                  |||                  :::      :::|||
Db         241 GATAAATTATCCCAGCAAGAAATCAACGACTTAGCAGCATTAGTATACTATCCGGAAGAA 300

Qy          95 SerLeuLysCysIleAlaAsnGlyValThrSerLysValPheLeuAlaIleArgArgCys 114
                  ||||||   :::   |||      |||      |||   |||
Db         301 AAACTAAAATTAGTTAAAAATAATTTCGATTCAATCGGAACATTAAATATTTGGTATATT 360

Qy         115 SerThrPheGlnArgMetIleAlaGluValGlnGluGluCysTyrSerLysLeuAsnVal 134
               :::|||   ||||||:::|||   ::::::         |||   ||||||
Db         361 ACAACCATTCAACGATTAATT---GATTTAATTACATATTGCTCATCAAAATATACACGT 417

Qy         135 CysSerIleAlaLysArgAsnProGlu-----------AlaIleThrGluValValGln 150
                  :::   |||      ||||||               |||   |||::::::
Db         418 TCAAAATTACGCAAAGCATTACCTGAACAATACGTTTATATTATTGAAGAGCTACTTTAC 477

Qy         151 LeuProAsnHisPheSerAsnArg------TyrTyrAsnArgLeuValArgSerLeuLeu 168
                  |||   |||   |||:::      ||||||      ||||||      ::::::
Db         478 AAGAGCAATGAATTTCATAATAAAAAGCCTTATTATGAAACATTAGTTAACCAAATTATT 537

Qy         169 GluCysAspGlu 172
               |||   ::::::
Db         538 GAATTAGAACAA 549

RESULT 12
US-08-353-700-2
; Sequence 2, Application US/08353700
; Patent No. 5599919
;  GENERAL INFORMATION:
;    APPLICANT:  YEN, TIMOTHY J.
;    APPLICANT:  RATTNER, JEROME B.
;    TITLE OF INVENTION:  NUCLEIC ACID ENCODING A
;    TITLE OF INVENTION:  TRANSIENTLY-EXPRESSED KINETOCHORE PROTEIN,
;    TITLE OF INVENTION:  AND METHODS OF USE
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  DANN, DORFMAN, HERRELL AND SKILLMAN
;      STREET:  1601 MARKET STREET, SUITE 720
;      CITY:  PHILADELPHIA
;      STATE:  PA
;      COUNTRY:  USA
;      ZIP:  19103-2307
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/353,700
;      FILING DATE:  09-DEC-1994
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  REED, JANET E.
;      REGISTRATION NUMBER:  36,252
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (215) 563-4100
;      TELEFAX:  (215) 563-4044
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  10136 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA to mRNA
;    HYPOTHETICAL:  NO
```

```
;    ANTI-SENSE:  NO
;    ORIGINAL SOURCE:
;      ORGANISM:  HUMAN
US-08-353-700-2

Alignment Scores:
Pred. No.:              12.7          Length:         10136
Score:                  84.00         Matches:        61
Percent Similarity:     34.41%        Conservative:   35
Best Local Similarity:  21.86%        Mismatches:     110
Query Match:            6.62%         Indels:         73
DB:                     1             Gaps:           11

US-09-705-500A-3 (1-247) x US-08-353-700-2 (1-10136)

Qy         11 LeuValIleSerAlaSerAlaThrHisGluAlaGluGlnAsnAspSerValSerProArg 30
              |||      :::             :::||||||||||||:::          |||
Db        131 TTATTTACAAATGTTGGAGTAATAAAGAAGGCAGAACAAAATGAGCTGGGCTTTGGAAGA 190

Qy         31 LysSerArgValAlaAla---GlnAsnSerAlaGluValValArgCysLeuAsnSerAla 49
                 |||   ||||||   :::||||||:::|||      |||         :::|||
Db        191 ATGGAAAGAAGGGCTGCCTACAAGAACTCTTCAGAAAATTCAAGAGCTTGAAGGACAGCT 250

Qy         50 LeuGlnVal-----------------------------------------------GlyCys 54
              |||                                                      ||||||
Db        251 TGACAAACTGAAGAAGGAAAAGCAGCAAAGGCAGTTTCAGCTTGACAGTCTCGAGGCTGC 310

Qy         55 GlyAlaPheAlaCysLeuGluAsn-SerThrCysAspThrAspGly-------------- 69
              |||   |||      |||              |||:::|||
Db        311 GCCGCAGAAGCAAACACAGAAGGTTGAAAATGAAAAAACCGAGGGTACAAACCTGAAAAG 370

Qy         70 ------------MetTyrAspIleCysLysSerPheLeuTyrSerAlaAlaLysPheAs 85
                        :::   :::||||||:::|||         :::      |||
Db        371 GGAGAATCAAAGATTGATGGAAATATGTGAAAGTCTGGAGAAAACTAAGCAGAAGATTTC 430

Qy         85 pThrGlnGlyLysAlaPheValLysGluSerLeuLysCysIleAlaAsnGlyValThrSe 105
              :::   :::      ||||||||||||              |||       ::
Db        431 TCATGAACTTCAA------GTCAAGGAGTCACAAGTGAATTTCCAGGAAGGACAACTGAA 484

Qy        105 r--------------------LysValPheLeuAlaIleArgArgCysSerThrPheGl 118
              :                    |||:::       ::::::||||||   :::
Db        485 TTCAGGCAAAAAACAAATAGAAAAACTGGAACAGGAACTTAAAAGGTGTAAATCTGAGCT 544

Qy        118 nArgMetIleAlaGluValGlnGluGluCysTyrSerLysLeuAsnValCysSerIleAl 138
                       :::      :::                 ||||||   |||:::
Db        545 TGAAAGAAGCCAACAAGCTGCGCAGTCTGCAGATGTCTCTCTGAATCCATGCAAT----- 599

Qy        138 aLysArgAsnProGluAlaIleThrGluValValGlnLeuProAsnHisPhe------Se 156
                    |||:::   |||                 |||:::   :::
Db        600 -------ACACCACAAAAAATTTTTACAACTCCACTAACACCAAGTCAATATTATAGTGG 652

Qy        156 rAsnArgTyr------------------TyrAsnArgLeuVal------ArgSerLeuLe 168
              ::::::|||                 ||||||:::   |||      |||      ||
Db        653 TTCCAAGTATGAAGATCTAAAAGAAAAATATAATAAAGAGGTTGAAGAACGAAAAAGATT 712

Qy        168 uGluCysAspGluAspThrValSerThrIleArgAspSerLeuMetGluLysIleGlyPr 188
              ||||   :::
Db        713 AGAGGCAGAG---------------------------------------------------- 722

Qy        188 oAsnMetAlaSerLeuPheHisIleLeuGlnThrAspHisCysAlaGlnThrHisProAr 208
                                 ||||||          :::||||||   |||::
Db        723 ----------------GTTAAAGCCTTGCAGGCTAAAAAAGCAAGCCAGACTCTTCCACA 766

Qy        208 gAlaAspPheAsnArgArgArgThrAsnGluProGlnLysLeuLysValLeuLeuArgAs 228
              :|||      |||   |||                |||          :::
Db        767 AGCCACCATGAATCACCGCGACATTGCCCGGCATCAGGCTTCATCATCTGTGTTCTCA-- 824

Qy        228 nLeuArgGlyGluGluAspSerProSerHisIleLysArgThrSerHisGluSer 246
                    :::|||   :::|||||||||:::          |||      :::
Db        825 ----TGGCAGCAAGAGAAGACCCCAAGTCATCTTTCATCTAATTCTCAAAGAACT 875

RESULT 13
PCT-US95-16216-2
```

```
; Sequence 2, Application PC/TUS9516216
; GENERAL INFORMATION:
;   APPLICANT:  Yen, Timothy J.
;   APPLICANT:  Rattner, Jerome B.
;   TITLE OF INVENTION:  Nucleic Acid Encoding a Transiently
;   TITLE OF INVENTION:  Expressed Kinetochore Protein, and Methods of Use
;   NUMBER OF SEQUENCES:  4
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE:  Dann, Dorfman, Herrell and Skillman
;     STREET:  1601 Market Street   Suite 720
;     CITY:  Philadelphia
;     STATE:  PA
;     COUNTRY:  USA
;     ZIP:  19103-2307
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE:  Floppy disk
;     COMPUTER:  IBM PC compatible
;     OPERATING SYSTEM:  PC-DOS/MS-DOS
;     SOFTWARE:  PatentIn Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER:  PCT/US95/16216
;     FILING DATE:
;     CLASSIFICATION:
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER:  US 08/353,700
;     FILING DATE:  09-DEC-1995
;   ATTORNEY/AGENT INFORMATION:
;     NAME:  Reed, Janet E.
;     REGISTRATION NUMBER:  36,252
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE:  (215) 563-4100
;     TELEFAX:  (215) 563-4044
;  INFORMATION FOR SEQ ID NO:  2:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH:  10136 base pairs
;     TYPE:  nucleic acid
;     STRANDEDNESS:  double
;     TOPOLOGY:  linear
;   MOLECULE TYPE:  DNA (genomic)
;   HYPOTHETICAL:  NO
;   ANTI-SENSE:  NO
PCT-US95-16216-2

Alignment Scores:
Pred. No.:              12.7          Length:         10136
Score:                  84.00         Matches:        61
Percent Similarity:     34.41%        Conservative:   35
Best Local Similarity:  21.86%        Mismatches:     110
Query Match:            6.62%         Indels:         73
DB:                     5             Gaps:           11

US-09-705-500A-3 (1-247) x PCT-US95-16216-2 (1-10136)

Qy         11 LeuValIleSerAlaSerAlaThrHisGluAlaGluGlnAsnAspSerValSerProArg 30
              |||      :::             :::||||||||||||:::          |||
Db        131 TTATTTACAAATGTTGGAGTAATAAAGAAGGCAGAACAAAATGAGCTGGGCTTTGGAAGA 190

Qy         31 LysSerArgValAlaAla---GlnAsnSerAlaGluValValArgCysLeuAsnSerAla 49
                 |||   ||||||   :::||||||:::|||      |||         :::|||
Db        191 ATGGAAAGAAGGGCTGCCTACAAGAACTCTTCAGAAAATTCAAGAGCTTGAAGGACAGCT 250

Qy         50 LeuGlnVal-----------------------------------------------GlyCys 54
              |||                                                      ||||||
Db        251 TGACAAACTGAAGAAGGAAAAGCAGCAAAGGCAGTTTCAGCTTGACAGTCTCGAGGCTGC 310

Qy         55 GlyAlaPheAlaCysLeuGluAsn-SerThrCysAspThrAspGly-------------- 69
              |||   |||      |||              |||:::|||
Db        311 GCCGCAGAAGCAAACACAGAAGGTTGAAAATGAAAAAACCGAGGGTACAAACCTGAAAAG 370

Qy         70 ------------MetTyrAspIleCysLysSerPheLeuTyrSerAlaAlaLysPheAs 85
                        :::   :::||||||:::|||         :::      |||
Db        371 GGAGAATCAAAGATTGATGGAAATATGTGAAAGTCTGGAGAAAACTAAGCAGAAGATTTC 430
```

```
Qy         85 pThrGlnGlyLysAlaPheValLysGluSerLeuLysCysIleAlaAsnGlyValThrSe 105
Db        431 TCATGAACTTCAA------GTCAAGGAGTCACAAGTGAATTTCCAGGAAGGACAACTGAA 484

Qy        105 r--------------------LysValPheLeuAlaIleArgArgCysSerThrPheGl 118
Db        485 TTCAGGCAAAAAACAAATAGAAAAACTGGAACAGGAACTTAAAAGGTGTAAATCTGAGCT 544

Qy        118 nArgMetIleAlaGluValGlnGluGluCysTyrSerLysLeuAsnValCysSerIleAl 138
Db        545 TGAAAGAAGCCAACAAGCTGCGCAGTCTGCAGATGTCTCTCTGAATCCATGCAAT----- 599

Qy        138 aLysArgAsnProGluAlaIleThrGluValValGlnLeuProAsnHisPhe------Se 156
Db        600 -------ACACCACAAAAAATTTTTACAACTCCACTAACACCAAGTCAATATTATAGTGG 652

Qy        156 rAsnArgTyr------------------TyrAsnArgLeuVal------ArgSerLeuLe 168
Db        653 TTCCAAGTATGAAGATCTAAAAGAAAAATATAATAAAGAGGTTGAAGAACGAAAAAGATT 712

Qy        168 uGluCysAspGluAspThrValSerThrIleArgAspSerLeuMetGluLysIleGlyPr 188
Db        713 AGAGGCAGAG---------------------------------------------------- 722

Qy        188 oAsnMetAlaSerLeuPheHisIleLeuGlnThrAspHisCysAlaGlnThrHisProAr 208
Db        723 ---------------GTTAAAGCCTTGCAGGCTAAAAAAGCAAGCCAGACTCTTCCACA 766

Qy        208 gAlaAspPheAsnArgArgArgThrAsnGluProGlnLysLeuLysValLeuLeuArgAs 228
Db        767 AGCCACCATGAATCACCGCGACATTGCCCGGCATCAGGCTTCATCATCTGTGTTCTCA-- 824

Qy        228 nLeuArgGlyGluGluAspSerProSerHisIleLysArgThrSerHisGluSer 246
Db        825 ----TGGCAGCAAGAGAAGACCCCAAGTCATCTTTCATCTAATTCTCAAAGAACT 875
```

RESULT 14
US-09-134-001C-973
; Sequence 973, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC-007
; CURRENT APPLICATION NUMBER: US/09/134,001C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 973
; LENGTH: 1254
; TYPE: DNA
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-973

Alignment Scores:

Pred. No.:	0.663	Length:	1254
Score:	83.00	Matches:	44
Percent Similarity:	38.97%	Conservative:	32
Best Local Similarity:	22.56%	Mismatches:	57
Query Match:	6.55%	Indels:	62
DB:	4	Gaps:	11

US-09-705-500A-3 (1-247) x US-09-134-001C-973 (1-1254)

```
Qy         57 PheAlaCysLeuGluAsnSerThrCysAspThrAsp--------------GlyMetTyr 71
Db        796 TTTATTAAATTTGAAGAAGCTACAATTGAAACTGATCATACATCTAAACAAGGACTTTAT 855

Qy         72 AspIleCysLysSerPheLeuTyrSerAlaAlaLysPheAspThrGlnGlyLysAlaPhe 91
Db        856 GATGTTATTCAATCTTTT---------AAAGATAAAGTAAGAACTGAAGGGAAATCATTT 906

Qy         92 ValLysGluSerLeuLysCysIleAlaAsnGlyValThrSerLysValPheLeuAlaIle 111
Db        907 TATAGATTGAACGTACGC--------------ATTAATAGTGAAGACATTATTGCACCA 951

Qy        112 ArgArgCysSerThrPheGlnArgMetIleAlaGluValGlnGluGluCysTyrSerLys 131
Db        952 CAAGATTTAATTCAATTAAAAGAAATGATTACTGAGTTCGAAGAAAAC------------ 999

Qy        132 LeuAsnValCysSerIleAlaLysArgAsnProGluAlaIleThrGluValValGlnLeu 151
Db        999 ------------------------------------------------------------ 999

Qy        152 ProAsnHisPheSerAsnArgTyrTyrAsnArgLeuValArgSerLeuLeuGluCysAsp 171
Db       1000 GAAAATCAATTTGTT------TTTATTGAAGATTTAAATCTTCAATATGTTCAAAATGAC 1053

Qy        172 GluAspThrValSerThrIleArgAspSerLeuMetGluLysIleGlyProAsnMet--- 190
Db       1054 GAAATGCCAATA--------------------GTTAAAGAGTTTTCACCAGAATTACTT 1092

Qy        191 ------AlaSerLeuPheHisIleLeuGlnThrAspHisCysAlaGlnThrHisProArg 208
Db       1093 GATGATGCGTCACTTTTTGATTCGGCAATGACTGAT------TTATATCTTAATCCAAGG 1146

Qy        209 Ala---------------AspPheAsnArg------------ArgArgThrAsnGluPro 219
Db       1147 GCTTCTAAGTTTTTAGATGACTATAATGAATTTGATAAAGTTGAGTTAGTCAATCATGCA 1206

Qy        220 GlnLysLeuLysValLeuLeuArgAsnLeuArgGlyGluGluAsp 234
Db       1207 GAAAGACTT------TTAAAGGATGAAATGAGAGGTGAACAAAAT 1245
```

RESULT 15
US-09-134-001C-1833
; Sequence 1833, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC-007
; CURRENT APPLICATION NUMBER: US/09/134,001C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 1833
; LENGTH: 1089
; TYPE: DNA
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-1833

Alignment Scores:

Pred. No.:	0.715	Length:	1089
Score:	82.00	Matches:	54
Percent Similarity:	36.96%	Conservative:	48
Best Local Similarity:	19.57%	Mismatches:	106
Query Match:	6.47%	Indels:	68
DB:	4	Gaps:	13

US-09-705-500A-3 (1-247) x US-09-134-001C-1833 (1-1089)

```
Qy          5 SerAlaValLeuLeuValLeu---ValIleSerAlaSerAlaThr--------------- 18
Db         94 AGTGCATTAACATTGGCACTCTATTTATTTAACAGTAACGTAACTGTGTATGCGGATGAA 153

Qy         19 HisGluAlaGluGlnAsnAspSerValSerProArgLysSerArgValAlaAlaGlnAsn 38
```

```
Db        154 AATACTGCAAACCAAAATCAAGGAACATCACCAAAAATTTCACAGACAGCACCTACAAAT 213

Qy         39 SerAlaGluValValArgCysLeuAsnSerAlaLeuGlnValGlyCysGlyAlaPheAla 58

Db        214 AATACTGAA-------------------------AATACAGATGCCACAGCCATAACA 246

Qy         59 CysLeuGluAsnSerThrCysAspThr------AspGlyMetTyrAspIleCysLysSer 76

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Qy         77 PheLeuTyrSerAlaAlaLysPheAspThrGlnGlyLysAlaPheValLysGluSerLeu 96

Db        301 ATTCTTTATGTAACTGTCTGGCTAGATGATCAAGGAAAT---ATTATTAAAGATGCTGTG 357

Qy         97 Lys------------------------------------------------------- 97

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Db        418 TATAGAACTTCTGTGAGTGACGGAATTACTAAGTTTATTTAT---------CGTAAAATT 468

Qy        115 SerThrPheGlnArgMetIleAlaGluValGlnGluGluCysTyrSerLysLeuAsnVal 134

Db        469 AGCACTGCACAATCACCTATAGTTGAAAATAATCAACAAGATAATAATACAAATAAAGTT 528

Qy        135 CysSerIleAlaLysArgAsnProGluAlaIleThrGluValValGlnLeuProAsnHis 154

Db        529 GTTGAAACAACCAATCAAAATAAAGATGAAGTGAATGGAAAAGAACAA------AATCAA 582

Qy        155 PheSerAsnArgTyrTyrAsnArgLeuValArgSerLeuLeuGluCysAspGluAspThr 174

Db        583 GCAAATACTTCAGTAACAAATACACAAATT---ACCAAAAACGAGAAAGACGAAGACACA 639

Qy        175 ValSerThrIleArgAspSerLeuMetGluLysIleGlyProAsnMetAlaSerLeuPhe 194

Db        640 ---AAAACACTAAAGAAAGATAAAGATGAGAAAGAATCTAAAGACACAAAAACA------ 690

Qy        195 HisIleLeuGlnThrAspHisCysAlaGlnThrHisProArgAlaAspPheAsnArgArg 214

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Qy        215 ArgThrAsnGluPro--------------GlnLysLeuLysValLeuLeuArgAsnLeu 229

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Qy        230 ArgGlyGluGluAspSerProSerHisIleLysArgThrSerHisGlu 245

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GenCore version 5.1.6

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Run on: June 12, 2003, 20:50:19 ; Search time 142 Seconds
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Title: US-09-705-500A-3
Perfect score: 1268
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Searched: 870385 seqs, 699768693 residues

Total number of hits satisfying chosen parameters: 1740770

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	1268	100.0	1283	10	US-09-840-989A-1	Sequence 1, Appli
3	1268	100.0	3765	12	US-10-044-090-638	Sequence 638, App
4	1268	100.0	3897	9	US-10-198-846-13651	Sequence 13651, A
5	1250	98.6	2572	10	US-09-925-300-486	Sequence 486, App
6	861	67.9	585	10	US-09-778-320-149	Sequence 149, App
7	861	67.9	585	10	US-09-910-689-149	Sequence 149, App
8	861	67.9	585	12	US-10-010-742-149	Sequence 149, App
c 9	689	54.3	473	9	US-10-060-036-2677	Sequence 2677, Ap
10	508	40.1	420	10	US-09-778-320-141	Sequence 141, App
11	508	40.1	420	10	US-09-910-689-141	Sequence 141, App
12	508	40.1	420	12	US-10-010-742-141	Sequence 141, App
13	396	31.2	436	9	US-09-918-995-33032	Sequence 33032, A
c 14	370	29.2	219	10	US-09-864-761-21309	Sequence 21309, A
15	354	27.9	2759	9	US-10-198-846-9993	Sequence 9993, Ap
16	354	27.9	4173	9	US-10-071-766-128	Sequence 128, App
17	352	27.8	892	10	US-09-361-736-1	Sequence 1, Appli
c 18	214	16.9	362	10	US-09-864-761-4563	Sequence 4563, Ap
19	95	7.5	4420	9	US-09-986-234-5	Sequence 5, Appli
20	91	7.2	4348	9	US-09-828-062-5	Sequence 5, Appli
21	90	7.1	1384	9	US-09-983-802-142	Sequence 142, App
c 22	86.5	6.8	1383	9	US-09-764-891-9703	Sequence 9703, Ap
c 23	86	6.8	1536	10	US-09-734-569-169	Sequence 169, App
c 24	84.5	6.7	591	10	US-09-734-569-119	Sequence 119, App
25	84	6.6	10096	10	US-09-960-253-163	Sequence 163, App
26	83	6.5	3574	10	US-09-962-832-241	Sequence 241, App
27	83	6.5	4386	9	US-10-198-846-9921	Sequence 9921, Ap
28	82.5	6.5	5204	9	US-09-938-842A-1432	Sequence 1432, Ap
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30	81	6.4	2160	10	US-09-419-305-5	Sequence 5, Appli
31	81	6.4	249487	9	US-10-026-188-3	Sequence 3, Appli
32	80	6.3	1067	9	US-10-198-846-13438	Sequence 13438, A
c 33	79	6.2	1690	9	US-10-115-928-27	Sequence 27, Appl
34	78	6.2	185695	9	US-10-020-141-11	Sequence 11, Appl
35	78	6.2	185695	9	US-10-017-721-1	Sequence 1, Appli
c 36	78	6.2	640681	10	US-09-790-988-1	Sequence 1, Appli
c 37	77.5	6.1	1392	9	US-09-938-842A-781	Sequence 781, App
38	77.5	6.1	1944	9	US-10-102-806-54	Sequence 54, Appl
c 39	77.5	6.1	4120	10	US-09-070-927A-473	Sequence 473, App
c 40	77	6.1	7359	9	US-10-092-154-1376	Sequence 1376, Ap
c 41	77	6.1	7359	9	US-10-092-154-1377	Sequence 1377, Ap
c 42	77	6.1	7359	10	US-09-764-847-1376	Sequence 1376, Ap
c 43	77	6.1	7359	10	US-09-764-847-1377	Sequence 1377, Ap
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ALIGNMENTS

RESULT 1
US-10-116-051-1
; Sequence 1, Application US/10116051
; Patent No. US20020146791A1
; GENERAL INFORMATION:
; APPLICANT: Olsen et al.
; TITLE OF INVENTION: CORPUSCLES OF STANNIUS PROTEIN, STANNIOCALCIN
; FILE REFERENCE: PF108P1D1C1
; CURRENT APPLICATION NUMBER: US/10/116,051
; CURRENT FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: 09/312,610
; PRIOR FILING DATE: 1999-05-17
; PRIOR APPLICATION NUMBER: 08/431,117
; PRIOR FILING DATE: 1995-04-28
; PRIOR APPLICATION NUMBER: 08/208,005
; PRIOR FILING DATE: 1994-03-08
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 771
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-116-051-1

Alignment Scores:
Pred. No.: 4.16e-169 Length: 771
Score: 1268.00 Matches: 247
Percent Similarity: 100.00% Conservative: 0

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Best Local Similarity:  100.00%        Mismatches:     0
Query Match:            100.00%        Indels:         0
DB:                     12             Gaps:           0

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Qy         21 AlaGluGlnAsnAspSerValSerProArgLysSerArgValAlaAlaGlnAsnSerAla 40
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Qy         61 GluAsnSerThrCysAspThrAspGlyMetTyrAspIleCysLysSerPheLeuTyrSer 80
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Qy         81 AlaAlaLysPheAspThrGlnGlyLysAlaPheValLysGluSerLeuLysCysIleAla 100
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Qy        121 IleAlaGluValGlnGluGluCysTyrSerLysLeuAsnValCysSerIleAlaLysArg 140
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RESULT 2
US-09-840-989A-1
; Sequence 1, Application US/09840989A
; Patent No. US20020042372A1
; GENERAL INFORMATION:
;  APPLICANT: Olsen et al.
;  TITLE OF INVENTION: Stanniocalcin Polynucleotides, Polypeptides, and Methods Based Th
;  FILE REFERENCE: PF108P2
;  CURRENT APPLICATION NUMBER: US/09/840,989A
;  CURRENT FILING DATE:  2001-04-25
;  PRIOR APPLICATION NUMBER: PCT/US00/29432
;  PRIOR FILING DATE: 2000-10-26
;  PRIOR APPLICATION NUMBER: US 60/161,740
;  PRIOR FILING DATE: 1999-10-27
;  NUMBER OF SEQ ID NOS: 12
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
;  LENGTH: 1283
;  TYPE: DNA
;  ORGANISM: Homo sapiens
;  FEATURE:
;  NAME/KEY: CDS
;  LOCATION: (45)..(788)
;  OTHER INFORMATION:
;  NAME/KEY: misc_feature
;  LOCATION: (857)..(857)
;  OTHER INFORMATION: n is equal to a, t, c, or g.
;  NAME/KEY: misc_feature
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;  OTHER INFORMATION: n is equal to a, t, c, or g.
US-09-840-989A-1

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Score:                  1268.00        Matches:        247
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US-09-705-500A-3 (1-247) x US-09-840-989A-1 (1-1283)

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Qy         61 GluAsnSerThrCysAspThrAspGlyMetTyrAspIleCysLysSerPheLeuTyrSer 80
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Qy        241 ArgThrSerHisGluSerAla 247
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Db        765 CGCACATCCCATGAGAGTGCA 785

RESULT 3
US-10-044-090-638
; Sequence 638, Application US/10044090
; Patent No. US20020137081A1
; GENERAL INFORMATION:
;  APPLICANT: Olga Bandman
;  TITLE OF INVENTION: GENES DIFFERENTIALLY EXPRESSED IN VASCULAR TISSUE ACTIVATION
;  FILE REFERENCE: PA-0028 US
;  CURRENT APPLICATION NUMBER: US/10/044,090
;  CURRENT FILING DATE:  2002-01-09
;  NUMBER OF SEQ ID NOS: 850
;  SOFTWARE: PERL Program
; SEQ ID NO 638
;   LENGTH: 3765
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: Incyte ID No. US20020137081A1 331181.1
;   NAME/KEY: unsure
;   LOCATION: 2378, 3184, 3187, 3194
;   OTHER INFORMATION: a, t, c, g, or other
US-10-044-090-638

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Pred. No.:              5.98e-168      Length:          3765
Score:                  1268.00        Matches:         247
Percent Similarity:     100.00%        Conservative:    0
Best Local Similarity:  100.00%        Mismatches:      0
Query Match:            100.00%        Indels:          0
DB:                     12             Gaps:            0

US-09-705-500A-3 (1-247) x US-10-044-090-638 (1-3765)

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Qy         41 GluValValArgCysLeuAsnSerAlaLeuGlnValGlyCysGlyAlaPheAlaCysLeu 60
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Qy         61 GluAsnSerThrCysAspThrAspGlyMetTyrAspIleCysLysSerPheLeuTyrSer 80
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Db        354 GAAAACTCCACCTGTGACACAGATGGGATGTATGACATCTGTAAATCCTTCTTGTACAGC 413

Qy         81 AlaAlaLysPheAspThrGlnGlyLysAlaPheValLysGluSerLeuLysCysIleAla 100
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Db        534 ATTGCTGAGGTGCAGGAAGAGTGCTACAGCAAGCTGAATGTGTGCAGCATCGCCAAGCGG 593

Qy        141 AsnProGluAlaIleThrGluValValGlnLeuProAsnHisPheSerAsnArgTyrTyr 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db        594 AACCCTGAAGCCATCACTGAGGTCGTCCAGCTGCCCAATCACTTCTCCAACAGATACTAT 653

Qy        161 AsnArgLeuValArgSerLeuGluCysAspGluAspThrValSerThrIleArgAsp 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        654 AACAGACTTGTCCGAAGCCTGCTGGAATGTGATGAAGACACAGTCAGCACAATCAGAGAC 713

Qy        181 SerLeuMetGluLysIleGlyProAsnMetAlaSerLeuPheHisIleLeuGlnThrAsp 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        714 AGCCTGATGGAGAAAATTGGGCCTAACATGGCCAGCCTCTTCCACATCCTGCAGACAGAC 773

Qy        201 HisCysAlaGlnThrHisProArgAlaAspPheAsnArgArgArgThrAsnGluProGln 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        774 CACTGTGCCCAAACACACCCACGAGCTGACTTCAACAGGAGACGCACCAATGAGCCGCAG 833

Qy        221 LysLeuLysValLeuLeuArgAsnLeuArgGlyGluGluAspSerProSerHisIleLys 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        834 AAGCTGAAAGTCCTCCTCAGGAACCTCCGAGGTGAGGAGGACTCTCCCTCCCACATCAAA 893

Qy        241 ArgThrSerHisGluSerAla 247
              |||||||||||||||||||||
Db        894 CGCACATCCCATGAGAGTGCA 914

RESULT 4
US-10-198-846-13651
; Sequence 13651, Application US/10198846
; Publication No. US20030099974A1
; GENERAL INFORMATION:
;  APPLICANT: Lillie, James
;  APPLICANT:  Xu, Yongyao
;  APPLICANT:  Wang, Youzhen
;  APPLICANT:  Steinmann, Kathleen
;  TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS
;  TITLE OF INVENTION:  FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
;  TITLE OF INVENTION:  THERAPY OF BREAST CANCER
;  FILE REFERENCE: MRI-049
;  CURRENT APPLICATION NUMBER: US/10/198,846
;  CURRENT FILING DATE:  2002-07-18
;  PRIOR APPLICATION NUMBER: 60/306,220
;  PRIOR FILING DATE: 2001-07-18
;  NUMBER OF SEQ ID NOS: 14084
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 13651
;   LENGTH: 3897
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: 3878, 3879, 3880, 3881, 3882, 3883, 3884, 3885, 3886, 3887,
;   LOCATION: 3888, 3889, 3890, 3891, 3892, 3893, 3894, 3895, 3896, 3897
;   OTHER INFORMATION: n = A,T,C or G
US-10-198-846-13651

Alignment Scores:
Pred. No.:              6.34e-168      Length:          3897
Score:                  1268.00        Matches:         247
Percent Similarity:     100.00%        Conservative:    0
Best Local Similarity:  100.00%        Mismatches:      0
Query Match:            100.00%        Indels:          0
DB:                     9              Gaps:            0

US-09-705-500A-3 (1-247) x US-10-198-846-13651 (1-3897)

Qy          1 MetLeuGlnAsnSerAlaValLeuLeuValLeuValIleSerAlaSerAlaThrHisGlu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        285 ATGCTCCAAAACTCAGCAGTGCTTCTGGTGCTGGTGATCAGTGCTTCTGCAACCCATGAG 344

Qy         21 AlaGluGlnAsnAspSerValSerProArgLysSerArgValAlaAlaGlnAsnSerAla 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        345 GCGGAGCAGAATGACTCTGTGAGCCCCAGGAAATCCCGAGTGGCGGCTCAAAACTCAGCT 404

Qy         41 GluValValArgCysLeuAsnSerAlaLeuGlnValGlyCysGlyAlaPheAlaCysLeu 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        405 GAAGTGGTTCGTTGCCTCAACAGTGCTCTACAGGTCGGCTGCGGGGCTTTTGCATGCCTG 464
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Qy         61 GluAsnSerThrCysAspThrAspGlyMetTyrAspIleCysLysSerPheLeuTyrSer 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        465 GAAAACTCCACCTGTGACACAGATGGGATGTATGACATCTGTAAATCCTTCTTGTACAGC 524

Qy         81 AlaAlaLysPheAspThrGlnGlyLysAlaPheValLysGluSerLeuLysCysIleAla 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        525 GCTGCTAAATTTGACACTCAGGGAAAAGCATTCGTCAAAGAGAGCTTAAAATGCATCGCC 584

Qy        101 AsnGlyValThrSerLysValPheLeuAlaIleArgArgCysSerThrPheGlnArgMet 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        585 AACGGGGTCACCTCCAAGGTCTTCCTCGCCATTCGGAGGTGCTCCACTTTCCAAAGGATG 644

Qy        121 IleAlaGluValGlnGluGluCysTyrSerLysLeuAsnValCysSerIleAlaLysArg 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        645 ATTGCTGAGGTGCAGGAAGAGTGCTACAGCAAGCTGAATGTGTGCAGCATCGCCAAGCGG 704

Qy        141 AsnProGluAlaIleThrGluValValGlnLeuProAsnHisPheSerAsnArgTyrTyr 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        705 AACCCTGAAGCCATCACTGAGGTCGTCCAGCTGCCCAATCACTTCTCCAACAGATACTAT 764

Qy        161 AsnArgLeuValArgSerLeuLeuGluCysAspGluAspThrValSerThrIleArgAsp 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        765 AACAGACTTGTCCGAAGCCTGCTGGAATGTGATGAAGACACAGTCAGCACAATCAGAGAC 824

Qy        181 SerLeuMetGluLysIleGlyProAsnMetAlaSerLeuPheHisIleLeuGlnThrAsp 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        825 AGCCTGATGGAGAAAATTGGGCCTAACATGGCCAGCCTCTTCCACATCCTGCAGACAGAC 884

Qy        201 HisCysAlaGlnThrHisProArgAlaAspPheAsnArgArgArgThrAsnGluProGln 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        885 CACTGTGCCCAAACACACCCACGAGCTGACTTCAACAGGAGACGCACCAATGAGCCGCAG 944

Qy        221 LysLeuLysValLeuLeuArgAsnLeuArgGlyGluGluAspSerProSerHisIleLys 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        945 AAGCTGAAAGTCCTCCTCAGGAACCTCCGAGGTGAGGAGGACTCTCCCTCCCACATCAAA 1004

Qy        241 ArgThrSerHisGluSerAla 247
              |||||||||||||||||||||
Db       1005 CGCACATCCCATGAGAGTGCA 1025

RESULT 5
US-09-925-300-486
; Sequence 486, Application US/09925300
; Patent No. US20020151681A1
; GENERAL INFORMATION:
;  APPLICANT: Craig Rosen,
;  APPLICANT:  Steve Ruben
;  TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
;  FILE REFERENCE: PA101
;  CURRENT APPLICATION NUMBER: US/09/925,300
;  CURRENT FILING DATE:  2001-08-10
;  PRIOR APPLICATION NUMBER: PCT/US00/05988
;  PRIOR FILING DATE: 2000-03-08
;  PRIOR APPLICATION NUMBER: 60/124,270
;  PRIOR FILING DATE: 1999-03-12
;  NUMBER OF SEQ ID NOS: 1890
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 486
;   LENGTH: 2572
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc feature
;   LOCATION: (823)
;   OTHER INFORMATION: n equals a,t,g, or c
US-09-925-300-486

Alignment Scores:
Pred. No.:              1.1e-165        Length:         2572
Score:                  1250.00         Matches:        246
Percent Similarity:     99.19%          Conservative:   0
Best Local Similarity:  99.19%          Mismatches:     1
Query Match:            98.58%          Indels:         1
DB:                     10              Gaps:           0

US-09-705-500A-3 (1-247) x US-09-925-300-486 (1-2572)

Qy          1 MetLeuGlnAsnSerAlaValLeuLeuValLeuValIleSerAlaSerAlaThrHisGlu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        265 ATGCTCCAAAACTCAGCAGTGCTTCTGGTGCTGGTGATCAGTGCTTCTGCAACCCATGAG 324

Qy         21 AlaGluGlnAsnAspSerValSerProArgLysSerArgValAlaAlaGlnAsnSerAla 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        325 GCGGAGCAGAATGACTCTGTGAGCCCCAGGAAATCCCGAGTGGCGGCTCAAAACTCAGCT 384

Qy         41 GluValValArgCysLeuAsnSerAlaLeuGlnValGlyCysGlyAlaPheAlaCysLeu 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        385 GAAGTGGTTCGTTGCCTCAACAGTGCTCTACAGGTCGGCTGCGGGGCTTTTGCATGCCTG 444

Qy         61 GluAsnSerThrCysAspThrAspGlyMetTyrAspIleCysLysSerPheLeuTyrSer 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        445 GAAAACTCCACCTGTGACACAGATGGGATGTATGACATCTGTAAATCCTTCTTGTACAGC 504

Qy         81 AlaAlaLysPheAspThrGlnGlyLysAlaPheValLysGluSerLeuLysCysIleAla 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        505 GCTGCTAAATTTGACACTCAGGGAAAAGCATTCGTCAAAGAGAGCTTAAAATGCATCGCC 564

Qy        101 AsnGlyValThrSerLysValPheLeuAlaIleArgArgCysSerThrPheGlnArgMet 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        565 AACGGGGTCACCTCCAAGGTCTTCCTCGCCATTCGGAGGTGCTCCACTTTCCAAAGGATG 624

Qy        121 IleAlaGluValGlnGluGluCysTyrSerLysLeuAsnValCysSerIleAlaLysArg 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        625 ATTGCTGAGGTGCAGGAAGAGTGCTACAGCAAGCTGAATGTGTGCAGCATCGCCAAGCGG 684

Qy        141 AsnProGluAlaIleThrGluValValGlnLeuProAsnHisPheSerAsnArgTyrTyr 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        685 AACCCTGAAGCCATCACTGAGGTCGTCCAGCTGCCCAATCACTTCTCCAACAGATACTAT 744

Qy        161 AsnArgLeuValArgSerLeuLeuGluCysAspGluAspThrValSerThrIleArgAsp 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        745 AACAGACTTGTCCGAAGCCTGCTGGAATGTGATGAAGACACAGTCAGCACAATCAGAGAC 804

Qy        181 SerLeuMetGlu-LysIleGlyProAsnMetAlaSerLeuPheHisIleLeuGlnThrAs 200
              |||||||||||| |||   ||||||||||||||||||||||||||||||||||||||||
Db        805 AGCCTGATGGAGRAAATTNGGGCCTAACATGGCCAGCCTCTTCCACATCCTGCAGACAGA 864

Qy        200 pHisCysAlaGlnThrHisProArgAlaAspPheAsnArgArgArgThrAsnGluProGl 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        865 CCACTGTGCCCAAACACACCCACGAGCTGACTTCAACAGGAGACGCACCAATGAGCCGCA 924

Qy        220 nLysLeuLysValLeuLeuArgAsnLeuArgGlyGluGluAspSerProSerHisIleLy 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        925 GAAGCTGAAAGTCCTCCTCAGGAACCTCCGAGGTGAGGAGGACTCTCCCTCCCACATCAA 984

Qy        240 sArgThrSerHisGluSerAla 247
              |||||||||||||||||||||
Db        985 ACGCACATCCCATGAGAGTGCA 1006

RESULT 6
US-09-778-320-149
; Sequence 149, Application US/09778320
; Patent No. US20010034052A1
; GENERAL INFORMATION:
;  APPLICANT:  Dillon, Davin C.
;  APPLICANT:  Day, Craig H.
;  APPLICANT:  Jiang, Yuqiu
;  APPLICANT:  Houghton, Raymond L.
;  APPLICANT:  Mitcham, Jennifer
;  APPLICANT:  Wang, TongTong
;  APPLICANT:  McNeill, Patricia D.
;  TITLE OF INVENTION:  COMPOSITIONS AND METHODS FOR THE THERAPY AND
;  TITLE OF INVENTION:  DIAGNOSIS OF BREAST CANCER
;  FILE REFERENCE:  210121.491C5
;  CURRENT APPLICATION NUMBER: US/09/778,320
```

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;  CURRENT FILING DATE:  2001-02-06
;  NUMBER OF SEQ ID NOS:  301
;  SOFTWARE:  FastSEQ for Windows Version 3.0
; SEQ ID NO 149
;   LENGTH: 585
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(585)
;   OTHER INFORMATION: n=A,T,C or G
US-09-778-320-149

Alignment Scores:
Pred. No.:              8.3e-112      Length:         585
Score:                  861.00        Matches:        166
Percent Similarity:     98.22%        Conservative:   0
Best Local Similarity:  98.22%        Mismatches:     3
Query Match:            67.90%        Indels:         0
DB:                     10            Gaps:           0

US-09-705-500A-3 (1-247) x US-09-778-320-149 (1-585)

Qy         79 TyrSerAlaAlaLysPheAspThrGlnGlyLysAlaPheValLysGluSerLeuLysCys 98
              |||      |||||||||||||||   |||||||||||||||||||||||||||||||||
Db          6 TACANCACTGCTAAATTTGACACTNANGGAAAAGCATTCGTCAAAGAGAGCTTAAAATGC 65

Qy         99 IleAlaAsnGlyValThrSerLysValPheLeuAlaIleArgArgCysSerThrPheGln 118
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         66 ATCGCCAACGGGGTCACCTCCAAGGTCTTCCTCGCCATTCGGAGGTGCTCCACTTTCCAA 125

Qy        119 ArgMetIleAlaGluValGlnGluGluCysTyrSerLysLeuAsnValCysSerIleAla 138
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        126 AGGATGATTGCTGAGGTGCAGGAAGAGTGCTACAGCAAGCTGAATGTGTGCAGCATCGCC 185

Qy        139 LysArgAsnProGluAlaIleThrGluValValGlnLeuProAsnHisPheSerAsnArg 158
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        186 AAGCGGAACCCTGAAGCCATCACTGAGGTCGTCCAGCTGCCCAATCACTTCTCCAACAGA 245

Qy        159 TyrTyrAsnArgLeuValArgSerLeuLeuGluCysAspGluAspThrValSerThrIle 178
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        246 TACTATAACAGACTTGTCCGAAGCCTGCTGGAATGTGATGAAGACACAGTCAGCACAATC 305

Qy        179 ArgAspSerLeuMetGluLysIleGlyProAsnMetAlaSerLeuPheHisIleLeuGln 198
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        306 AGAGACAGCCTGATGGAGAAAATTGGGCCTAACATGGCCAGCCTCTTCCACATCCTGCAG 365

Qy        199 ThrAspHisCysAlaGlnThrHisProArgAlaAspPheAsnArgArgArgThrAsnGlu 218
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        366 ACAGACCACTGTGCCCAAACACACCCACGAGCTGACTTCAACAGGAGACGCACCAATGAG 425

Qy        219 ProGlnLysLeuLysValLeuLeuArgAsnLeuArgGlyGluGluAspSerProSerHis 238
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        426 CCGCAGAAGCTGAAAGTCCTCCTCAGGAACCTCCGAGGTGAGGAGGACTCTCCCTCCCAC 485

Qy        239 IleLysArgThrSerHisGluSerAla 247
              |||||||||||||||||||||||||||
Db        486 ATCAAACGCACATCCCATGAGAGTGCA 512

RESULT 7
US-09-910-689-149
; Sequence 149, Application US/09910689
; Patent No. US20020081609A1
; GENERAL INFORMATION:
;  APPLICANT: Dillon, Davin C.
;  APPLICANT:  Day, Craig H.
;  APPLICANT:  Jiang, Yuqiu
;  APPLICANT:  Houghton, Raymond L.
;  APPLICANT:  Mitcham, Jennifer
;  APPLICANT:  Wang, Tongtong
;  APPLICANT:  McNeill, Patricia D.
;  APPLICANT:  Harlocker, Susan L.
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
;  TITLE OF INVENTION:  DIAGNOSIS OF BREAST CANCER
;  FILE REFERENCE: 210121.491C6
;  CURRENT APPLICATION NUMBER: US/09/910,689
;  CURRENT FILING DATE:  2001-07-20
;  NUMBER OF SEQ ID NOS: 307
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 149
;   LENGTH: 585
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: 10, 30, 32, 527, 565
;   OTHER INFORMATION: n = A,T,C or G
US-09-910-689-149

Alignment Scores:
Pred. No.:              8.3e-112      Length:         585
Score:                  861.00        Matches:        166
Percent Similarity:     98.22%        Conservative:   0
Best Local Similarity:  98.22%        Mismatches:     3
Query Match:            67.90%        Indels:         0
DB:                     10            Gaps:           0

US-09-705-500A-3 (1-247) x US-09-910-689-149 (1-585)

Qy         79 TyrSerAlaAlaLysPheAspThrGlnGlyLysAlaPheValLysGluSerLeuLysCys 98
              |||      |||||||||||||||   |||||||||||||||||||||||||||||||||
Db          6 TACANCACTGCTAAATTTGACACTNANGGAAAAGCATTCGTCAAAGAGAGCTTAAAATGC 65

Qy         99 IleAlaAsnGlyValThrSerLysValPheLeuAlaIleArgArgCysSerThrPheGln 118
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         66 ATCGCCAACGGGGTCACCTCCAAGGTCTTCCTCGCCATTCGGAGGTGCTCCACTTTCCAA 125

Qy        119 ArgMetIleAlaGluValGlnGluGluCysTyrSerLysLeuAsnValCysSerIleAla 138
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        126 AGGATGATTGCTGAGGTGCAGGAAGAGTGCTACAGCAAGCTGAATGTGTGCAGCATCGCC 185

Qy        139 LysArgAsnProGluAlaIleThrGluValValGlnLeuProAsnHisPheSerAsnArg 158
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        186 AAGCGGAACCCTGAAGCCATCACTGAGGTCGTCCAGCTGCCCAATCACTTCTCCAACAGA 245

Qy        159 TyrTyrAsnArgLeuValArgSerLeuLeuGluCysAspGluAspThrValSerThrIle 178
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        246 TACTATAACAGACTTGTCCGAAGCCTGCTGGAATGTGATGAAGACACAGTCAGCACAATC 305

Qy        179 ArgAspSerLeuMetGluLysIleGlyProAsnMetAlaSerLeuPheHisIleLeuGln 198
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        306 AGAGACAGCCTGATGGAGAAAATTGGGCCTAACATGGCCAGCCTCTTCCACATCCTGCAG 365

Qy        199 ThrAspHisCysAlaGlnThrHisProArgAlaAspPheAsnArgArgArgThrAsnGlu 218
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        366 ACAGACCACTGTGCCCAAACACACCCACGAGCTGACTTCAACAGGAGACGCACCAATGAG 425

Qy        219 ProGlnLysLeuLysValLeuLeuArgAsnLeuArgGlyGluGluAspSerProSerHis 238
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        426 CCGCAGAAGCTGAAAGTCCTCCTCAGGAACCTCCGAGGTGAGGAGGACTCTCCCTCCCAC 485

Qy        239 IleLysArgThrSerHisGluSerAla 247
              |||||||||||||||||||||||||||
Db        486 ATCAAACGCACATCCCATGAGAGTGCA 512

RESULT 8
US-10-010-742-149
; Sequence 149, Application US/10010742
; Patent No. US20020146727A1
; GENERAL INFORMATION:
;  APPLICANT: Dillon, Davin C.
;  APPLICANT:  Day, Craig H.
;  APPLICANT:  Jiang, Yuqiu
;  APPLICANT:  Houghton, Raymond L.
;  APPLICANT:  Mitcham, Jennifer L.
;  APPLICANT:  Wang, Tongtong
```

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;  APPLICANT:  McNeill, Patricia D.
;  APPLICANT:  Harlocker, Susan L.
;  APPLICANT:  Bennington, Angela Ann
;  APPLICANT:  Zehentner, Barbara
;  APPLICANT:  Fanger, Gary R.
;  APPLICANT:  Retter, Marc W.
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
;  TITLE OF INVENTION:  DIAGNOSIS OF BREAST CANCER
;  FILE REFERENCE: 210121.491C7
;  CURRENT APPLICATION NUMBER: US/10/010,742
;  CURRENT FILING DATE:  2001-11-30
;  NUMBER OF SEQ ID NOS: 307
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 149
;   LENGTH: 585
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: 10, 30, 32, 527, 565
;   OTHER INFORMATION: n = A,T,C or G
US-10-010-742-149

Alignment Scores:
Pred. No.:              8.3e-112        Length:         585
Score:                  861.00          Matches:        166
Percent Similarity:     98.22%          Conservative:   0
Best Local Similarity:  98.22%          Mismatches:     3
Query Match:            67.90%          Indels:         0
DB:                     12              Gaps:           0

US-09-705-500A-3 (1-247) x US-10-010-742-149 (1-585)

Qy          79 TyrSerAlaAlaLysPheAspThrGlnGlyLysAlaPheValLysGluSerLeuLysCys 98
               |||      ||||||||||||||||   ||||||||||||||||||||||||||||||||
Db           6 TACANCACTGCTAAATTTGACACTNANGGAAAAGCATTCGTCAAAGAGAGCTTAAAATGC 65

Qy          99 IleAlaAsnGlyValThrSerLysValPheLeuAlaIleArgArgCysSerThrPheGln 118
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          66 ATCGCCAACGGGGTCACCTCCAAGGTCTTCCTCGCCATTCGGAGGTGCTCCACTTTCCAA 125

Qy         119 ArgMetIleAlaGluValGlnGluGluCysTyrSerLysLeuAsnValCysSerIleAla 138
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         126 AGGATGATTGCTGAGGTGCAGGAAGAGTGCTACAGCAAGCTGAATGTGTGCAGCATCGCC 185

Qy         139 LysArgAsnProGluAlaIleThrGluValValGlnLeuProAsnHisPheSerAsnArg 158
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         186 AAGCGGAACCCTGAAGCCATCACTGAGGTCGTCCAGCTGCCCAATCACTTCTCCAACAGA 245

Qy         159 TyrTyrAsnArgLeuValArgSerLeuLeuGluCysAspGluAspThrValSerThrIle 178
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         246 TACTATAACAGACTTGTCCGAAGCCTGCTGGAATGTGATGAAGACACAGTCAGCACAATC 305

Qy         179 ArgAspSerLeuMetGluLysIleGlyProAsnMetAlaSerLeuPheHisIleLeuGln 198
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         306 AGAGACAGCCTGATGGAGAAAATTGGGCCTAACATGGCCAGCCTCTTCCACATCCTGCAG 365

Qy         199 ThrAspHisCysAlaGlnThrHisProArgAlaAspPheAsnArgArgArgThrAsnGlu 218
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         366 ACAGACCACTGTGCCCAAACACACCCACGAGCTGACTTCAACAGGAGACGCACCAATGAG 425

Qy         219 ProGlnLysLeuLysValLeuLeuArgAsnLeuArgGlyGluGluAspSerProSerHis 238
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         426 CCGCAGAAGCTGAAAGTCCTCCTCAGGAACCTCCGAGGTGAGGAGGACTCTCCCTCCCAC 485

Qy         239 IleLysArgThrSerHisGluSerAla 247
               |||||||||||||||||||||||||||
Db         486 ATCAAACGCACATCCCATGAGAGTGCA 512

RESULT 9
US-10-060-036-2677/c
; Sequence 2677, Application US/10060036
; Publication No. US20030073144A1
; GENERAL INFORMATION:
;  APPLICANT: Benson, Darin R.
;  APPLICANT:  Kalos, Michael D.
;  APPLICANT:  Lodes, Michael J.
;  APPLICANT:  Persing, David H.
;  APPLICANT:  Hepler, William T.
;  APPLICANT:  Jiang, Yuqiu
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
;  TITLE OF INVENTION:  AND DIAGNOSIS OF PANCREATIC CANCER
;  FILE REFERENCE: 210121.566
;  CURRENT APPLICATION NUMBER: US/10/060,036
;  CURRENT FILING DATE:  2002-01-30
;  NUMBER OF SEQ ID NOS: 4560
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2677
;   LENGTH: 473
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-060-036-2677

Alignment Scores:
Pred. No.:              1.16e-87        Length:         473
Score:                  689.00          Matches:        132
Percent Similarity:     100.00%         Conservative:   0
Best Local Similarity:  100.00%         Mismatches:     0
Query Match:            54.34%          Indels:         0
DB:                     9               Gaps:           0

US-09-705-500A-3 (1-247) x US-10-060-036-2677 (1-473)

Qy         116 ThrPheGlnArgMetIleAlaGluValGlnGluGluCysTyrSerLysLeuAsnValCys 135
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         472 ACTTTCCAAAGGATGATTGCTGAGGTGCAGGAAGAGTGCTACAGCAAGCTGAATGTGTGC 413

Qy         136 SerIleAlaLysArgAsnProGluAlaIleThrGluValValGlnLeuProAsnHisPhe 155
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         412 AGCATCGCCAAGCGGAACCCTGAAGCCATCACTGAGGTCGTCCAGCTGCCCAATCACTTC 353

Qy         156 SerAsnArgTyrTyrAsnArgLeuValArgSerLeuLeuGluCysAspGluAspThrVal 175
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         352 TCCAACAGATACTATAACAGACTTGTCCGAAGCCTGCTGGAATGTGATGAAGACACAGTC 293

Qy         176 SerThrIleArgAspSerLeuMetGluLysIleGlyProAsnMetAlaSerLeuPheHis 195
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         292 AGCACAATCAGAGACAGCCTGATGGAGAAAATTGGGCCTAACATGGCCAGCCTCTTCCAC 233

Qy         196 IleLeuGlnThrAspHisCysAlaGlnThrHisProArgAlaAspPheAsnArgArgArg 215
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         232 ATCCTGCAGACAGACCACTGTGCCCAAACACACCCACGAGCTGACTTCAACAGGAGACGC 173

Qy         216 ThrAsnGluProGlnLysLeuLysValLeuLeuArgAsnLeuArgGlyGluGluAspSer 235
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         172 ACCAATGAGCCGCAGAAGCTGAAAGTCCTCCTCAGGAACCTCCGAGGTGAGGAGGACTCT 113

Qy         236 ProSerHisIleLysArgThrSerHisGluSerAla 247
               ||||||||||||||||||||||||||||||||||||
Db         112 CCCTCCCACATCAAACGCACATCCCATGAGAGTGCA 77

RESULT 10
US-09-778-320-141
; Sequence 141, Application US/09778320
; Patent No. US20010034052A1
; GENERAL INFORMATION:
;  APPLICANT:  Dillon, Davin C.
;  APPLICANT:  Day, Craig H.
;  APPLICANT:  Jiang, Yuqiu
;  APPLICANT:  Houghton, Raymond L.
;  APPLICANT:  Mitcham, Jennifer
;  APPLICANT:  Wang, TongTong
;  APPLICANT:  McNeill, Patricia D.
;  TITLE OF INVENTION:  COMPOSITIONS AND METHODS FOR THE THERAPY AND
;  TITLE OF INVENTION:  DIAGNOSIS OF BREAST CANCER
;  FILE REFERENCE:  210121.491C5
```

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;  CURRENT APPLICATION NUMBER: US/09/778,320
;  CURRENT FILING DATE:  2001-02-06
;  NUMBER OF SEQ ID NOS:  301
;  SOFTWARE:  FastSEQ for Windows Version 3.0
; SEQ ID NO 141
;   LENGTH: 420
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(420)
;   OTHER INFORMATION: n = A,T,C or G
US-09-778-320-141

Alignment Scores:
Pred. No.:              3.54e-62        Length:         420
Score:                  508.00          Matches:        116
Percent Similarity:     82.27%          Conservative:   0
Best Local Similarity:  82.27%          Mismatches:     19
Query Match:            40.06%          Indels:         6
DB:                     10              Gaps:           0

US-09-705-500A-3 (1-247) x US-09-778-320-141 (1-420)

Qy         85 AspThrGlnGlyLysAlaPheValLysGluSerLeuLysCysIleAlaAsnGlyValThr 104
              ||||||||||||||||||      |||   ||||||||||||||||||||||||||||||
Db          1 GACACTCAGGGAAAAGCATNNGNCAAANAGAGCTTAAAATGCATCGCCAACGGGGTCACC 60

Qy        105 SerLysValPheLeuAlaIleArgArgCysSerThrPheGlnArgMetIleAlaGluVal 124
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TCCAAGGTCTTCCTCGCCATTCGGAGGTGCTCCACTTTCCAAAGGATGATTGCTGAGGTG 120

Qy        125 GlnGluGluCysTyrSerLysLeuAsnValCysSerIleAlaLysArgAsnProGluAla 144
              ||||||||||||||||||||||||||||      ||||||||||||||||||||||||||
Db        121 CAGGAAGAGTGCTACAGCAAGCTGAATGTGCGCANCATCGCCAAGCGGAACCCNGAAGCC 180

Qy        145 IleThrGluValValGlnLeuProAsnHisPheSerAsnArgTyrTyrAsnArgLeuVal 164
              ||||||||||||||||||||||||||||||||||||   ||||||||||||||||||||
Db        181 ATCACTGAGGTCGTGCAGCTGCCCAATCACTTCTCCAACANATACTATAACAGACTTGNN 240

Qy        165 ArgSerLeuLeuGluCysAspGluAspThr-ValSerThrIleArg-AspSerLeuMetG 184
              ||||||||||||||   ||||||   |||    ||||||||||| ||||||||||||
Db        241 CGAAGCCTGCTGGAATGNGATGAANACACAGGGCAGCACAATCAGGAGACAGCCTGATGG 300

Qy        184 luLysIleGlyProAsnMetAla-SerLeuPheHisIleLeu--GlnThrAspHisCysA 203
                |||   ||||||   ||||||    ||||||||||||||     ||||||||||||
Db        301 ANAAAANTGGGCCTANCATGGCCAGGCCTCTTCCACATCCTNGCANGACAGACCACTGTG 360

Qy        203 laGlnThrHisProArg-AlaAspPheAsnArgArgArgThrAsnGluPro 219
              ||||||||||||||   ||||||      ||||||||||||   ||||||
Db        361 CCCAAACACACCCNCTGAGCTGACTTNNACAGGAGACGCACNAAGGAGCCC 411

RESULT 11
US-09-910-689-141
; Sequence 141, Application US/09910689
; Patent No. US20020081609A1
; GENERAL INFORMATION:
;  APPLICANT: Dillon, Davin C.
;  APPLICANT:  Day, Craig H.
;  APPLICANT:  Jiang, Yuqiu
;  APPLICANT:  Houghton, Raymond L.
;  APPLICANT:  Mitcham, Jennifer
;  APPLICANT:  Wang, Tongtong
;  APPLICANT:  McNeill, Patricia D.
;  APPLICANT:  Harlocker, Susan L.
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
;  TITLE OF INVENTION:  DIAGNOSIS OF BREAST CANCER
;  FILE REFERENCE: 210121.491C6
;  CURRENT APPLICATION NUMBER: US/09/910,689
;  CURRENT FILING DATE:  2001-07-20
;  NUMBER OF SEQ ID NOS: 307
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 141
;   LENGTH: 420
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: 20, 21, 23, 28, 155, 174, 221, 239, 240, 258, 265, 302, 307,
;   LOCATION: 316, 342, 346, 374, 387, 388, 402, 418
;   OTHER INFORMATION: n = A,T,C or G
US-09-910-689-141

Alignment Scores:
Pred. No.:              3.54e-62        Length:         420
Score:                  508.00          Matches:        116
Percent Similarity:     82.27%          Conservative:   0
Best Local Similarity:  82.27%          Mismatches:     19
Query Match:            40.06%          Indels:         6
DB:                     10              Gaps:           0

US-09-705-500A-3 (1-247) x US-09-910-689-141 (1-420)

Qy         85 AspThrGlnGlyLysAlaPheValLysGluSerLeuLysCysIleAlaAsnGlyValThr 104
              ||||||||||||||||||      |||   ||||||||||||||||||||||||||||||
Db          1 GACACTCAGGGAAAAGCATNNGNCAAANAGAGCTTAAAATGCATCGCCAACGGGGTCACC 60

Qy        105 SerLysValPheLeuAlaIleArgArgCysSerThrPheGlnArgMetIleAlaGluVal 124
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TCCAAGGTCTTCCTCGCCATTCGGAGGTGCTCCACTTTCCAAAGGATGATTGCTGAGGTG 120

Qy        125 GlnGluGluCysTyrSerLysLeuAsnValCysSerIleAlaLysArgAsnProGluAla 144
              ||||||||||||||||||||||||||||      ||||||||||||||||||||||||||
Db        121 CAGGAAGAGTGCTACAGCAAGCTGAATGTGCGCANCATCGCCAAGCGGAACCCNGAAGCC 180

Qy        145 IleThrGluValValGlnLeuProAsnHisPheSerAsnArgTyrTyrAsnArgLeuVal 164
              ||||||||||||||||||||||||||||||||||||   ||||||||||||||||||||
Db        181 ATCACTGAGGTCGTGCAGCTGCCCAATCACTTCTCCAACANATACTATAACAGACTTGNN 240

Qy        165 ArgSerLeuLeuGluCysAspGluAspThr-ValSerThrIleArg-AspSerLeuMetG 184
              ||||||||||||||   ||||||   |||    ||||||||||| ||||||||||||
Db        241 CGAAGCCTGCTGGAATGNGATGAANACACAGGGCAGCACAATCAGGAGACAGCCTGATGG 300

Qy        184 luLysIleGlyProAsnMetAla-SerLeuPheHisIleLeu--GlnThrAspHisCysA 203
                |||   ||||||   ||||||    ||||||||||||||     ||||||||||||
Db        301 ANAAAANTGGGCCTANCATGGCCAGGCCTCTTCCACATCCTNGCANGACAGACCACTGTG 360

Qy        203 laGlnThrHisProArg-AlaAspPheAsnArgArgArgThrAsnGluPro 219
              ||||||||||||||   ||||||      ||||||||||||   ||||||
Db        361 CCCAAACACACCCNCTGAGCTGACTTNNACAGGAGACGCACNAAGGAGCCC 411

RESULT 12
US-10-010-742-141
; Sequence 141, Application US/10010742
; Patent No. US20020146727A1
; GENERAL INFORMATION:
;  APPLICANT: Dillon, Davin C.
;  APPLICANT:  Day, Craig H.
;  APPLICANT:  Jiang, Yuqiu
;  APPLICANT:  Houghton, Raymond L.
;  APPLICANT:  Mitcham, Jennifer L.
;  APPLICANT:  Wang, Tongtong
;  APPLICANT:  McNeill, Patricia D.
;  APPLICANT:  Harlocker, Susan L.
;  APPLICANT:  Bennington, Angela Ann
;  APPLICANT:  Zehentner, Barbara
;  APPLICANT:  Fanger, Gary R.
;  APPLICANT:  Retter, Marc W.
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
;  TITLE OF INVENTION:  DIAGNOSIS OF BREAST CANCER
;  FILE REFERENCE: 210121.491C7
;  CURRENT APPLICATION NUMBER: US/10/010,742
;  CURRENT FILING DATE:  2001-11-30
;  NUMBER OF SEQ ID NOS: 307
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 141
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;   LENGTH: 420
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: 20, 21, 23, 28, 155, 174, 221, 239, 240, 258, 265, 302, 307,
;   LOCATION: 316, 342, 346, 374, 387, 388, 402, 418
;   OTHER INFORMATION: n = A,T,C or G
US-10-010-742-141

Alignment Scores:
Pred. No.:              3.54e-62        Length:         420
Score:                  508.00          Matches:        116
Percent Similarity:     82.27%          Conservative:   0
Best Local Similarity:  82.27%          Mismatches:     19
Query Match:            40.06%          Indels:         6
DB:                     12              Gaps:           0

US-09-705-500A-3 (1-247) x US-10-010-742-141 (1-420)

Qy         85 AspThrGlnGlyLysAlaPheValLysGluSerLeuLysCysIleAlaAsnGlyValThr 104
              ||||||||||||||||||    |||   ||||||||||||||||||||||||||||||
Db          1 GACACTCAGGGAAAAGCATNNGNCAAANAGAGCTTAAAATGCATCGCCAACGGGGTCACC 60

Qy        105 SerLysValPheLeuAlaIleArgArgCysSerThrPheGlnArgMetIleAlaGluVal 124
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TCCAAGGTCTTCCTCGCCATTCGGAGGTGCTCCACTTTCCAAAGGATGATTGCTGAGGTG 120

Qy        125 GlnGluGluCysTyrSerLysLeuAsnValCysSerIleAlaLysArgAsnProGluAla 144
              ||||||||||||||||||||||||||||||      ||||||||||||||||||||||
Db        121 CAGGAAGAGTGCTACAGCAAGCTGAATGTGCGCANCATCGCCAAGCGGAACCCNGAAGCC 180

Qy        145 IleThrGluValValGlnLeuProAsnHisPheSerAsnArgTyrTyrAsnArgLeuVal 164
              ||||||||||||||||||||||||||||||||||||   ||||||||||||||||
Db        181 ATCACTGAGGTCGTGCAGCTGCCCAATCACTTCTCCAACANATACTATAACAGACTTGNN 240

Qy        165 ArgSerLeuLeuGluCysAspGluAspThr-ValSerThrIleArg-AspSerLeuMetG 184
              ||||||||||||||   ||||||   |||    ||||||||||| ||||||||||||
Db        241 CGAAGCCTGCTGGAATGNGATGAANACACAGGGCAGCACAATCAGGAGACAGCCTGATGG 300

Qy        184 luLysIleGlyProAsnMetAla-SerLeuPheHisIleLeu--GlnThrAspHisCysA 203
                |||   ||||||   ||||||    ||||||||||||||     ||||||||||||
Db        301 ANAAAANTGGGCCTANCATGGCCAGGCCTCTTCCACATCCTNGCANGACAGACCACTGTG 360

Qy        203 laGlnThrHisProArg-AlaAspPheAsnArgArgArgThrAsnGluPro 219
              |||||||||||||    ||||||     ||||||||||||   ||||||
Db        361 CCCAAACACACCCNCTGAGCTGACTTNNACAGGAGACGCACNAAGGAGCCC 411

RESULT 13
US-09-918-995-33032
; Sequence 33032, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
;  APPLICANT: Hyseq, Inc.
;  TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
;  TITLE OF INVENTION:  FROM VARIOUS cDNA LIBRARIES
;  FILE REFERENCE: 20411-756
;  CURRENT APPLICATION NUMBER: US/09/918,995
;  CURRENT FILING DATE:  2001-07-30
;  PRIOR APPLICATION NUMBER: US/09/235,076
;  PRIOR FILING DATE: 1999-01-20
;  NUMBER OF SEQ ID NOS: 38054
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 33032
;   LENGTH: 436
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-918-995-33032

Alignment Scores:
Pred. No.:              2.51e-46        Length:         436
Score:                  396.00          Matches:        76
Percent Similarity:     100.00%         Conservative:   0
Best Local Similarity:  100.00%         Mismatches:     0
Query Match:            31.23%          Indels:         0
DB:                     9               Gaps:           0

US-09-705-500A-3 (1-247) x US-09-918-995-33032 (1-436)

Qy        172 GluAspThrValSerThrIleArgAspSerLeuMetGluLysIleGlyProAsnMetAla 191
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 GAAGACACAGTCAGCACAATCAGAGACAGCCTGATGGAGAAAATTGGGCCTAACATGGCC 61

Qy        192 SerLeuPheHisIleLeuGlnThrAspHisCysAlaGlnThrHisProArgAlaAspPhe 211
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 AGCCTCTTCCACATCCTGCAGACAGACCACTGTGCCCAAACACACCCACGAGCTGACTTC 121

Qy        212 AsnArgArgArgThrAsnGluProGlnLysLeuLysValLeuLeuArgAsnLeuArgGly 231
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        122 AACAGGAGACGCACCAATGAGCCGCAGAAGCTGAAAGTCCTCCTCAGGAACCTCCGAGGT 181

Qy        232 GluGluAspSerProSerHisIleLysArgThrSerHisGluSerAla 247
              |||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 GAGGAGGACTCTCCCTCCCACATCAAACGCACATCCCATGAGAGTGCA 229

RESULT 14
US-09-864-761-21309/c
; Sequence 21309, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
;  APPLICANT: Penn, Sharron G.
;  APPLICANT:  Rank, David R.
;  APPLICANT:  Hanzel, David K.
;  APPLICANT:  Chen, Wensheng
;  TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
;  TITLE OF INVENTION:  GENE EXPRESSION ANALYSIS BY MICROARRAY
;  FILE REFERENCE: Aeomica-X-1
;  CURRENT APPLICATION NUMBER: US/09/864,761
;  CURRENT FILING DATE:  2001-05-23
;  PRIOR APPLICATION NUMBER: US 60/180,312
;  PRIOR FILING DATE: 2000-02-04
;  PRIOR APPLICATION NUMBER: US 60/207,456
;  PRIOR FILING DATE: 2000-05-26
;  PRIOR APPLICATION NUMBER: US 09/632,366
;  PRIOR FILING DATE: 2000-08-03
;  PRIOR APPLICATION NUMBER: GB 24263.6
;  PRIOR FILING DATE: 2000-10-04
;  PRIOR APPLICATION NUMBER: US 60/236,359
;  PRIOR FILING DATE: 2000-09-27
;  PRIOR APPLICATION NUMBER: PCT/US01/00666
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00667
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00664
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00669
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00665
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00668
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00663
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00662
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00661
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00670
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: US 60/234,687
;  PRIOR FILING DATE: 2000-09-21
;  PRIOR APPLICATION NUMBER: US 09/608,408
;  PRIOR FILING DATE: 2000-06-30
;  PRIOR APPLICATION NUMBER: US 09/774,203
;  PRIOR FILING DATE: 2001-01-29
;  NUMBER OF SEQ ID NOS: 49117
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;  SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 21309
;   LENGTH: 219
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: MAP TO AC012119.1
;   OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.7
;   OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 2.4
;   OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 2.8
;   OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 2.8
;   OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 2.4
;   OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 3.1
;   OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 1.8
;   OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.7
;   OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 2.2
;   OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 2.7
;   OTHER INFORMATION: SWISSPROT HIT: P52823, EVALUE 2.00e-36
;   OTHER INFORMATION: NT HIT: AF098463.1, EVALUE 1.00e-120
;   OTHER INFORMATION: EST_HUMAN HIT: AW954342.1, EVALUE 1.00e-116
US-09-864-761-21309

Alignment Scores:
Pred. No.:               3.72e-43       Length:          219
Score:                   370.00         Matches:         72
Percent Similarity:      100.00%        Conservative:    0
Best Local Similarity:   100.00%        Mismatches:      0
Query Match:             29.18%         Indels:          0
DB:                      10             Gaps:            0

US-09-705-500A-3 (1-247) x US-09-864-761-21309 (1-219)

Qy          88 GlyLysAlaPheValLysGluSerLeuLysCysIleAlaAsnGlyValThrSerLysVal 107
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         219 GGAAAAGCATTCGTCAAAGAGAGCTTAAAATGCATCGCCAACGGGGTCACCTCCAAGGTC 160

Qy         108 PheLeuAlaIleArgArgCysSerThrPheGlnArgMetIleAlaGluValGlnGluGlu 127
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         159 TTCCTCGCCATTCGGAGGTGCTCCACTTTCCAAAGGATGATTGCTGAGGTGCAGGAAGAG 100

Qy         128 CysTyrSerLysLeuAsnValCysSerIleAlaLysArgAsnProGluAlaIleThrGlu 147
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          99 TGCTACAGCAAGCTGAATGTGTGCAGCATCGCCAAGCGGAACCCTGAAGCCATCACTGAG 40

Qy         148 ValValGlnLeuProAsnHisPheSerAsnArgTyr 159
               |||||||||||||||||||||||||||||||||||
Db          39 GTCGTCCAGCTGCCCAATCACTTCTCCAACAGGTAC 4

RESULT 15
US-10-198-846-9993
; Sequence 9993, Application US/10198846
; Publication No. US20030099974A1
; GENERAL INFORMATION:
;  APPLICANT: Lillie, James
;  APPLICANT:  Xu, Yongyao
;  APPLICANT:  Wang, Youzhen
;  APPLICANT:  Steinmann, Kathleen
;  TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS
;  TITLE OF INVENTION:  FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
;  TITLE OF INVENTION:  THERAPY OF BREAST CANCER
;  FILE REFERENCE: MRI-049
;  CURRENT APPLICATION NUMBER: US/10/198,846
;  CURRENT FILING DATE:  2002-07-18
;  PRIOR APPLICATION NUMBER: 60/306,220
;  PRIOR FILING DATE: 2001-07-18
;  NUMBER OF SEQ ID NOS: 14084
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 9993
;   LENGTH: 2759
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: 1, 2, 3, 2758, 2759
;   OTHER INFORMATION: n = A,T,C or G
US-10-198-846-9993

Alignment Scores:
Pred. No.:               4.8e-39        Length:          2759
Score:                   354.00         Matches:         82
Percent Similarity:      52.32%         Conservative:    42
Best Local Similarity:   34.60%         Mismatches:      102
Query Match:             27.92%         Indels:          12
DB:                      9              Gaps:            4

US-09-705-500A-3 (1-247) x US-10-198-846-9993 (1-2759)

Qy           9 LeuValLeuValIleSer--------------------AlaSerAlaThrHisGluAla 21
               |||   ||||||::::::                    |||||||:::
Db         288 CTGGCTTTGGTGTTGGCCACCTTTGACCCGGCGCGGGGGACCGACGCCACCAACCCACCC 347

Qy          22 Glu---GlnAsnAspSerValSerProArgLysSerArgValAlaAlaGlnAsnSerAla 40
               |||         |||      |||  :::|||  |||::::::  |||||:::|||
Db         348 GAGGGTCCCCAAGACAGGAGCTCCCAGCAGAAAGGCCGCCTGTCCCTGCAGAATACAGCG 407

Qy          41 GluValValArgCysLeuAsnSerAlaLeuGlnValGlyCysGlyAlaPheAlaCysLeu 60
               |||:::      ||||||  :::|||      ||||||||||||  |||  |||
Db         408 GAGATCCAGCACTGTTTGGTCAACGCTGGCGATGTGGGGTGTGGCGTGTTTGAATGTTTC 467

Qy          61 GluAsnSerThrCysAspThrAspGlyMetTyrAspIleCysLysSerPheLeuTyrSer 80
               ||||||::::::|||:::      |||::::::  ||||||  :::||||||::::::
Db         468 GAGAACAACTCTTGTGAGATTCGGGGCTTACATGGGATTTGCATGACTTTTCTGCACAAC 527

Qy          81 AlaAlaLysPheAspThrGlnGlyLysAlaPheValLysGluSerLeuLysCysIleAla 100
               |||  |||||||||  |||||||||:::|||:::|||::::::||||||||  |||
Db         528 GCTGGAAAATTTGATGCCCAGGGCAAGTCATTCATCAAAGACGCCTTGAAATGTAAGGCC 587

Qy         101 AsnGlyValThrSerLysValPheLeuAlaIleArgArgCysSerThrPheGlnArgMet 120
               :::  :::      :::                |||:::|||         :::  |||
Db         588 CACGCTCTGCGGCACAGGTTCGGCTGCATAAGCCGGAAGTGCCCGGCCATCAGGGAAATG 647

Qy         121 IleAlaGluValGlnGluGluCysTyrSerLysLeuAsnValCysSerIleAlaLysArg 140
               ::::::::::|||  |||||||||  |||  ::::::|||:::  |||:::
Db         648 GTGTCCCAGTTGCAGCGGGAATGCTACCTCAAGCACGACCTGTGCGCGGCTGCCCAGGAG 707

Qy         141 AsnProGluAlaIleThrGluValValGlnLeuProAsnHisPheSerAsnArgTyrTyr 160
               |||      |||  |||::::::      :::      :::      |||
Db         708 AACACCCGGGTGATAGTGGAGATGATCCATTTCAAGGACTTGCTGCTGCACGAACCCTAC 767

Qy         161 AsnArgLeuValArgSerLeuLeuGluCysAspGluAspThrValSerThrIleArgAsp 180
                 ||||||  ||||||  |||  |||:::          |||
Db         768 GTGGACCTCGTGAACTTGCTGCTGACCTGTGGGGAGGAGGTGAAGGAGGCCATCACCCAC 827

Qy         181 SerLeuMetGluLysIleGlyProAsnMetAlaSerLeuPheHisIleLeuGlnThrAsp 200
               |||:::      :::      |||      ||||||      ||||||
Db         828 AGCGTGCAGGTTCAGTGTGAGCAGAACTGGGGAAGCCTGTGCTCCATCTTG------AGC 881

Qy         201 HisCysAlaGlnThrHisProArgAlaAspPheAsnArgArgArgThrAsnGluProGln 220
                  |||        ||||||  |||                |||        |||
Db         882 TTCTGCACCTCGGC-CATCCAGAAGCCTCCCACGGCGCCCCCCGAGCGCCAGCCCCAGGT 940

Qy         221 LysLeuLysValLeuLeuArgAsn---LeuArgGlyGluGluAspSerPro 236
                         |||:::        ||||||        ||||||
Db         941 GGACAGAACCAAGCTCTCCAGGGCCCACCACGGGGAAGCAGGACATCACCT 991


Search completed: June 12, 2003, 22:05:22
Job time : 149 secs
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GenCore version 5.1.6

OM protein - nucleic search, using frame_plus_p2n model

Run on: June 12, 2003, 20:11:29 ; Search time 1418 Seconds
(without alignments)
2821.076 Million cell updates/sec

Title: US-09-705-500A-3
Perfect score: 1268
Sequence: 1 MLQNSAVLLVLVISASATHE.....NLRGEEDSPSHIKRTSHESA 247

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlp
-Q=/cgn2_1/USPTO_spool/US09705500/runat_06062003_113612_7466/app_query.fasta_1.391
-DB=EST -QFMT=fastap -SUFFIX=rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09705500_@CGN_1_1_1525_@runat_06062003_113612_7466 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pln:*
21: em_gss_vrt:*
22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1248	98.4	869	14	BQ672018	BQ672018 AGENCOURT
2	1196	94.3	739	9	AI115911	AI115911 ue96d11.y
3	1087	85.7	1057	14	BQ225453	BQ225453 AGENCOURT
4	1076	84.9	648	13	BM311682	BM311682 ig60f04.x
5	1075	84.8	644	10	AW965863	AW965863 EST377936
c 6	1066	84.1	617	13	BM311087	BM311087 ig60f04.y
7	1041	82.1	915	13	BI182587	BI182587 UNL-P-FN-
8	1038	81.9	915	14	BQ894224	BQ894224 AGENCOURT
9	980.5	77.3	646	10	AW954342	AW954342 EST366412
10	876	69.1	782	9	AL549427	AL549427 AL549427
11	849	67.0	577	14	BQ308414	BQ308414 MR0-BT450
12	848	66.9	560	12	BF042539	BF042539 BP250022A
13	839	66.2	513	10	BE476621	BE476621 159962 BA
14	839	66.2	908	9	AL550611	AL550611 AL550611
15	817	64.4	1010	14	BM924595	BM924595 AGENCOURT
16	777.5	61.3	907	9	AU122680	AU122680 AU122680
17	763	60.2	623	13	BI081334	BI081334 602879386
c 18	678	53.5	437	10	AW996662	AW996662 QV3-BN004
19	649.5	51.2	563	10	BB856959	BB856959 BB856959
20	630	49.7	483	14	R72337	R72337 yj89d08.r1
21	627	49.4	930	12	BF303368	BF303368 602030289
22	602	47.5	719	13	BI764976	BI764976 603051122
23	600	47.3	417	12	BF849408	BF849408 QV4-EN009
24	548	43.2	619	13	BI010260	BI010260 MR2-EN009
25	544	42.9	879	13	BI769460	BI769460 603054789
26	543	42.8	605	13	BI010412	BI010412 MR2-EN009
27	515	40.6	388	10	BE491299	BE491299 db71b12.y
28	514	40.5	531	10	AW466127	AW466127 BP230022A
c 29	512	40.4	530	12	BF854554	BF854554 MR2-EN009
30	507	40.0	774	13	BI918756	BI918756 603179881
31	506.5	39.9	366	14	R73246	R73246 yl09f01.r1
32	478	37.7	543	14	BQ636799	BQ636799 he01f01.y
33	466	36.8	412	14	R48681	R48681 yj65b07.r1
34	457	36.0	301	9	AA297962	AA297962 EST113548
35	454	35.8	524	14	BM708153	BM708153 UI-E-CI1-
36	443	34.9	492	10	BE235128	BE235128 142476 MA
37	434	34.2	543	9	AL702795	AL702795 DKFZp686H
38	415	32.7	251	13	BI975654	BI975654 484119 MA
39	396	31.2	375	14	BM720350	BM720350 UI-E-EJ0-
40	378.5	29.9	461	10	AW463836	AW463836 BP230013B
41	366	28.9	422	10	AW784374	AW784374 zb61h07.g
42	354.5	28.0	880	9	AL556729	AL556729 AL556729
43	354.5	28.0	990	11	AK002527	AK002527 Mus muscu
44	354.5	28.0	1607	11	AK010318	AK010318 Mus muscu
45	354	27.9	933	14	BQ928761	BQ928761 AGENCOURT

ALIGNMENTS

RESULT 1
BQ672018
LOCUS BQ672018 869 bp mRNA linear EST 15-JUL-2002
DEFINITION AGENCOURT_8032625 NIH_MGC_102 Homo sapiens cDNA clone IMAGE:6213518 5', mRNA sequence.
ACCESSION BQ672018
VERSION BQ672018.1 GI:21782852
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 869)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

```
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC
             cDNA Library Preparation: Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM2379  row: f  column: 15
            High quality sequence stop: 673.
FEATURES             Location/Qualifiers
     source          1. .869
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:6213518"
                     /clone_lib="NIH_MGC_102"
                     /tissue_type="epidermoid carcinoma, cell line"
                     /lab_host="DH10B (phage-resistant)"
                     /note="Organ: salivary gland; Vector: pOTB7; Site_1: XhoI;
                     Site_2: EcoRI; cDNA made by oligo-dT priming.
                     Directionally cloned into EcoRI/XhoI sites using the
                     following 5' adaptor: GGCACGAG(G).  Library constructed
                     by Ling Hong in the laboratory of Gerald M. Rubin
                     (University of  California, Berkeley) using ZAP-cDNA
                     synthesis kit (Stratagene) and Superscript II RT (Life
                     Technologies). Note: this is a NIH_MGC Library."
BASE COUNT      234 a    231 c    214 g    188 t      2 others
ORIGIN

Alignment Scores:
Pred. No.:              6.82e-143       Length:         869
Score:                  1248.00         Matches:        244
Percent Similarity:     98.79%          Conservative:   0
Best Local Similarity:  98.79%          Mismatches:     3
Query Match:            98.42%          Indels:         0
DB:                     14              Gaps:           0

US-09-705-500A-3 (1-247) x BQ672018 (1-869)

Qy          1 MetLeuGlnAsnSerAlaValLeuLeuValLeuValIleSerAlaSerAlaThrHisGlu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         21 ATGCTCCAAAACTCAGCAGTGCTTCTGGTGCTGGTGATCAGTGCTTCTGCAACCCATGAG 80

Qy         21 AlaGluGlnAsnAspSerValSerProArgLysSerArgValAlaAlaGlnAsnSerAla 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         81 GCGGAGCAGAATGACTCTGTGAGCCCCAGGAAATCCCGAGTGGCGGCTCAAAACTCAGCT 140

Qy         41 GluValValArgCysLeuAsnSerAlaLeuGlnValGlyCysGlyAlaPheAlaCysLeu 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        141 GAAGTGGTTCGTTGCCTCAACAGTGCTCTACAGGTCGGCTGCGGGGCTTTTGCATGCCTG 200

Qy         61 GluAsnSerThrCysAspThrAspGlyMetTyrAspIleCysLysSerPheLeuTyrSer 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        201 GAAAACTCCACCTGTGACACAGATGGGATGTATGACATCTGTAAATCCTTCTTGTACAGC 260

Qy         81 AlaAlaLysPheAspThrGlnGlyLysAlaPheValLysGluSerLeuLysCysIleAla 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        261 GCTGCTAAATTTGACACTCAGGGAAAAGCATTCGTCAAAGAGAGCTTAAAATGCATCGCC 320

Qy        101 AsnGlyValThrSerLysValPheLeuAlaIleArgArgCysSerThrPheGlnArgMet 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        321 AACGGGGTCACCTCCAAGGTCTTCCTCGCCATTCGGAGGTGCTCCACTTTCCAAAGGATG 380

Qy        121 IleAlaGluValGlnGluGluCysTyrSerLysLeuAsnValCysSerIleAlaLysArg 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        381 ATTGCTGAGGTGCAGGAAGAGTGCTACAGCAAGCTGAATGTGTGCAGCATCGCCAAGCGG 440

Qy        141 AsnProGluAlaIleThrGluValValGlnLeuProAsnHisPheSerAsnArgTyrTyr 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        441 AACCCTGAAGCCATCACTGAGGTCGTCCAGCTGCCCAATCACTTCTCCAACAGATACTAT 500

Qy        161 AsnArgLeuValArgSerLeuLeuGluCysAspGluAspThrValSerThrIleArgAsp 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        501 AACAGACTTGTCCGAAGCCTGCTGGAATGTGATGAAGACACAGTCAGCACAATCAGAGAC 560

Qy        181 SerLeuMetGluLysIleGlyProAsnMetAlaSerLeuPheHisIleLeuGlnThrAsp 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        561 AGCCTGATGGAGAAAATTGGGCCTAACATGGCCAGCCTCTTCCACATCCTGCAGACAGAC 620

Qy        201 HisCysAlaGlnThrHisProArgAlaAspPheAsnArgArgArgThrAsnGluProGln 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        621 CACTGTGCCCAAACACACCCACGAGCTGACTTCAACAGGAGACGCACCAATGAGCCGCAG 680

Qy        221 LysLeuLysValLeuLeuArgAsnLeuArgGlyGluGluAspSerProSerHisIleLys 240
              ||||||||||||||||||||||||          ||||||||||||||||||||||||||
Db        681 AAGCTGAAAGTCCTCCTCAGGAACCCTCCGAGTGAGGAAGACTCTCCCTCCCACATCAAA 740

Qy        241 ArgThrSerHisGluSerAla 247
              |||||||||||||||||||||
Db        741 CGCACATCCCATGAGAGTGCA 761

RESULT 2
AI115911
LOCUS       AI115911                739 bp    mRNA    linear   EST 02-SEP-1998
DEFINITION  ue96d11.y1 Sugano mouse embryo mewa Mus musculus cDNA clone
            IMAGE:1498965 5' similar to SW:CSTP_HUMAN P52823 STANNIOCALCIN
            PRECURSOR. [2] SW:CSTP_HUMAN ;, mRNA sequence.
ACCESSION   AI115911
VERSION     AI115911.1  GI:3516235
KEYWORDS    EST.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 739)
  AUTHORS   Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
            Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
            Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
            Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
            Waterston,R.
  TITLE     The WashU-HHMI Mouse EST Project
  JOURNAL   Unpublished (1996)
COMMENT     Contact: Marra M/Mouse EST Project
            WashU-HHMI Mouse EST Project
            Washington University School of MedicineP
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: mouseest@watson.wustl.edu
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            MGI:936569
            Possible reversed clone: similarity on wrong strand
            Seq primer: custom primer used
            High quality sequence stop: 515.
FEATURES             Location/Qualifiers
     source          1. .739
                     /organism="Mus musculus"
                     /strain="C57BL"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:1498965"
                     /clone_lib="Sugano mouse embryo mewa"
                     /dev_stage="embryo, 14 dpc"
                     /lab_host="DH10B"
                     /note="Vector: pME18S-FL3; Site_1: DraIII (CACTGTGTG);
                     Site_2: DraIII (CACCATGTG); 1st strand cDNA was primed
                     with an oligo(dT) primer  [ATGTGGCCTTTTTTTTTTTTTTTT];
                     double-stranded cDNA was ligated to a  DraIII adaptor
                     [TGTTGGCCTACTGG], digested and cloned into distinct DraIII
                     sites of the pME18S-FL3 vector (5' site CACTGTGTG, 3' site
                     CACCATGTG). XhoI should be used to isolate the cDNA
                     insert.  Size selection was performed to exclude fragments
                     <1.5kb.  Library constructed by Dr. Sumio Sugano
                     (University of Tokyo Institute of Medical Science).
```

Custom primers for sequencing: 5' end primer
CTTCTGCTCTAAAAGCTGCG and 3' end primer
CGACCTGCAGCTCGAGCACA."
BASE COUNT 205 a 197 c 184 g 146 t 7 others
ORIGIN

Alignment Scores:

Pred. No.:	1.31e-136	Length:	739
Score:	1196.00	Matches:	231
Percent Similarity:	96.73%	Conservative:	6
Best Local Similarity:	94.29%	Mismatches:	8
Query Match:	94.32%	Indels:	0
DB:	9	Gaps:	0

US-09-705-500A-3 (1-247) x AI115911 (1-739)

```
Qy          3 GlnAsnSerAlaValLeuLeuValLeuValIleSerAlaSerAlaThrHisGluAlaGlu 22
              :::|||||||||||||:::|||   |||||||||||||||:::|||   ||||||||||||
Db          5 AAAAACTCAGCAGTGATTCTGGCGCTGGTCATCAGTGCAGCTGCAGCGCACGAGGCGGAA 64

Qy         23 GlnAsnAspSerValSerProArgLysSerArgValAlaAlaGlnAsnSerAlaGluVal 42
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         65 CAAAATGATTCTGTGAGCCCCAGAAAATCCCGGGTGGCGGCTCAAAATTCAGCTGAAGTG 124

Qy         43 ValArgCysLeuAsnSerAlaLeuGlnValGlyCysGlyAlaPheAlaCysLeuGluAsn 62
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        125 GTTCGCTGCCTCAACAGTGCCCTGCAGGTTGGCTGCGGGGCTTTTGCATGCCTGGAAAAC 184

Qy         63 SerThrCysAspThrAspGlyMetTyrAspIleCysLysSerPheLeuTyrSerAlaAla 82
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        185 TCCACATGTGACACAGATGGGATGTACGACATTTGTAAATCCTTCTTGTACAGTGCTGCT 244

Qy         83 LysPheAspThrGlnGlyLysAlaPheValLysGluSerLeuLysCysIleAlaAsnGly 102
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        245 AAATTTGACACTCAGGGAAAAGCATTTGTCAAAGAGAGCTTAAAGTGCATCGCCAATGGG 304

Qy        103 ValThrSerLysValPheLeuAlaIleArgArgCysSerThrPheGlnArgMetIleAla 122
              :::||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        305 ATCACCTCCAAGGTATTCCTTGCCATTCGGAGGTGTTCGACTTTCCAGAGGATGATCGCC 364

Qy        123 GluValGlnGluGluCysTyrSerLysLeuAsnValCysSerIleAlaLysArgAsnPro 142
              ||||||||||||:::||||||||||||||||||||||||||||||||||||||||||||
Db        365 GAGGTGCAGGAGGACTGCTACAGCAAGCTTAACGTTTGCAGCATCGCCAAGCGCAACCCG 424

Qy        143 GluAlaIleThrGluValValGlnLeuProAsnHisPheSerAsnArgTyrTyrAsnArg 162
              ||||||||||||||||||:::||||||||||||||||||||||||||||||||||||||||
Db        425 GAAGCCATCACTGAAGTCATACAGCTGCCCAATCACTTCTCCAACAGATACTACAACAGA 484

Qy        163 LeuValArgSerLeuLeuGluCysAspGluAspThrValSerThrIleArgAspSerLeu 182
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        485 CTTGTCCGAAGCCTTCTGGAATGTGATGAAGACACGGTCAGTACAATCAGAGACAGCCTG 544

Qy        183 MetGluLysIleGlyProAsnMetAlaSerLeuPheHisIleLeuGlnThrAspHisCys 202
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        545 ATGGAGAAGATCGGGCCCAACATGGCCAGCCTCTTCCACATCCTGCAGACAGACCACTGT 604

Qy        203 AlaGlnThrHisProArgAlaAspPheAsnArgArgArgThrAsnGluProGlnLysLeu 222
              ||||||||||||||||||||||||||||||||||||||||   ||||||||||||||||
Db        605 GCCCAGACACACCCCAGAGCTGACTTCAATAGGAGGCGCACANATGAGCCACAGAAGCTG 664

Qy        223 LysValLeuLeuArgAsnLeuArgGlyGluGluAspSerProSerHisIleLysArgThr 242
              |||||||||||||||||||||||||||||||   ||||||   |||||||||   ||||||
Db        665 AAAGTCCTNCTCAGGAACCTNCGAGGTGAGGNGGACTCTNCCTCACACATCANACGCACC 724

Qy        243 SerHisGluSerAla 247
              |||||||||
Db        725 TNCCAAGAGAGTGCG 739
```

RESULT 3
BQ225453
LOCUS BQ225453 1057 bp mRNA linear EST 02-MAY-2002
DEFINITION AGENCOURT_7257225 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:5773821 5', mRNA sequence.
ACCESSION BQ225453
VERSION BQ225453.1 GI:20406853
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1057)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP/Gazdar
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM12842 row: e column: 22
High quality sequence stop: 578.
FEATURES Location/Qualifiers
source 1. .1057
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5773821"
/clone_lib="NIH_MGC_68"
/tissue_type="large cell carcinoma"
/lab_host="DH10B (phage-resistant)"
/note="Organ: lung; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.8 kb. Library constructed by Life Technologies. "
BASE COUNT 291 a 293 c 219 g 254 t
ORIGIN

Alignment Scores:

Pred. No.:	6.95e-123	Length:	1057
Score:	1087.00	Matches:	208
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	85.73%	Indels:	0
DB:	14	Gaps:	0

US-09-705-500A-3 (1-247) x BQ225453 (1-1057)

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Qy         40 AlaGluValValArgCysLeuAsnSerAlaLeuGlnValGlyCysGlyAlaPheAlaCys 59
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Db          4 GCTGAAGTGGTTCGTTGCCTCAACAGTGCTCTACAGGTCGGCTGCGGGGCTTTTGCATGC 63

Qy         60 LeuGluAsnSerThrCysAspThrAspGlyMetTyrAspIleCysLysSerPheLeuTyr 79
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         64 CTGGAAAACTCCACCTGTGACACAGATGGGATGTATGACATCTGTAAATCCTTCTTGTAC 123

Qy         80 SerAlaAlaLysPheAspThrGlnGlyLysAlaPheValLysGluSerLeuLysCysIle 99
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        124 AGCGCTGCTAAATTTGACACTCAGGGAAAAGCATTCGTCAAAGAGAGCTTAAAATGCATC 183

Qy        100 AlaAsnGlyValThrSerLysValPheLeuAlaIleArgArgCysSerThrPheGlnArg 119
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        184 GCCAACGGGGTCACCTCCAAGGTCTTCCTCGCCATTCGGAGGTGCTCCACTTTCCAAAGG 243

Qy        120 MetIleAlaGluValGlnGluGluCysTyrSerLysLeuAsnValCysSerIleAlaLys 139
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        244 ATGATTGCTGAGGTGCAGGAAGAGTGCTACAGCAAGCTGAATGTGTGCAGCATCGCCAAG 303

Qy        140 ArgAsnProGluAlaIleThrGluValValGlnLeuProAsnHisPheSerAsnArgTyr 159
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        304 CGGAACCCTGAAGCCATCACTGAGGTCGTCCAGCTGCCCAATCACTTCTCCAACAGATAC 363

Qy        160 TyrAsnArgLeuValArgSerLeuLeuGluCysAspGluAspThrValSerThrIleArg 179
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        364 TATAACAGACTTGTCCGAAGCCTGCTGGAATGTGATGAAGACACAGTCAGCACAATCAGA 423

Qy        180 AspSerLeuMetGluLysIleGlyProAsnMetAlaSerLeuPheHisIleLeuGlnThr 199
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        424 GACAGCCTGATGGAGAAAATTGGGCCTAACATGGCCAGCCTCTTCCACATCCTGCAGACA 483

Qy        200 AspHisCysAlaGlnThrHisProArgAlaAspPheAsnArgArgArgThrAsnGluPro 219
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        484 GACCACTGTGCCCAAACACACCCACGAGCTGACTTCAACAGGAGACGCACCAATGAGCCG 543

Qy        220 GlnLysLeuLysValLeuLeuArgAsnLeuArgGlyGluGluAspSerProSerHisIle 239
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        544 CAGAAGCTGAAAGTCCTCCTCAGGAACCTCCGAGGTGAGGAGGACTCTCCCTCCCACATC 603

Qy        240 LysArgThrSerHisGluSerAla 247
              |||||||||||||||||||||||
Db        604 AAACGCACATCCCATGAGAGTGCA 627

RESULT 4
BM311682
LOCUS       BM311682                 648 bp    mRNA    linear   EST 03-JAN-2002
DEFINITION  ig60f04.x1 HR85 islet Homo sapiens cDNA 3' similar to SW:STC1_HUMAN
            P52823 STANNIOCALCIN 1 PRECURSOR ;, mRNA sequence.
ACCESSION   BM311682
VERSION     BM311682.1  GI:18046027
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 648)
  AUTHORS   Melton,D., Brown,J., Kenty,G., Permutt,A., Lee,C., Kaestner,K.,
            Lemishka,I., Scearce,M., Brestelli,J., Gradwohl,G., Clifton,S.,
            Hillier,L., Marra,M., Pape,D., Wylie,T., Martin,J., Blistain,A.,
            Schmitt,A., Theising,B., Ritter,E., Ronko,I., Bennett,J., Cardenas
            ,M., Gibbons,M., McCann,R., Cole,R., Tsagareishvili,R., Williams,T.
            , Jackson,Y. and Bowers,Y.
  TITLE     Endocrine Pancreas Consortium
  JOURNAL   Unpublished (2000)
COMMENT     Other_ESTs: ig60f04.y1
            Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
            Endocrine Pancreas Consortium
            Harvard University, Howard Hughes Medical Institute
            Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
            MA 02138
            Tel: 617-495-1812
            Fax: 617-495-8557
            Email: dmelton@biohp.harvard.edu
            Library was constructed by Dr. Hiroshi Inoue DNA sequencing by:
            Washington University Genome Sequencing Center For information on
            obtaining a clone please contact: Dr. Hiroshi Inoue
            (hinoue@im.wustl.edu)
            Possible reversed clone: similarity on wrong strand
            Seq primer: -40UP from Gibco
            High quality sequence stop: 475.
FEATURES             Location/Qualifiers
     source          1. .648
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone_lib="HR85 islet"
                     /tissue_type="Purified pancreatic islet"
                     /lab_host="DH10B"
                     /note="Organ: Pancreas; Vector: pBluescript SK(-); Site_1:
                     NotI; Site_2: XhoI; cDNA made by oligo-dT priming.
                     Size-selected on agarose gel. Average insert size ~1kb. 5'
                     XhoI site was destroyed after directional cloning.
                     Amplified once. Contact information: Hiroshi Inoue, MD,
                     Metabolism Div. (Alan Permutt Lab), Washington University
                     School of Medicine, Box 8127, 660 South Euclid Ave., St.
                     Louis, MO 63110, E-mail: hinoue@imgate.wustl.edu, Tel:
                     314-362-1916, Fax: 314-747-2692."
BASE COUNT      175 a    179 c    164 g    130 t
ORIGIN

Alignment Scores:
Pred. No.:                6.47e-122      Length:          648
Score:                    1076.00        Matches:         207
Percent Similarity:       100.00%        Conservative:    0
Best Local Similarity:    100.00%        Mismatches:      0
Query Match:              84.86%         Indels:          0
DB:                       13             Gaps:            0

US-09-705-500A-3 (1-247) x BM311682 (1-648)

Qy         13 IleSerAlaSerAlaThrHisGluAlaGluGlnAsnAspSerValSerProArgLysSer 32
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         28 ATCAGTGCTTCTGCAACCCATGAGGCGGAGCAGAATGACTCTGTGAGCCCCAGGAAATCC 87

Qy         33 ArgValAlaAlaGlnAsnSerAlaGluValValArgCysLeuAsnSerAlaLeuGlnVal 52
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         88 CGAGTGGCGGCTCAAAACTCAGCTGAAGTGGTTCGTTGCCTCAACAGTGCTCTACAGGTC 147

Qy         53 GlyCysGlyAlaPheAlaCysLeuGluAsnSerThrCysAspThrAspGlyMetTyrAsp 72
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        148 GGCTGCGGGGCTTTTGCATGCCTGGAAAACTCCACCTGTGACACAGATGGGATGTATGAC 207

Qy         73 IleCysLysSerPheLeuTyrSerAlaAlaLysPheAspThrGlnGlyLysAlaPheVal 92
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        208 ATCTGTAAATCCTTCTTGTACAGCGCTGCTAAATTTGACACTCAGGGAAAAGCATTCGTC 267

Qy         93 LysGluSerLeuLysCysIleAlaAsnGlyValThrSerLysValPheLeuAlaIleArg 112
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        268 AAAGAGAGCTTAAAATGCATCGCCAACGGGGTCACCTCCAAGGTCTTCCTCGCCATTCGG 327

Qy        113 ArgCysSerThrPheGlnArgMetIleAlaGluValGlnGluGluCysTyrSerLysLeu 132
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        328 AGGTGCTCCACTTTCCAAAGGATGATTGCTGAGGTGCAGGAAGAGTGCTACAGCAAGCTG 387

Qy        133 AsnValCysSerIleAlaLysArgAsnProGluAlaIleThrGluValValGlnLeuPro 152
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        388 AATGTGTGCAGCATCGCCAAGCGGAACCCTGAAGCCATCACTGAGGTCGTCCAGCTGCCC 447

Qy        153 AsnHisPheSerAsnArgTyrTyrAsnArgLeuValArgSerLeuLeuGluCysAspGlu 172
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        448 AATCACTTCTCCAACAGATACTATAACAGACTTGTCCGAAGCCTGCTGGAATGTGATGAA 507

Qy        173 AspThrValSerThrIleArgAspSerLeuMetGluLysIleGlyProAsnMetAlaSer 192
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        508 GACACAGTCAGCACAATCAGAGACAGCCTGATGGAGAAAATTGGGCCTAACATGGCCAGC 567

Qy        193 LeuPheHisIleLeuGlnThrAspHisCysAlaGlnThrHisProArgAlaAspPheAsn 212
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        568 CTCTTCCACATCCTGCAGACAGACCACTGTGCCCAAACACACCCACGAGCTGACTTCAAC 627

Qy        213 ArgArgArgThrAsnGluPro 219
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Db        628 AGGAGACGCACCAATGAGCCG 648

RESULT 5
AW965863
LOCUS       AW965863                 644 bp    mRNA    linear   EST 01-JUN-2000
DEFINITION  EST377936 MAGE resequences, MAGI Homo sapiens cDNA, mRNA sequence.
ACCESSION   AW965863
VERSION     AW965863.1  GI:8155699
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 644)
  AUTHORS   Hegde,P., Qi,R., Abernathy,K., Dharap,S., Gaspard,R., Gay,C., Holt
            ,I.E., Saeed,A.I., Sharov,V., Lee,N.H., Yeatman,T.J. and
            Quackenbush,J.
  TITLE     Assessment of gene expression patterns in a model of colon tumor
            metastasis using a 19,200 element cDNA microarray
  JOURNAL   Unpublished (2000)
```

```
COMMENT     Contact: John Quackenbush
            The Institute for Genomic Research
            9712 Medical Center Dr., Rockville, MD 20850, USA
            Tel: 301 838 3528
            Fax: 301 838 0208
            Email: johnq@tigr.org
            Plate: 220
            Seq primer: Reverse.
FEATURES             Location/Qualifiers
     source          1. .644
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone_lib="MAGE resequences, MAGI"
                     /note="Vector: pBluescriptSKm"
BASE COUNT      171 a    175 c    164 g    134 t
ORIGIN

Alignment Scores:
Pred. No.:              8.49e-122       Length:         644
Score:                  1075.00         Matches:        213
Percent Similarity:     99.07%          Conservative:   0
Best Local Similarity:  99.07%          Mismatches:     2
Query Match:            84.78%          Indels:         1
DB:                     10              Gaps:           0

US-09-705-500A-3 (1-247) x AW965863 (1-644)

Qy          5 SerAlaValLeuLeuValLeuValIleSerAlaSerAlaThrHisGluAlaGluGlnAsn 24
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 TCAGCAGTGCTTCTGGTGCTGGTGATCAGTGCTTCTGCAACCCATGAGGCGGAGCAGAAT 60

Qy         25 AspSerValSerProArgLysSerArgValAlaAlaGlnAsnSerAlaGluValValArg 44
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GACTCTGTGAGCCCCAGGAAATCCCGAGTGGCGGCTCAAAACTCAGCTGAAGTGGTTCGT 120

Qy         45 CysLeuAsnSerAlaLeuGlnValGlyCysGlyAlaPheAlaCysLeuGluAsnSerThr 64
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TGCCTCAACAGTGCTCTACAGGTCGGCTGCGGGGCTTTTGCATGCCTGGAAAACTCCACC 180

Qy         65 CysAspThrAspGlyMetTyrAspIleCysLysSerPheLeuTyrSerAlaAlaLysPhe 84
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TGTGACACAGATGGGATGTATGACATCTGTAAATCCTTCTTGTACAGCGCTGCTAAATTT 240

Qy         85 AspThrGlnGlyLysAlaPheValLysGluSerLeuLysCysIleAlaAsnGlyValThr 104
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GACACTCAGGGAAAAGCATTCGTCAAAGAGAGCTTAAAATGCATCGCCAACGGGGTCACC 300

Qy        105 SerLysValPheLeuAlaIleArgArgCysSerThrPheGlnArgMetIleAlaGluVal 124
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TCCAAGGTCTTCCTCGCCATTCGGAGGTGCTCCACTTTCCAAAGGATGATTGCTGAGGTG 360

Qy        125 GlnGluGluCysTyrSerLysLeuAsnValCysSerIleAlaLysArgAsnProGluAla 144
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CAGGAAGAGTGCTACAGCAAGCTGAATGTGTGCAGCATCGCCAAGCGGAACCCTGAAGCC 420

Qy        145 IleThrGluValValGlnLeuProAsnHisPheSerAsnArgTyrTyrAsnArgLeuVal 164
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ATCACTGAGGTCGTCCAGCTGCCCAATCACTTCTCCAACAGATACTATAACAGACTGGTC 480

Qy        165 ArgSerLeuLeuGluCysAspGluAspThrValSerThrIleArgAspSerLeuMetGlu 184
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 CGAAGCCTGCTGGAATGTGATGAAGACACAGTCAGCACAATCAGAGACAGCCTGATGGAG 540

Qy        185 LysIleGlyProAsnMetAlaSerLeuPheHisIleLeuGlnThrAspHisCysAlaGln 204
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||   |||
Db        541 AAAATTGGGCCTAACATGGCCAGCCTCTTCCACATCCTGCAGACGGACCATTGTGC-CAA 599

Qy        205 ThrHisProArgAlaAspPheAsnArgArgArgThrAsnGluPro 219
              |||||||||||||||||||||   |||||||||||||||||||||
Db        600 ACACACCCACGAGCTGACTTCACCAGGAGACGCACCAATGAGCCA 644

RESULT 6
BM311087/c
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LOCUS       BM311087                617 bp    mRNA    linear   EST 03-JAN-2002
DEFINITION  ig60f04.y1 HR85 islet Homo sapiens cDNA 5' similar to SW:STC1_HUMAN
            P52823 STANNIOCALCIN 1 PRECURSOR ;, mRNA sequence.
ACCESSION   BM311087
VERSION     BM311087.1  GI:18045432
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 617)
  AUTHORS   Melton,D., Brown,J., Kenty,G., Permutt,A., Lee,C., Kaestner,K.,
            Lemishka,I., Scearce,M., Brestelli,J., Gradwohl,G., Clifton,S.,
            Hillier,L., Marra,M., Pape,D., Wylie,T., Martin,J., Blistain,A.,
            Schmitt,A., Theising,B., Ritter,E., Ronko,I., Bennett,J., Cardenas
            ,M., Gibbons,M., McCann,R., Cole,R., Tsagareishvili,R., Williams,T.
            , Jackson,Y. and Bowers,Y.
  TITLE     Endocrine Pancreas Consortium
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
            Endocrine Pancreas Consortium
            Harvard University, Howard Hughes Medical Institute
            Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
            MA 02138
            Tel: 617-495-1812
            Fax: 617-495-8557
            Email: dmelton@biohp.harvard.edu
            Library was constructed by Dr. Hiroshi Inoue DNA sequencing by:
            Washington University Genome Sequencing Center For information on
            obtaining a clone please contact: Dr. Hiroshi Inoue
            (hinoue@im.wustl.edu)
            Possible reversed clone: similarity on wrong strand
            Seq primer: -40RP from Gibco
            High quality sequence stop: 441.
FEATURES             Location/Qualifiers
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                     /tissue_type="Purified pancreatic islet"
                     /lab_host="DH10B"
                     /note="Organ: Pancreas; Vector: pBluescript SK(-); Site_1:
                     NotI; Site_2: XhoI; cDNA made by oligo-dT priming.
                     Size-selected on agarose gel. Average insert size ~1kb. 5'
                     XhoI site was destroyed after directional cloning.
                     Amplified once. Contact information: Hiroshi Inoue, MD,
                     Metabolism Div. (Alan Permutt Lab), Washington University
                     School of Medicine, Box 8127, 660 South Euclid Ave., St.
                     Louis, MO 63110, E-mail: hinoue@imgate.wustl.edu, Tel:
                     314-362-1916, Fax: 314-747-2692."
BASE COUNT      123 a    155 c    168 g    171 t
ORIGIN

Alignment Scores:
Pred. No.:              1.01e-120       Length:         617
Score:                  1066.00         Matches:        205
Percent Similarity:     100.00%         Conservative:   0
Best Local Similarity:  100.00%         Mismatches:     0
Query Match:            84.07%          Indels:         0
DB:                     13              Gaps:           0

US-09-705-500A-3 (1-247) x BM311087 (1-617)

Qy         20 GluAlaGluGlnAsnAspSerValSerProArgLysSerArgValAlaAlaGlnAsnSer 39
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        617 GAGGCGGAGCAGAATGACTCTGTGAGCCCCAGGAAATCCCGAGTGGCGGCTCAAAACTCA 558

Qy         40 AlaGluValValArgCysLeuAsnSerAlaLeuGlnValGlyCysGlyAlaPheAlaCys 59
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        557 GCTGAAGTGGTTCGTTGCCTCAACAGTGCTCTACAGGTCGGCTGCGGGGCTTTTGCATGC 498

Qy         60 LeuGluAsnSerThrCysAspThrAspGlyMetTyrAspIleCysLysSerPheLeuTyr 79
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Db        497 CTGGAAAACTCCACCTGTGACACAGATGGGATGTATGACATCTGTAAATCCTTCTTGTAC 438

Qy         80 SerAlaAlaLysPheAspThrGlnGlyLysAlaPheValLysGluSerLeuLysCysIle 99
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        437 AGCGCTGCTAAATTTGACACTCAGGGAAAAGCATTCGTCAAAGAGAGCTTAAAATGCATC 378

Qy        100 AlaAsnGlyValThrSerLysValPheLeuAlaIleArgArgCysSerThrPheGlnArg 119
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        377 GCCAACGGGGTCACCTCCAAGGTCTTCCTCGCCATTCGGAGGTGCTCCACTTTCCAAAGG 318

Qy        120 MetIleAlaGluValGlnGluGluCysTyrSerLysLeuAsnValCysSerIleAlaLys 139
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Db        317 ATGATTGCTGAGGTGCAGGAAGAGTGCTACAGCAAGCTGAATGTGTGCAGCATCGCCAAG 258

Qy        140 ArgAsnProGluAlaIleThrGluValValGlnLeuProAsnHisPheSerAsnArgTyr 159
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        257 CGGAACCCTGAAGCCATCACTGAGGTCGTCCAGCTGCCCAATCACTTCTCCAACAGATAC 198

Qy        160 TyrAsnArgLeuValArgSerLeuLeuGluCysAspGluAspThrValSerThrIleArg 179
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        197 TATAACAGACTTGTCCGAAGCCTGCTGGAATGTGATGAAGACACAGTCAGCACAATCAGA 138

Qy        180 AspSerLeuMetGluLysIleGlyProAsnMetAlaSerLeuPheHisIleLeuGlnThr 199
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        137 GACAGCCTGATGGAGAAAATTGGGCCTAACATGGCCAGCCTCTTCCACATCCTGCAGACA 78

Qy        200 AspHisCysAlaGlnThrHisProArgAlaAspPheAsnArgArgArgThrAsnGluPro 219
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Db         77 GACCACTGTGCCCAAACACACCCACGAGCTGACTTCAACAGGAGACGCACCAATGAGCCG 18

Qy        220 GlnLysLeuLysVal 224
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Db         17 CAGAAGCTGAAAGTC 3
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RESULT 7
BI182587
LOCUS       BI182587                915 bp    mRNA    linear   EST 10-JUL-2001
DEFINITION  UNL-P-FN-bj-f-06-0-UNL.s1 UNL-P-FN Sus scrofa cDNA clone
            UNL-P-FN-bj-f-06-0-UNL 3', mRNA sequence.
ACCESSION   BI182587
VERSION     BI182587.1  GI:14656996
KEYWORDS    EST.
SOURCE      pig.
  ORGANISM  Sus scrofa
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE   1  (bases 1 to 915)
  AUTHORS   Caetano,A.R., Johnson,R.K.and Pomp,D.
  TITLE     Generation and sequence characterization of a normalized cDNA
            library from swine ovarian follicles
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Pomp, D
            Department of Animal Science
            University of Nebraska, Lincoln
            Lincoln, NE 68583-0908, USA
            Tel: 402 472 6416
            Fax: 402 472 6362
            Email: dpomp@unl.edu
            Oligo-dT track not found, Not I site shown in beginning of sequence
            is likely internal to the message.
            Seq primer: M13 -29
            POLYA=No.
FEATURES             Location/Qualifiers
     source          1. .915
                     /organism="Sus scrofa"
                     /strain="University of Nebraska, Lincoln Swine Selection
                     Lines"
                     /db_xref="taxon:9823"
                     /clone="UNL-P-FN-bj-f-06-0-UNL"
                     /clone_lib="UNL-P-FN"
                     /dev_stage="ADULT"
                     /lab_host="DH10B (Life Technologies)"
                     /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
                     polylinker; Site_1: Not I; Site_2: Eco RI; The UNL-P-FN
                     library is a normalized library representing porcine
                     ovarian follicles, ranging between 2.0 to 10.0 mm in
                     diameter, collected during 7 days of the follicular phase
                     of the pig estrous cycle. This library was derived from
                     the library UNL-P-F2. The tag is a string of 5-6
                     nucleotides present between the Not I site and the
                     oligo-dT track. The library was constructed as described
                     by Bonaldo, Lennon and Soares, Genome Research 6: 791-806
                     , 1996.
                     TAG_SEQ=None found"
BASE COUNT      221 a    249 c    219 g    216 t     10 others
ORIGIN
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```
Alignment Scores:
Pred. No.:                2.51e-117      Length:          915
Score:                    1041.00        Matches:         203
Percent Similarity:       95.00%         Conservative:    6
Best Local Similarity:    92.27%         Mismatches:      9
Query Match:              82.10%         Indels:          2
DB:                       13             Gaps:            0

US-09-705-500A-3 (1-247) x BI182587 (1-915)

Qy         29 ProArgLysSerArgVal-AlaAlaGlnAsnSerAlaGluValValArgCysLeuAsnSe 48
              |||  ||||||||||| |||  |||||||||  |||:::||||||||||||||||||
Db         24 CCANNGAAATCCCGNGTTGGCAGGTCAGAACTCAGTTGAAATGGTTCGCTGCCTCAACAG 83

Qy         48 rAlaLeuGlnValGlyCysGlyAlaPheAlaCysLeuGluAsnSerThrCysAspThrAs 68
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         84 CGCTCTGCAGGTTGGCTGTGGAGCTTTTGCCTGCCTGGAAAACTCCACCTGTGACACAGA 143

Qy         68 pGlyMetTyrAspIleCysLysSerPheLeuTyrSerAlaAla-LysPheAspThrGlnG 88
              |||||||||||||||||||||||||||||||||||||||||    ||||||||||||
Db        144 TGGGATGTACGACATCTGTAAATCCTTCTTGTACAGCGCTGCTANAATTTGACACTCAGG 203

Qy         88 lyLysAlaPheValLysGluSerLeuLysCysIleAlaAsnGlyValThrSerLysValP 108
              ||||||||||||||||||||||||||||||||||||||||||||||||||||:::|||||||
Db        204 GAAAAGCCTTTGTCAAAGAGAGTTTAAAGTGCATCGCCAACGGGGTCACCGCCAAGGTCT 263

Qy        108 heLeuAlaIleArgArgCysSerThrPheGlnArgMetIleAlaGluValGlnGluGluC 128
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        264 TCCTCGCCATTCGGAGATGCTCTACTTTCCAGCGGATGATTGCCGAGGTGCAGGAGGAGT 323

Qy        128 ysTyrSerLysLeuAsnValCysSerIleAlaLysArgAsnProGluAlaIleThrGluV 148
              |||||:::|||||||||||||||||:::|||||||||||||||||||||||||||||||
Db        324 GCTACACCAAGCTGAACGTGTGCAGTGTCGCCAAGCGGAACCCCGAAGCCATCACGGAAG 383

Qy        148 alValGlnLeuProAsnHisPheSerAsnArgTyrTyrAsnArgLeuValArgSerLeuL 168
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        384 TCGTCCAGCTCCCCAATCACTTCTCCAACAGATACTACAACAGACTTGTTCGCAGCCTGC 443

Qy        168 euGluCysAspGluAspThrValSerThrIleArgAspSerLeuMetGluLysIleGlyP 188
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        444 TGGAATGTGACGAAGACACGGTCAGCACCATCAGAGACAGCCTGATGGAGAAAATTGGGC 503

Qy        188 roAsnMetAlaSerLeuPheHisIleLeuGlnThrAspHisCysAlaGlnThrHisProA 208
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        504 CCAACATGGCCAGCCTCTTCCACATCCTGCAGACGGATCACTGTGCCCACACGCACCAGC 563

Qy        208 rgAlaAspPheAsnArgArgArgThrAsnGluProGlnLysLeuLysValLeuLeuArgA 228
              ||||||||||||||||:::|||  ||||||||||||||||||||||||||||||||||||
Db        564 GAGCTGACTTCAACAGAAAACGTGCCAACGAGCCACAGAAGCTGAAAGTCCTCCTCAGGA 623

Qy        228 snLeuArgGlyGluGluAspSerProSerHisIleLysArgThrSerHisGluSer 246
              |||||||||||||||     ||||||:::||||||||||||||||||||||||||
Db        624 ACCTCCGAGGTGAGGTGGCCTCCCCCGCCCACATCAAACGCACCTCCCACGAGAGT 679
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```
RESULT 8
BQ894224
LOCUS       BQ894224                915 bp    mRNA    linear   EST 16-AUG-2002
DEFINITION  AGENCOURT_8489564 Lupski_dorsal_root_ganglion Homo sapiens cDNA
            clone IMAGE:6180797 5', mRNA sequence.
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ACCESSION   BQ894224
VERSION     BQ894224.1  GI:22286238
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 915)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. James R. Lupski
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM13564  row: c  column: 06
            High quality sequence stop: 638.
FEATURES             Location/Qualifiers
     source          1. .915
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:6180797"
                     /clone_lib="Lupski_dorsal_root_ganglion"
                     /sex="male"
                     /tissue_type="dorsal root ganglia"
                     /dev_stage="adult, 36 yr"
                     /lab_host="DH10B"
                     /note="Vector: pCMV-SPORT6 (Life Technologies); Site_1:
                     NotI; Site_2: SalI; cDNA made by oligo-dT priming.
                     Directionally cloned using the following adaptors:
                     5'-TCGACCCACGCGTCCG-3' and
                     5'-GACTAGTTCTAGATCGCGAGCGGCCGCCCT(15)-3'. Size selected >
                     1 kb for average insert length 1.7 kb. This is a primary
                     library, non-amplified. Library constructed by Life
                     Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor
                     College of Medicine) and is available through Life
                     Technologies."
BASE COUNT      271 a    247 c    235 g    161 t      1 others
ORIGIN

Alignment Scores:
Pred. No.:                5.89e-117      Length:          915
Score:                    1038.00        Matches:         210
Percent Similarity:       97.26%         Conservative:    3
Best Local Similarity:    95.89%         Mismatches:      3
Query Match:              81.86%         Indels:          3
DB:                       14             Gaps:            0

US-09-705-500A-3 (1-247) x BQ894224 (1-915)

Qy          1 MetLeuGlnAsnSerAlaValLeuLeuValLeuValIleSerAlaSerAlaThrHisGlu 20
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        256 ATGCTCCAAAACTCAGCAGTGCTTCTGGTGCTGGTGATCAGTGCTTCTGCAACCCATGAG 315

Qy         21 AlaGluGlnAsnAspSerValSerProArgLysSerArgValAlaAlaGlnAsnSerAla 40
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        316 GCGGAGCAGAATGACTCTGTGAGCCCCAGGAAATCCCGAGTGGCGGCTCAAAACTCAGCT 375

Qy         41 GluValValArgCysLeuAsnSerAlaLeuGlnValGlyCysGlyAlaPheAlaCysLeu 60
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        376 GAAGTGGTTCGTTGCCTCAACAGTGCTCTACAGGTCGGCTGCGGGGCTTTTGCATGCCTG 435

Qy         61 GluAsnSerThrCysAspThrAspGlyMetTyrAspIleCysLysSerPheLeuTyrSer 80
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        436 GAAAACTCCACCTGTGACACAGATGGGATGTATGACATCTGTAAATCCTTCTTGTACAGC 495

Qy         81 AlaAlaLysPheAspThrGlnGlyLysAlaPheValLysGluSerLeuLysCysIleAla 100
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db        496 GCTGCTAAATTTGACACTCAGGGAAAAGCATTCGTCAAAGAGAGCTTAAAATGCATCGCC 555

Qy        101 AsnGlyValThrSerLysValPheLeuAlaIleArgArgCysSerThrPheGlnArgMet 120
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        556 AACGGGGTCACCTCCAAGGTCTTCCTCGCCATTCGGAGGTGCTCCACTTTCCAAAGGATG 615

Qy        121 IleAlaGluValGlnGluGluCysTyrSerLysLeuAsnValCysSerIleAlaLysArg 140
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        616 ATTGCTGAGGTGCAGGAAGAGTGCTACAGCAAGCTGAATGTGTGCAGCATCGCCAAGCGG 675

Qy        141 AsnProGluAlaIleThrGluValValGlnLeuProAsnHisPheSerAsnArgTyrTyr 160
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        676 AACCCTGAAGCCATCACTGAGGTCGTCCAGCTGCCCAATCACTTCTCCAACAGATACTAT 735

Qy        161 AsnArgLeuValArgSerLeuLeuGluCysAspGluAspThrValSerThrIleArgAsp 180
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        736 AACAGACTTGTCCGAAGCCTGCTGGGATGTGATGAAGACACAGTCAGCACAATCAGAGAC 795

Qy        181 SerLeuMetGluLysIleGlyProAsnMetAlaSerLeuPheHisIleLeuGlnThrAsp 200
              |||||||||||||||:::|||||||||||||   |||||||||||||||||||||||||:::
Db        796 AGCCTGATGGAGAAAATGGGGCCTAACATGGNCAGCCTCTTCCACATCCTGCAGACAGAA 855

Qy        201 HisCys-AlaGlnThrHisProArg-AlaAspPheAsnArg-ArgArgThr 216
              |||    |||:::|||||||||||| ||||||||||||| |||||||||
Db        856 CACTGGTGCCAAAACACACCCACGAAGCTGACTTCAACAGGGAGACGCACC 906

RESULT 9
AW954342
LOCUS       AW954342                646 bp    mRNA    linear   EST 01-JUN-2000
DEFINITION  EST366412 MAGE resequences, MAGC Homo sapiens cDNA, mRNA sequence.
ACCESSION   AW954342
VERSION     AW954342.1  GI:8144025
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 646)
  AUTHORS   Hegde,P., Qi,R., Abernathy,K., Dharap,S., Gaspard,R., Gay,C., Holt
            ,I.E., Saeed,A.I., Sharov,V., Lee,N.H., Yeatman,T.J. and
            Quackenbush,J.
  TITLE     Assessment of gene expression patterns in a model of colon tumor
            metastasis using a 19,200 element cDNA microarray
  JOURNAL   Unpublished (2000)
COMMENT     Contact: John Quackenbush
            The Institute for Genomic Research
            9712 Medical Center Dr., Rockville, MD 20850, USA
            Tel: 301 838 3528
            Fax: 301 838 0208
            Email: johnq@tigr.org
            Plate: 62
            Seq primer: Reverse.
FEATURES             Location/Qualifiers
     source          1. .646
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone_lib="MAGE resequences, MAGC"
                     /note="Vector: pBluescriptSKm"
BASE COUNT      171 a    178 c    161 g    135 t      1 others
ORIGIN

Alignment Scores:
Pred. No.:                3.84e-110      Length:          646
Score:                    980.50         Matches:         208
Percent Similarity:       97.22%         Conservative:    2
Best Local Similarity:    96.30%         Mismatches:      6
Query Match:              77.33%         Indels:          5
DB:                       10             Gaps:            0

US-09-705-500A-3 (1-247) x AW954342 (1-646)

Qy          5 SerAlaValLeuLeuValLeuValIleSerAlaSerAlaThrHisGluAlaGluGlnAsn 24
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db          1 TCAGCAGTGCTTCTGGTGCTGGTGATCAGTGCTTCTGCAACCCATGAGGCGGAGCAGAAT 60

Qy         25 AspSerValSerProArgLysSerArgValAlaAlaGlnAsnSerAlaGluValValArg 44
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GACTCTGTGAGCCCCAGGAAATCCCGAGTGGCGGCTCAAAACTCAGCTGAAGTGGTTCGT 120

Qy         45 CysLeuAsnSerAlaLeuGlnValGlyCysGlyAlaPheAlaCysLeuGluAsnSerThr 64
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TGCCTCAACAGTGCTCTACAGGTCGGCTGCGGGGCTTTTGCATGCCTGGAAAACTCCACC 180

Qy         65 CysAspThrAspGlyMetTyrAspIleCysLysSerPheLeuTyrSerAlaAlaLysPhe 84
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TGTGACACAGATGGGATGTATGACATCTGTAAATCCTTCTTGTACAGCGCTGCTAAATTT 240

Qy         85 AspThrGlnGlyLysAlaPheValLysGluSerLeuLysCysIleAlaAsnGlyValThr 104
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GACACTCAGGGAAAAGCATTCGTCAAAGAGAGCTTAAAATGCATCGCCAACGGGGTCACC 300

Qy        105 SerLysValPheLeuAlaIleArgArgCysSerThrPheGlnArgMetIleAlaGluVal 124
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TCCAAGGTCTTCCTCGCCATTCGGAGGTGCTCCACTTTCCAAAGGATGATTGCTGAGGTG 360

Qy        125 GlnGluGluCysTyrSerLysLeuAsnValCysSerIleAlaLysArgAsnProGluAla 144
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CAGGAAGAGTGCTACAGCAAGCTGAATGTGTGCAGCATCGCCAAGCGGAACCCTGAAGCC 420

Qy        145 IleThrGluValValGlnLeuProAsnHisPheSerAsnArgTyrTyrAsnArgLeuVal 164
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ATCACTGAGGTCGTCCAGCTGCCCAATCACTTCTCCAACAGATACTATAACAGACTTGTC 480

Qy        165 ArgSerLeuLeuGluCysAspGluAspThrValSerThrIleArgAspSerLeuMetGlu 184
              |||||||||||||||||||||   ||||||||||||||||||||||||||||||||||||
Db        481 CGAAGCCTGCTGGAATGTGATGAANACACAGTCAGCACAATCAGAGACAGCCTGATGGAG 540

Qy        185 LysIleGlyProAsnMetAlaSerLeuPheHisIleLeuGlnThrAspHisCysAlaGln 204
              ||||||||||||   :::||||||||||||||||||||||||||   |||||||||
Db        541 AAAATTGGGCCTAC-ATTGCCAGCCTCTTCCACATCCTGCAGACAGA-CACTGTGCCCA- 597

Qy        205 ThrHisProArgAlaAspPheAsnArgArgArgThrAsnGluProGln 220
              ||||||||||||||||||||   |||||||||   :::|||||||||
Db        598 ACACACCCACGAGCTGACTTCAC-AGGAGACGCCC-CATGAGCCGCAA 643

RESULT 10
AL549427
LOCUS       AL549427                782 bp    mRNA    linear   EST 16-FEB-2001
DEFINITION  AL549427 LTI_NFL006_PL2 Homo sapiens cDNA clone CS0DI044YI18 5
            prime, mRNA sequence.
ACCESSION   AL549427
VERSION     AL549427.1  GI:12885398
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 782)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE     Full-length cDNA libraries and normalization
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Genoscope
            Genoscope - Centre National de Sequencage
            BP 191 91006 EVRY cedex - France
            Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
FEATURES             Location/Qualifiers
     source          1. .782
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="CS0DI044YI18"
                     /clone_lib="LTI_NFL006_PL2"
                     /tissue_type="placenta"
                     /note="Vector: pCMVSPORT 6; Site_1: NotI; 1st strand cDNA
                     was primed with a NotI-oligo(dT) primer.  Five prime end
                     enriched, double-stranded cDNA was digested with Not I and
                     cloned into the Not I and Eco RV sites of the pCMVSPORT 6
                     vector. Library was normalized. Library was constructed by
                     Life Technologies. Contact : Feng Liang Life Technologies,
                     a division of Invitrogen 9800 Medical Center Drive
                     Rockville, Maryland 20850, USA Fax : (1) 301 610 8371
                     Email : fliang@lifetech.com URL :
                     http://fulllength.invitrogen.com"
BASE COUNT      230 a    204 c    202 g    144 t      2 others
ORIGIN

Alignment Scores:
Pred. No.:                4.19e-97        Length:          782
Score:                    876.00          Matches:         177
Percent Similarity:       98.88%          Conservative:    0
Best Local Similarity:    98.88%          Mismatches:      2
Query Match:              69.09%          Indels:          1
DB:                       9               Gaps:            0

US-09-705-500A-3 (1-247) x AL549427 (1-782)

Qy          1 MetLeuGlnAsnSerAlaValLeuLeuValLeuValIleSerAlaSerAlaThrHisGlu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        245 ATGCTCCAAAACTCAGCAGTGCTTCTGGTGCTGGTGATCAGTGCTTCTGCAACCCATGAG 304

Qy         21 AlaGluGlnAsnAspSerValSerProArgLysSerArgValAlaAlaGlnAsnSerAla 40
              |||   ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        305 GCGGA-SAGAATGACTCTGTGAGCCCCAGGAAATCCCGAGTGGCGGCTCAAAACTCAGCT 363

Qy         41 GluValValArgCysLeuAsnSerAlaLeuGlnValGlyCysGlyAlaPheAlaCysLeu 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        364 GAAGTGGTTCGTTGCCTCAACAGTGCTCTACAGGTCGGCTGCGGGGCTTTTGCATGCCTG 423

Qy         61 GluAsnSerThrCysAspThrAspGlyMetTyrAspIleCysLysSerPheLeuTyrSer 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        424 GAAAACTCCACCTGTGACACAGATGGGATGTATGACATCTGTAAATCCTTCTTGTACAGC 483

Qy         81 AlaAlaLysPheAspThrGlnGlyLysAlaPheValLysGluSerLeuLysCysIleAla 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        484 GCTGCTAAATTTGACACTCAGGGAAAAGCATTCGTCAAAGAGAGCTTAAAATGCATCGCC 543

Qy        101 AsnGlyValThrSerLysValPheLeuAlaIleArgArgCysSerThrPheGlnArgMet 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        544 AACGGGGTCACCTCCAAGGTCTTCCTCGCCATTCGGAGGTGCTCCACTTTCCAAAGGATG 603

Qy        121 IleAlaGluValGlnGluGluCysTyrSerLysLeuAsnValCysSerIleAlaLysArg 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        604 ATTGCTGAGGTGCAGGAAGAGTGCTACAGCAAGCTGAATGTGTGCAGCATCGCCAAGCGG 663

Qy        141 AsnProGluAlaIleThrGluValValGlnLeuProAsnHisPheSerAsnArgTyrTyr 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        664 AACCCTGAAGCCATCACTGAGGTCGTCCAGCTGCCCAATCACTTCTCCAACAGATACTAT 723

Qy        161 AsnArgLeuValArgSerLeuLeuGluCysAspGluAspThrValSerThrIleArg 179
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        724 AACAGACTTGTCCGAAGCCTGCTGGAATGTGATGAAGACACAGTYAGCACAATCAGA 780

RESULT 11
BQ308414
LOCUS       BQ308414                577 bp    mRNA    linear   EST 16-MAY-2002
DEFINITION  MR0-BT4501-280601-103-c11 BT4501 Homo sapiens cDNA, mRNA sequence.
ACCESSION   BQ308414
VERSION     BQ308414.1  GI:20849730
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 577)
  AUTHORS   Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
            Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
            Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
            Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
            ,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
            Simpson,A.J.
```

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  TITLE     Shotgun sequencing of the human transcriptome with ORF expressed
            sequence tags
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
  MEDLINE   20202663
COMMENT     Contact: Simpson A.J.G.
            Laboratory of Cancer Genetics
            Ludwig Institute for Cancer Research
            Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
            Brazil
            Tel: +55-11-2704922
            Fax: +55-11-2707001
            Email: asimpson@ludwig.org.br
            This sequence was derived from the FAPESP/LICR Human Cancer Genome
            Project. This entry can be seen in the following URL
            (http://www.ludwig.org.br/scripts/gethtml2.pl?t1=MR0&t2=MR0-BT4501-
            280601-103-c11&t3=2001-06-28&t4=1)
            Seq primer: puc 18 forward
            High quality sequence stop: 576.
FEATURES             Location/Qualifiers
     source          1. .577
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone_lib="BT4501"
                     /dev_stage="Adult"
                     /note="Organ: breast; Vector: puc18; Site_1: SmaI; Site_2:
                     SmaI; A mini-library was made by cloning products derived
                     from  ORESTES PCR (U.S. Letters Patent application No. 196
                     ,716 -  Ludwig Institute for Cancer Research) profiles
                     into the pUC 18 vector. Reverse transcription of tissue
                     mRNA and cDNA amplification were performed under low
                     stringency conditions."
BASE COUNT      161 a    159 c    140 g    117 t
ORIGIN

Alignment Scores:
Pred. No.:              5.13e-94        Length:         577
Score:                  849.00          Matches:        183
Percent Similarity:     96.83%          Conservative:   0
Best Local Similarity:  96.83%          Mismatches:     4
Query Match:            66.96%          Indels:         6
DB:                     14              Gaps:           0

US-09-705-500A-3 (1-247) x BQ308414 (1-577)

Qy         38 AsnSerAlaGluValValArgCysLeuAsnSerAlaLeuGlnValGlyCysGlyAlaPhe 57
              ||||||||||||||||||  ||||||||||||||||||||||||||||||||||    |||
Db          1 AACTCAGCTGAAGTGGTTC--TGCCTCAACAGTGCTCTACAGGTCGGCTGCGGGGC-TTT 57

Qy         58 AlaCysLeuGluAsnSerThrCysAspThr-AspGlyMetTyrAspIleCysLysSerPh 77
              |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db         58 GCATGCCTGGAAAACTCCACCTGTGACACAGGATGGGATGTATGACATCTGTAAATCCTT 117

Qy         77 eLeuTyrSerAlaAlaLysPheAspThrGlnGlyLysAlaPheValLysGluSerLeuLy 97
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        118 CTTGTACAGCGCTGCTAAATTTGACACTCAGGGAAAAGCATTCGTCAAAGAGAGCTTAAA 177

Qy         97 sCysIleAlaAsnGlyValThrSerLysValPheLeuAlaIleArgArgCysSerThrPh 117
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        178 ATGCATCGCCAACGGGGTCACCTCCAAGGTCTTCCTCGCCATTCGGAGGTGCTCCACTTT 237

Qy        117 eGlnArgMetIleAlaGluValGlnGluGluCysTyrSerLysLeuAsnValCysSerIl 137
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        238 CCAAAGGATGATTGCTGAGGTGCAGGAAGAGTGCTACAGCAAGCTGAATGTGTGCAGCAT 297

Qy        137 eAlaLysArgAsnProGluAlaIleThrGluValValGlnLeuProAsnHisPheSerAs 157
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        298 CGCCAAGCGGAACCCTGAAGCCATCACTGAGGTCGTCCAGCTGCCCAATCACTTCTCCAA 357

Qy        157 nArgTyrTyrAsnArgLeuValArgSerLeuLeuGluCysAspGluAspThrValSerTh 177
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        358 CAGATACTATAACAGACTTGTCCGAAGCCTGCTGGAATGTGATGAAGACACAGTCAGCAC 417

Qy        177 rIleArgAspSerLeuMetGluLysIleGlyPro-AsnMetAlaSerLeuPheHisIleL 197
              ||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Db        418 AATCAGAGACAGCCTGATGGAGAAAATTGGGCCTAAACATGGCCAGCCTCTTCCACATCC 477

Qy        197 euGlnThrAspHisCysAlaGlnThrHisProArgAlaAspPheAsnArgArgArgThrA 217
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||    |
Db        478 TGCAGACAGACCACTGTGCCCAAACACACCCACGAGCTGACTTCAACAGGAGACGCCC-A 536

Qy        217 snGluProGlnLysLeuLysVal 224
              ||||||||  ||||||||||||
Db        537 ATGAGCCGAA-AAGCTGAAAGTC 558

RESULT 12
BF042539
LOCUS       BF042539                 560 bp    mRNA    linear   EST 10-OCT-2000
DEFINITION  BP250022A10G7 Soares normalized bovine placenta Bos taurus cDNA
            clone BP250022A10G7 5', mRNA sequence.
ACCESSION   BF042539
VERSION     BF042539.1  GI:10759594
KEYWORDS    EST.
SOURCE      cow.
  ORGANISM  Bos taurus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
            Bovidae; Bovinae; Bos.
REFERENCE   1  (bases 1 to 560)
  AUTHORS   Lewin,H.A., Soares,M.B., Rebeiz,M., Pardinas,J., Liu,L. and Larson
            ,J.H.
  TITLE     Bovine ESTs
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Lewin, H. A.
            W. M. Keck Center for Comparative and Functional Genomics
            University of Illinois at Urbana-Champaign
            340 Edward R. Madigan Laboratory, 1201 W. Gregory Dr., Urbana, IL
            61801, USA
            Tel: 217 333 5998
            Fax: 217 244 5617
            Email: h-lewin@uiuc.edu
            Funding for cattle EST sequencing was provided by the USDA National
            Research Initiative, Animal Genome Resource Grant AG 99-3205-8534
            to H. A. Lewin and J. E. Womack. Base Calling/Quality Scores: PHRED
            from Washington University Genome Center. Vector Trimmi g:
            Cross_match from Washington University Genome Center PHRAP suite.
            This sequence is vector free and at least 200 bp in length.
            PCR PRimers
            FORWARD: TAATACGACTCACTATAGGG
            BACKWARD: ATTAACCCTCACTAAAG
            Insert Length: 560   Std Error: 0.00
            Plate: BP250022A10  row: G  column: 7
            Seq primer: AGCGGATAACAATTTCACACAGGA
            High quality sequence stop: 560.
FEATURES             Location/Qualifiers
     source          1. .560
                     /organism="Bos taurus"
                     /db_xref="taxon:9913"
                     /clone="BP250022A10G7"
                     /clone_lib="Soares normalized bovine placenta"
                     /sex="female"
                     /lab_host="DH10B"
                     /note="Organ: placenta; Vector: pT7T3Pac; Site_1: EcoRI;
                     Site_2: NotI; The cDNA library was contributed by the
                     Soares laboratory and it  was constructed and normalized
                     as described by Bonaldo, M.F.,  Lennon, G. and Soares,
                     M.B. (1996), Genome Research 6(9): 791-806. "
BASE COUNT      150 a    142 c    146 g    122 t
ORIGIN

Alignment Scores:
Pred. No.:              6.45e-94        Length:         560
Score:                  848.00          Matches:        165
Percent Similarity:     99.41%          Conservative:   4
Best Local Similarity:  97.06%          Mismatches:     1
Query Match:            66.88%          Indels:         0
DB:                     12              Gaps:           0
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```
US-09-705-500A-3 (1-247) x BF042539 (1-560)

Qy          1 MetLeuGlnAsnSerAlaValLeuLeuValLeuValIleSerAlaSerAlaThrHisGlu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         49 ATGCTCCAAAACTCAGCAGTGCTTCTGGTGCTGGTGATCAGTGCTTCTGCAACCCATGAG 108

Qy         21 AlaGluGlnAsnAspSerValSerProArgLysSerArgValAlaAlaGlnAsnSerAla 40
              ||||||||||||||||||||||    ||||||||||||||||||||||||||||||||
Db        109 GCGGAGCAGAATGATTCTGTGAGCCTCAGGAAATCCCGGGTGGCAGCTCAGAACTCAGCT 168

Qy         41 GluValValArgCysLeuAsnSerAlaLeuGlnValGlyCysGlyAlaPheAlaCysLeu 60
              ||||||:::||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        169 GAAGTGATTCGCTGCCTCAACAGCGCGCTGCAGGTTGGCTGTGGAGCTTTTGCATGCCTG 228

Qy         61 GluAsnSerThrCysAspThrAspGlyMetTyrAspIleCysLysSerPheLeuTyrSer 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        229 GAGAACTCCACCTGTGACACAGATGGGATGTACGACATCTGTAAATCCTTCTTGTACAGC 288

Qy         81 AlaAlaLysPheAspThrGlnGlyLysAlaPheValLysGluSerLeuLysCysIleAla 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        289 GCTGCTAAATTTGACACTCAGGGAAAAGCATTTGTCAAAGAGAGCTTAAAGTGCATCGCC 348

Qy        101 AsnGlyValThrSerLysValPheLeuAlaIleArgArgCysSerThrPheGlnArgMet 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        349 AACGGGGTCACCTCCAAGGTCTTCCTGGCCATTCGGAGGTGCTCTACTTTCCAGAGGATG 408

Qy        121 IleAlaGluValGlnGluGluCysTyrSerLysLeuAsnValCysSerIleAlaLysArg 140
              ||||||||||||||||||||||||:::||||||||||||||||:::|||||||||||||||
Db        409 ATTGCCGAAGTCCAGGAGGAGTGCTACACCAAGCTGAACGTGTGCAGTGTCGCCAAGCGG 468

Qy        141 AsnProGluAlaIleThrGluValValGlnLeuProAsnHisPheSerAsnArgTyrTyr 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        469 AACCCGGAAGCCATCACGGAAGTCGTCCAGCTCCCTAATCATTTCTCCAACAGATACTAT 528

Qy        161 AsnArgLeuValArgSerLeuLeuGluCys 170
              ||||||||||||||||||||||:::|||
Db        529 AACAGACTTGTCCGAAGCCTACTGGACTGT 558

RESULT 13
BE476621
LOCUS       BE476621                513 bp    mRNA    linear   EST 28-AUG-2000
DEFINITION  159962 BARC 5BOV Bos taurus cDNA 5', mRNA sequence.
ACCESSION   BE476621
VERSION     BE476621.1  GI:9596154
KEYWORDS    EST.
SOURCE      cow.
  ORGANISM  Bos taurus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
            Bovidae; Bovinae; Bos.
REFERENCE   1  (bases 1 to 513)
  AUTHORS   Sonstegard,T.S., Capuco,A.V., Van Tassell,C.P., Ashwell,M.S. and
            Wells,K.D.
  TITLE     Mapping of Expressed Sequence Tags from a normalized bovine mammary
            gland cDNA library
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Sonstegard TS
            USDA, ARS, Beltsville Agricultural Research Center
            Bdlg. 200 Rm 2A, Beltsville, MD 20705, USA
            Tel: 301 504 8416
            Fax: 301 504 8414
            Email: tads@anri.barc.usda.gov
            Single pass sequencing. Bases called and alt_trimmed with phred
            v0.980904.e. Vector identified by cross_match with the -minscore 18
            and -minmatch 12 options.
            PCR PRimers
            FORWARD: AGGAAACAGCTATGACCAT
            BACKWARD: GTTTTCCCAGTCACGACG
            Plate: 28  row: D  column: 7
            Seq primer: ATTTAGGTGACACTATAG.
FEATURES             Location/Qualifiers
     source          1. .513
                     /organism="Bos taurus"
                     /db_xref="taxon:9913"
                     /clone_lib="BARC 5BOV"
                     /tissue_type="pooled"
                     /lab_host="DH10B"
                     /note="Vector: pCMV SPORT6; Site_1: NotI; Site_2: SalI;
                     Library made from pooled mRNA isolated from mammary
                     tissues at eight physiological, developmental, and disease
                     states."
BASE COUNT      129 a    133 c    135 g    116 t
ORIGIN

Alignment Scores:
Pred. No.:                7.08e-93        Length:          513
Score:                    839.00          Matches:         164
Percent Similarity:       99.41%          Conservative:    4
Best Local Similarity:    97.04%          Mismatches:      1
Query Match:              66.17%          Indels:          0
DB:                       10              Gaps:            0

US-09-705-500A-3 (1-247) x BE476621 (1-513)

Qy          1 MetLeuGlnAsnSerAlaValLeuLeuValLeuValIleSerAlaSerAlaThrHisGlu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          6 ATGCTCCAAAACTCAGCAGTGCTTCTGGTGCTGGTGATCAGTGCTTCTGCAACCCATGAG 65

Qy         21 AlaGluGlnAsnAspSerValSerProArgLysSerArgValAlaAlaGlnAsnSerAla 40
              ||||||||||||||||||||||    ||||||||||||||||||||||||||||||||
Db         66 GCGGAGCAGAATGATTCTGTGAGCCTCAGGAAATCCCGGGTGGCAGCTCAGAACTCAGCT 125

Qy         41 GluValValArgCysLeuAsnSerAlaLeuGlnValGlyCysGlyAlaPheAlaCysLeu 60
              ||||||:::||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        126 GAAGTGATTCGCTGCCTCAACAGCGCGCTGCAGGTTGGCTGTGGAGCTTTTGCATGCCTG 185

Qy         61 GluAsnSerThrCysAspThrAspGlyMetTyrAspIleCysLysSerPheLeuTyrSer 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        186 GAGAACTCCACCTGTGACACAGATGGGATGTACGACATCTGTAAATCCTTCTTGTACAGC 245

Qy         81 AlaAlaLysPheAspThrGlnGlyLysAlaPheValLysGluSerLeuLysCysIleAla 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        246 GCTGCTAAATTTGACACTCAGGGAAAAGCATTTGTCAAAGAGAGCTTAAAGTGCATCGCC 305

Qy        101 AsnGlyValThrSerLysValPheLeuAlaIleArgArgCysSerThrPheGlnArgMet 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        306 AACGGGGTCACCTCCAAGGTCTTCCTGGCCATTCGGAGGTGCTCTACTTTCCAGAGGATG 365

Qy        121 IleAlaGluValGlnGluGluCysTyrSerLysLeuAsnValCysSerIleAlaLysArg 140
              ||||||||||||||||||||||||||:::|||||||||||||||||:::||||||||||||
Db        366 ATTGCCGAAGTCCAGGAGGAGTGCTACACCAAGCTGAACGTGTGCAGTGTCGCCAAGCGG 425

Qy        141 AsnProGluAlaIleThrGluValValGlnLeuProAsnHisPheSerAsnArgTyrTyr 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        426 AACCCGGAAGCCATCACGGAAGTCGTCCAGCTCCCTAATCATTTCTCCAACAGATACTAT 485

Qy        161 AsnArgLeuValArgSerLeuLeuGlu 169
              ||||||||||||||||||||||:::
Db        486 AACAGACTTGTCCGAAGCCTACTGGAC 512

RESULT 14
AL550611
LOCUS       AL550611                908 bp    mRNA    linear   EST 16-FEB-2001
DEFINITION  AL550611 LTI_NFL006_PL2 Homo sapiens cDNA clone CS0DI058YD08 5
            prime, mRNA sequence.
ACCESSION   AL550611
VERSION     AL550611.1  GI:12887746
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 908)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE     Full-length cDNA libraries and normalization
```

```
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Genoscope
            Genoscope - Centre National de Sequencage
            BP 191 91006 EVRY cedex - France
            Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
FEATURES             Location/Qualifiers
     source          1. .908
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="CS0DI058YD08"
                     /clone_lib="LTI_NFL006_PL2"
                     /tissue_type="placenta"
                     /note="Vector: pCMVSPORT 6;.Site_1: NotI; 1st strand cDNA
                     was primed with a NotI-oligo(dT) primer.  Five prime end
                     enriched, double-stranded cDNA was digested with Not I and
                     cloned into the Not I and Eco RV sites of the pCMVSPORT 6
                     vector. Library was normalized. Library was constructed by
                     Life Technologies. Contact : Feng Liang Life Technologies,
                     a division of Invitrogen 9800 Medical Center Drive
                     Rockville, Maryland 20850, USA Fax : (1) 301 610 8371
                     Email : fliang@lifetech.com URL :
                     http://fulllength.invitrogen.com"
BASE COUNT      262 a    246 c    181 g    215 t      4 others
ORIGIN

Alignment Scores:
Pred. No.:              2.01e-92        Length:         908
Score:                  839.00          Matches:        162
Percent Similarity:     98.18%          Conservative:   0
Best Local Similarity:  98.18%          Mismatches:     3
Query Match:            66.17%          Indels:         0
DB:                     9               Gaps:           0

US-09-705-500A-3 (1-247) x AL550611 (1-908)

Qy         83 LysPheAspThrGlnGlyLysAlaPheValLysGluSerLeuLysCysIleAlaAsnGly 102
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 AAATTTGACACTCAGGGAAAAGCATTCGTCAAAGAGAGCTTAAAATGCATCGCCAACGGG 60

Qy        103 ValThrSerLysValPheLeuAlaIleArgArgCysSerThrPheGlnArgMetIleAla 122
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GTCACCTCCAAGGTCTTCCTCGCCATTCGGAGGTGCTCCACTTTCCAAAGGATGATTGCT 120

Qy        123 GluValGlnGluGluCysTyrSerLysLeuAsnValCysSerIleAlaLysArgAsnPro 142
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GAGGTGCAGGAAGAGTGCTACAGCAAGCTGAATGTGTGCAGCATCGCCAAGCGGAACCCT 180

Qy        143 GluAlaIleThrGluValValGlnLeuProAsnHisPheSerAsnArgTyrTyrAsnArg 162
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GAAGCCATCACTGAGGTCGTCCAGCTGCCCAATCACTTCTCCAACAGATACTATAACAGA 240

Qy        163 LeuValArgSerLeuLeuGluCysAspGluAspThrValSerThrIleArgAspSerLeu 182
              |||||||||||||||   ||||||||||||||||||||||||||||||   |||||||||
Db        241 CTTGTCCGAAGCCTGCYGGAATGTGATGAAGACACAGTCAGCACAATCARAGACAGCCTG 300

Qy        183 MetGluLysIleGlyProAsnMetAlaSerLeuPheHisIleLeuGlnThrAspHisCys 202
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 ATGGAGAAAATTGGGCCTAACATGGCCAGCCTCTTCCACATCCTGCAGACAGACCACTGT 360

Qy        203 AlaGlnThrHisProArgAlaAspPheAsnArgArgArgThrAsnGluProGlnLysLeu 222
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GCCCAAACACACCCACGAGCTGACTTCAACAGGAGACGCACCAATGAGCCGCAGAAGCTG 420

Qy        223 LysValLeuLeuArgAsnLeuArgGlyGluGluAspSerProSerHisIleLysArgThr 242
              ||||||||||||||||||   ||||||||||||||||||||||||||||||||||||||||
Db        421 AAAGTCCTCCTCAGGAACCTCCSAGGTGAGGAGGACTCTCCCTCCCACATCAAACGCACA 480

Qy        243 SerHisGluSerAla 247
              ||||||||||||||||
Db        481 TCCCATGAGAGTGCA 495

RESULT 15
BM924595

LOCUS       BM924595               1010 bp    mRNA    linear   EST 12-MAR-2002
DEFINITION  AGENCOURT_6767843 NIH_MGC_116 Homo sapiens cDNA clone IMAGE:5760977
            5', mRNA sequence.
ACCESSION   BM924595
VERSION     BM924595.1  GI:19374974
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1010)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Life Technologies, Inc.
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Agencourt Bioscience Corporation
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM12808  row: n  column: 18
            High quality sequence stop: 614.
FEATURES             Location/Qualifiers
     source          1. .1010
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:5760977"
                     /clone_lib="NIH_MGC_116"
                     /lab_host="DH10B"
                     /note="Organ: pooled colon, kidney, stomach; Vector:
                     pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA
                     source anonymous pool of 3 colons, age 26 yo male, 49 yo
                     female, 71 yo male colon; 46 yo male kidney, and pool of 2
                     stomachs, 62 yo male and 70 yo female.  Library is
                     oligo-dT primed and  directionally cloned (EcoRV site is
                     destroyed upon cloning).  Average insert size 1.4 kb,
                     insert size range 1-3 kb.  Library is normalized and
                     enriched for full-length clones and was constructed by C.
                     Gruber  (Invitrogen).  Research Genetics tracking code
                     023. Note: this is a NIH_MGC Library."
BASE COUNT      305 a    285 c    251 g    169 t
ORIGIN

Alignment Scores:
Pred. No.:              1.26e-89        Length:         1010
Score:                  817.00          Matches:        183
Percent Similarity:     79.75%          Conservative:   10
Best Local Similarity:  75.62%          Mismatches:     22
Query Match:            64.43%          Indels:         27
DB:                     14              Gaps:           6

US-09-705-500A-3 (1-247) x BM924595 (1-1010)

Qy          1 MetLeuGlnAsnSerAlaValLeuLeuValLeuValIleSerAlaSerAlaThrHisGlu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        263 ATGCTCCAAAACTCAGCAGTGCTTCTGGTGCTGGTGATCAGTGCTTCTGCAACCCATGAG 322

Qy         21 AlaGluGlnAsnAspSerValSerProArgLysSerArgValAlaAlaGlnAsnSerAla 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        323 GCGGAGCAGAATGACTCTGTGAGCCCCAGGAAATCCCGAGTGGCGGCTCAAAACTCAGCT 382

Qy         41 GluValValArgCysLeuAsnSerAlaLeuGlnValGlyCysGlyAlaPheAlaCysLeu 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        383 GAAGTGGTTCGTTGCCTCAACAGTGCTCTACAGGTCGGCTGCGGGGCTTTTGCATGCCTG 442

Qy         61 GluAsnSerThrCysAspThrAspGlyMetTyrAspIleCysLysSerPheLeuTyrSer 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        443 GAAAACTCCACCTGTGACACAGATGGGATGTATGACATCTGTAAATCCTTCTTGTACAGC 502

Qy         81 AlaAlaLysPheAspThrGlnGlyLysAlaPheValLysGluSerLeuLysCysIleAla 100
```

```
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          503 GCTGCTAAATTTGACACTCAGGGAAAAGCATTCGTCAAAGAGAGCTTAAAATGCATCGCC 562

Qy          101 AsnGlyValThrSerLysValPheLeuAlaIleArgArgCysSerThrPheGlnArgMet 120
                ||||||||||||||||||||||||||||||||||||||||||||||||||||:::|||
Db          563 AACGGGGTCACCTCCAAGGTCTTCCTCGCCATTCGGAGGTGCTCCACTTTCCAAAAGATG 622

Qy          121 IleAlaGluValGlnGluGluCysTyrSerLysLeuAsnValCysSerIleAlaLysArg 140
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          623 ATTGCTGAGGTGCAGGAAGAGTGCTACAGCAAGCTGAATGTGTGCAGCATCGCCAAGCGG 682

Qy          141 AsnPro-GluAlaIleThrGluValValGlnLeuProAsnHis-PheSerAsnArgTyrT 160
                |||||| |||||||||||||||||||||||||||||||||| |||||||||||||||
Db          683 AACCCTGGAAGCCATCACTGAGGTCGTCCAGCTGCCCAATCACTTTCTCCAACAGATACT 742

Qy          160 yrAsnArgLeuValArgSerLeuLeuGluCysAspGluAspThrValSerThrIleArgA 180
                |||||||                  |||   :::      :::      :::
Db          743 ATAACAGA-----------------ACTTGTCCCAAAGCCCTGCTGGGAATGGTGATGA 784

Qy          180 spSerLeuMet----------------------------GluLysIle--GlyProAs 189
                  :::   :::                          |||||||||  ||||||||
Db          785 AAAACACAGTTCAGCACAAATCAAAAGACAGCCCTGAGGGAGAAAAAATTGGGGCCCTAA 844

Qy          189 nMetAla---SerLeuPheHisIle-LeuGlnThr---AspHisCysAlaGlnThrHis- 206
                ||||      :::   |||||||||  ||||||      |||                |||
Db          845 CATGGGCCAGGCCTCCTTCCACATCCCTGCAGAACAGAACCCATTGGGGCCCCAAACACC 904

Qy          207 -----ProArgAlaAspPheAsnArgArgArgThr------AsnGluProGlnLys 221
                    |||:::   ||||||         :::|||         ||||||:::|||
Db          905 CCCCACCGAAGCTGGACTTCCAACACGGGAAAACCCCCCCAATGGAACCCCGCAAA 960

Search completed: June 12, 2003, 21:14:01
Job time : 1425 secs
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: June 12, 2003, 17:27:49 ; Search time 60 Seconds
(without alignments)
548.548 Million cell updates/sec

Title: US-09-705-500A-3
Perfect score: 1268
Sequence: 1 MLQNSAVLLVLVISASATHE.....NLRGEEDSPSHIKRTSHESA 247

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_101002:*
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22: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA2001.DAT:*
23: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1268	100.0	247	16	AAR84522	Stanniocalcin from
2	1268	100.0	247	21	AAB23264	Human stanniocalci
3	1268	100.0	247	21	AAY92901	Human stanniocalci
4	1268	100.0	247	21	AAY55750	Human stanniocalci
5	1268	100.0	247	21	AAY57166	Human corpuscles o
6	1268	100.0	247	22	AAB62690	Lng108, a diagnost
7	1268	100.0	247	22	AAB62473	Human stanniocalci
8	1268	100.0	247	23	ABB06259	Human staniocalcin
9	937	73.9	276	21	AAB56848	Human prostate can
10	680.5	53.7	261	9	AAP82968	Corpuscles of Stan
11	662.5	52.2	256	22	AAB62474	Coho salmon stanni
12	628	49.5	170	21	AAY55749	A. australis stann
13	358	28.2	70	22	ABB31928	Peptide #4579 enco
14	358	28.2	70	22	ABB37166	Peptide #4672 enco
15	358	28.2	70	22	ABB22472	Protein #4471 enco
16	358	28.2	70	22	AAM57878	Human brain expres
17	358	28.2	70	22	AAM70300	Human bone marrow
18	358	28.2	70	22	AAM18134	Peptide #4568 enco
19	358	28.2	70	22	AAM30637	Peptide #4674 enco
20	358	28.2	70	22	AAM05763	Peptide #4445 enco
21	358	28.2	70	23	ABG39940	Human peptide enco
22	354.5	28.0	296	21	AAY67926	Mouse stanniocalci
23	354.5	28.0	296	22	AAB61623	Murine stanniocalc
24	354	27.9	293	20	AAY41255	Adipogenesis inhib
25	354	27.9	293	21	AAB26872	Human adipocytogen
26	354	27.9	293	22	AAB93965	Human protein sequ
27	354	27.9	302	21	AAY67925	Human stanniocalci
28	354	27.9	302	22	AAB98971	Human adipogenesis
29	354	27.9	302	22	AAB95330	Human protein sequ
30	354	27.9	302	22	AAB31797	Amino acid sequenc
31	354	27.9	302	22	AAB61621	Human stanniocalci
32	335.5	26.5	251	17	AAR97978	Stanniocalcin alph
33	333.5	26.3	251	21	AAY55748	Human stanniocalci
34	111	8.8	40	20	AAY41254	Adipogenesis inhib
35	111	8.8	40	21	AAB26871	N-terminal amino a
36	111	8.8	40	22	AAB98970	Adipogenesis inhib
37	99	7.8	40	20	AAY41253	Adipogenesis inhib
38	99	7.8	40	21	AAB26870	N-terminal amino a
39	99	7.8	40	22	AAB98969	Adipogenesis inhib
40	93	7.3	19	21	AAY82531	Human stanniocalci
41	91	7.2	901	23	AAG66003	P. patens cell cyc
42	90.5	7.1	783	23	ABP35616	Fungal ZBC protein
43	90	7.1	282	20	AAY02781	Human secreted pro
44	90	7.1	331	23	ABP41192	Human ovarian anti
45	89.5	7.1	10182	23	ABP38314	Staphylococcus epi

ALIGNMENTS

RESULT 1
AAR84522
ID AAR84522 standard; Protein; 247 AA.
XX
AC AAR84522;
XX
DT 19-APR-1996 (first entry)
XX
DE Stanniocalcin from Corpuscles of Stannius.
XX
KW stanniocalcin; Corpuscles of Stannius; hypocalcaemia; hypercalcaemia;
KW electrolyte disorder; osteoporosis; Paget's disease; treatment.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Region 1..33
FT /label= prepro_region
FT Protein 34..247
FT /label= mature_stanniocalcin
XX
PN WO9524411-A1.
XX
PD 14-SEP-1995.
XX
PF 09-MAY-1994; 94WO-US05136.
XX
PR 08-MAR-1994; 94US-0208005.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Adams MD, Olsen H;
XX

DR WPI; 1995-328227/42.
DR N-PSDB; AAT02438.
XX
PT Human corpuscles of Stannius polypeptide(s) - used to treat
PT hypercalcaemia, hypocalcaemia and other electrolyte disorders
XX
PS Claim 14; Fig 1; 41pp; English.
XX
CC Stanniocalcin, a Corpuscles of Stannius polypeptide is encoded by
CC AAT02438. Stanniocalcin functions as a hypocalcaemic agent, and can be
CC used for the treatment of e.g. electrolyte disorders which lead to renal,
CC bone and heart diseases, hypertension, hypercalcaemia and disorders due
CC to elevated bone resorption, e.g. osteoporosis and Paget's disease.
XX
SQ Sequence 247 AA;

Query Match 100.0%; Score 1268; DB 16; Length 247;
Best Local Similarity 100.0%; Pred. No. 5.9e-124;
Matches 247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLQNSAVLLVLVISASATHEAEQNDSVSPRKSRVAAQNSAEVVRCLNSALQVGCGAFACL 60
Db 1 MLQNSAVLLVLVISASATHEAEQNDSVSPRKSRVAAQNSAEVVRCLNSALQVGCGAFACL 60

Qy 61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM 120
Db 61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM 120

Qy 121 IAEVQEECYSKLNVCSIAKRNPEAITEVVQLPNHFSNRYYNRLVRSLLECDEDTVSTIRD 180
Db 121 IAEVQEECYSKLNVCSIAKRNPEAITEVVQLPNHFSNRYYNRLVRSLLECDEDTVSTIRD 180

Qy 181 SLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRRTNEPQKLKVLLRNLRGEEDSPSHIK 240
Db 181 SLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRRTNEPQKLKVLLRNLRGEEDSPSHIK 240

Qy 241 RTSHESA 247
Db 241 RTSHESA 247

RESULT 2
AAB23264
ID AAB23264 standard; Protein; 247 AA.
XX
AC AAB23264;
XX
DT 02-FEB-2001 (first entry)
XX
DE Human stanniocalcin.
XX
KW Human; stanniocalcin; STC; osteogenesis; bone disease; osteoporosis;
KW mineral metabolism regulator; prophylaxis; therapy.
XX
OS Homo sapiens.
XX
PN JP2000229880-A.
XX
PD 22-AUG-2000.
XX
PF 10-FEB-1999; 99JP-0033262.
XX
PR 10-FEB-1999; 99JP-0033262.
XX
PA (SNOW) SNOW BRAND MILK PROD CO LTD.
XX
DR WPI; 2000-605236/58.
DR N-PSDB; AAA97594.
XX
PT An osteogenesis promoter useful in the prevention and/or treatment of
PT bone diseases such as osteoporosis -
XX
PS Example 1; Page 5-6; 6pp; Japanese.
XX
CC The invention relates to a novel osteogenesis-promoting composition
CC which contains stanniocalcin (STC) as the active component.
CC Stanniocalcin is a possible regulator of mineral metabolism. The
CC composition is useful as a prophylactic and/or therapeutic agent for
CC bone diseases such as osteoporosis. The present sequence represents
CC human stanniocalcin which was used in an exemplification of the
CC invention.
XX
SQ Sequence 247 AA;

Query Match 100.0%; Score 1268; DB 21; Length 247;
Best Local Similarity 100.0%; Pred. No. 5.9e-124;
Matches 247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLQNSAVLLVLVISASATHEAEQNDSVSPRKSRVAAQNSAEVVRCLNSALQVGCGAFACL 60
Db 1 MLQNSAVLLVLVISASATHEAEQNDSVSPRKSRVAAQNSAEVVRCLNSALQVGCGAFACL 60

Qy 61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM 120
Db 61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM 120

Qy 121 IAEVQEECYSKLNVCSIAKRNPEAITEVVQLPNHFSNRYYNRLVRSLLECDEDTVSTIRD 180
Db 121 IAEVQEECYSKLNVCSIAKRNPEAITEVVQLPNHFSNRYYNRLVRSLLECDEDTVSTIRD 180

Qy 181 SLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRRTNEPQKLKVLLRNLRGEEDSPSHIK 240
Db 181 SLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRRTNEPQKLKVLLRNLRGEEDSPSHIK 240

Qy 241 RTSHESA 247
Db 241 RTSHESA 247

RESULT 3
AAY92901
ID AAY92901 standard; Protein; 247 AA.
XX
AC AAY92901;
XX
DT 26-SEP-2000 (first entry)
XX
DE Human stanniocalcin protein.
XX
KW PCR primer; human; stanniocalcin; inhibitor; differentiation; maturation;
KW adipocyte; obesity; diabetes; hypertension; heart disease.
XX
OS Homo sapiens.
XX
PN WO200016795-A1.
XX
PD 30-MAR-2000.
XX
PF 17-SEP-1999; 99WO-JP05080.
XX
PR 17-SEP-1998; 98JP-0263004.
XX
PA (SNOW) SNOW BRAND MILK PROD CO LTD.
XX
PI Goto M, Tomoyasu A, Yamaguchi K, Kinosaki M, Nakagawa N;
XX
DR WPI; 2000-283445/24.
DR N-PSDB; AAA11145.
XX
PT Treating or preventing obesity, which is a risk factor for diabetes,
PT hypertension and heart disease, comprises administering an agent
PT containing stanniocalcin -
XX
PS Example 1; Page 16; 19pp; Japanese.
XX
CC This sequence represents the human stanniocalcin protein. Stanniocalcin

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CC   is an inhibitor of the differentiation and maturation of adipocytes. The
CC   protein is used for preventing and treating obesity which is a risk
CC   factor for diabetes, hypertension, and heart disease. The coding sequence
CC   was isolated from IMR-90 cells.
XX
SQ   Sequence   247 AA;

  Query Match             100.0%;  Score 1268;  DB 21;  Length 247;
  Best Local Similarity   100.0%;  Pred. No. 5.9e-124;
  Matches  247;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MLQNSAVLLVLVISASATHEAEQNDSVSPRKSRVAAQNSAEVVRCLNSALQVGCGAFACL 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MLQNSAVLLVLVISASATHEAEQNDSVSPRKSRVAAQNSAEVVRCLNSALQVGCGAFACL 60

Qy         61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM 120

Qy        121 IAEVQEECYSKLNVCSIAKRNPEAITEVVQLPNHFSNRYYNRLVRSLLECDEDTVSTIRD 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 IAEVQEECYSKLNVCSIAKRNPEAITEVVQLPNHFSNRYYNRLVRSLLECDEDTVSTIRD 180

Qy        181 SLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRRTNEPQKLKVLLRNLRGEEDSPSHIK 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 SLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRRTNEPQKLKVLLRNLRGEEDSPSHIK 240

Qy        241 RTSHESA 247
              |||||||
Db        241 RTSHESA 247


RESULT 4
AAY55750
ID   AAY55750 standard; Protein; 247 AA.
XX
AC   AAY55750;
XX
DT   11-FEB-2000  (first entry)
XX
DE   Human stanniocalcin polypeptide.
XX
KW   Stanniocalcin-alpha polypeptide; teleocalcin; hypocalcin; hypercalcemic;
KW   anti-hypercalcemic glycoprotein hormone; corpuscles of stannius; PTH;
KW   parathyroid hormone; bone reabsorption; osteoporosis; gene therapy; bone;
KW   electrolyte disorder; renal; heart disease; osteopetrosis; human;
KW   Paget's disease; hypercalcemia.
XX
OS   Homo sapiens.
XX
PN   US5994103-A.
XX
PD   30-NOV-1999.
XX
PF   02-JUN-1995;   95US-0460529.
XX
PR   10-NOV-1994;   94WO-US13206.
XX
PA   (HUMA-) HUMAN GENOME SCI INC.
XX
PI   Fleischmann RD,  Olsen HS;
XX
DR   WPI; 2000-038260/03.
XX
PT   Isolated nucleic acids encoding human stanniocalcin-alpha useful for
PT   treating electrolyte disorders which lead to renal, bone and heart
PT   diseases, osteoporosis and Paget's disease -
XX
PS   Disclosure; Fig 3; 21pp; English.
XX
CC   The invention provides a human stanniocalcin-alpha polypeptide (also
CC   called teleocalcin and hypocalcin). Stanniocalcin-alpha is an anti-
CC   hypercalcemic glycoprotein hormone produced by the corpuscles of
CC   stannius. It has a similar reported biological activity to that of
CC   parathyroid hormone (PTH) and both these proteins exhibit dual functions
CC   in mammals. They exert hypercalcemic activity due to stimulation of bone
CC   reabsorption. Further PTH has a biphasic action on bone metabolism (i.e.
CC   at low doses it increases bone formation and at high doses it increases
CC   bone reabsorption. Accordingly, human stanniocalcin-alpha and antagonists
CC   of it (under different circumstances) may be used to treat osteoporosis.
CC   The DNA may be used to produce human stanniocalcin-alpha according to
CC   standard recombinant DNA methodologies. The human stanniocalcin-alpha may
CC   be produced either in vitro in a fermentation culture or in vivo as part
CC   of a gene therapy protocol, and may be used to treat electrolyte
CC   disorders which lead to renal, bone and heart diseases. Due to the
CC   biphasic nature of stanniocalcin-alpha it may be used to treat
CC   osteoporosis, osteopetrosis and Paget's disease. Alternatively, the
CC   polypeptides may be used as antigens in the production of antibodies to
CC   stanniocalcin-alpha and to assay for agonists and antagonists of its
CC   activity. The antibodies and antagonists may be used to inhibit the
CC   activity of stanniocalcin-alpha and may be used to treat osteoporosis and
CC   hypercalcemia. The present sequence represents a human stanniocalcin.
XX
SQ   Sequence   247 AA;

  Query Match             100.0%;  Score 1268;  DB 21;  Length 247;
  Best Local Similarity   100.0%;  Pred. No. 5.9e-124;
  Matches  247;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MLQNSAVLLVLVISASATHEAEQNDSVSPRKSRVAAQNSAEVVRCLNSALQVGCGAFACL 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MLQNSAVLLVLVISASATHEAEQNDSVSPRKSRVAAQNSAEVVRCLNSALQVGCGAFACL 60

Qy         61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM 120

Qy        121 IAEVQEECYSKLNVCSIAKRNPEAITEVVQLPNHFSNRYYNRLVRSLLECDEDTVSTIRD 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 IAEVQEECYSKLNVCSIAKRNPEAITEVVQLPNHFSNRYYNRLVRSLLECDEDTVSTIRD 180

Qy        181 SLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRRTNEPQKLKVLLRNLRGEEDSPSHIK 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 SLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRRTNEPQKLKVLLRNLRGEEDSPSHIK 240

Qy        241 RTSHESA 247
              |||||||
Db        241 RTSHESA 247


RESULT 5
AAY57166
ID   AAY57166 standard; Protein; 247 AA.
XX
AC   AAY57166;
XX
DT   11-FEB-2000  (first entry)
XX
DE   Human corpuscles of stanius polypeptide.
XX
KW   Corpuscles of stanius polypeptide; calcium; inhibition; human; renal;
KW   therapeutic; bone; heart disease; hypocalcemia; osteoperosis.
XX
OS   Homo sapiens.
XX
PN   US5994301-A.
XX
PD   30-NOV-1999.
XX
PF   28-APR-1995;   95US-0431117.
XX
PR   08-MAR-1994;   94US-0208005.
XX
PA   (HUMA-) HUMAN GENOME SCI INC.
XX
PI   Adams MD,  Olsen HS;
```

XX
DR WPI; 2000-038269/03.
DR N-PSDB; AAZ39520.
XX
PT Human corpuscles of stanius polypeptides used to inhibit calcium uptake
PT -
XX
PS Claim 4; Fig 1A-B; 23pp; English.
XX
CC This represents a human corpuscles of stanius polypeptide, having a
CC calcium uptake inhibitory activity. The cDNA is deposited under the
CC accession number ATCC Deposit No. 75652. The polypeptide can be used in a
CC method for the treatment of a patient having need to inhibit uptake of
CC calcium. The method is also used for the therapeutic treatment of renal,
CC bone, and heart diseases, and the antagonist (may be an antibody) may be
CC used for treating hypocalcemia., and osteoperosis.
XX
SQ Sequence 247 AA;

Query Match 100.0%; Score 1268; DB 21; Length 247;
Best Local Similarity 100.0%; Pred. No. 5.9e-124;
Matches 247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MLQNSAVLLVLVISASATHEAEQNDSVSPRKSRVAAQNSAEVVRCLNSALQVGCGAFACL 60

Qy         61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM 120

Qy        121 IAEVQEECYSKLNVCSIAKRNPEAITEVVQLPNHFSNRYYNRLVRSLLECDEDTVSTIRD 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 IAEVQEECYSKLNVCSIAKRNPEAITEVVQLPNHFSNRYYNRLVRSLLECDEDTVSTIRD 180

Qy        181 SLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRRTNEPQKLKVLLRNLRGEEDSPSHIK 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 SLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRRTNEPQKLKVLLRNLRGEEDSPSHIK 240

Qy        241 RTSHESA 247
              |||||||
Db        241 RTSHESA 247
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RESULT 6
AAB62690
ID AAB62690 standard; Protein; 247 AA.
XX
AC AAB62690;
XX
DT 06-AUG-2001 (first entry)
XX
DE Lng108, a diagnostic marker for cancer.
XX
KW Lng108; cancer; diagnostic marker; cytotoxic; immune response; imaging.
XX
OS Homo sapiens.
XX
PN WO200132209-A1.
XX
PD 10-MAY-2001.
XX
PF 03-NOV-2000; 2000WO-US30482.
XX
PR 04-NOV-1999; 99US-0163444.
XX
PA (DIAD-) DIADEXUS INC.
XX
PI Recipon H, Macina RA, Chen S, Sun Y;
XX
DR WPI; 2001-316386/33.
DR N-PSDB; AAF83823.
XX
PT Novel assay for diagnosing and monitoring cancer, involves determining
PT levels of Lng108 in cells, tissues or bodily fluids of the patient, and
PT comparing with control -
XX
PS Disclosure; Page 33-34; 36pp; English.
XX
CC The invention relates to diagnosing the presence of cancer or diagnosing
CC metastases of cancer in a patient that involves determining levels of
CC Lng108 in a sample of cells, tissues or bodily fluids in a patient, and
CC comparing the determined levels with levels of Lng108 a normal human
CC control. The method is useful for diagnosing the presence of cancer,
CC diagnosing metastases of cancer, staging cancer, monitoring cancer, and
CC monitoring a change in stage of the cancer, in a patient. A therapeutic
CC agent which is an antibody labeled with paramagnetic ions or a
CC radioisotope, and conjugated with a cytotoxic agent is useful for imaging
CC cancer in a patient. A molecule which downregulates the expression or
CC activity of Lng108, is useful for treating cancer in a patient. Lng108
CC protein is useful for inducing an immune response against a target cell
CC expressing Lng108. The present sequence represents the human Lng108
CC polypeptide.
XX
SQ Sequence 247 AA;

Query Match 100.0%; Score 1268; DB 22; Length 247;
Best Local Similarity 100.0%; Pred. No. 5.9e-124;
Matches 247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 MLQNSAVLLVLVISASATHEAEQNDSVSPRKSRVAAQNSAEVVRCLNSALQVGCGAFACL 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MLQNSAVLLVLVISASATHEAEQNDSVSPRKSRVAAQNSAEVVRCLNSALQVGCGAFACL 60

Qy         61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM 120

Qy        121 IAEVQEECYSKLNVCSIAKRNPEAITEVVQLPNHFSNRYYNRLVRSLLECDEDTVSTIRD 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 IAEVQEECYSKLNVCSIAKRNPEAITEVVQLPNHFSNRYYNRLVRSLLECDEDTVSTIRD 180

Qy        181 SLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRRTNEPQKLKVLLRNLRGEEDSPSHIK 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 SLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRRTNEPQKLKVLLRNLRGEEDSPSHIK 240

Qy        241 RTSHESA 247
              |||||||
Db        241 RTSHESA 247
```

RESULT 7
AAB62473
ID AAB62473 standard; Protein; 247 AA.
XX
AC AAB62473;
XX
DT 09-JUL-2001 (first entry)
XX
DE Human stanniocalcin (STC) protein.
XX
KW Stanniocalcin; STC; neuroprotective; antiinflammatory; antianemic;
KW antirheumatic; antiarthritic; dermatological; antiallergic; human;
KW nephrotropic; antithyroid; immunosuppressive; antidiabetic; vulnerary;
KW antiasthmatic; hemostatic; antiarrhythmic; vasotropic; antipsoriatic;
KW antitumor; anti HIV; antiparkinsonian; nootropic; cell proliferation;
KW hemostatic; thrombolytic.
XX
OS Homo sapiens.
XX
PN WO200130969-A2.
XX
PD 03-MAY-2001.
XX
PF 20-OCT-2000; 2000WO-US29432.
XX

PR 27-OCT-1999; 99US-0161740.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
PA (UYHE-) UNIV HELSINKI.
XX
PI Olsen HS, Zhang K, Lindsberg P, Tatlisumak T, Kaste M;
PI Andersson LC;
XX
DR WPI; 2001-308626/32.
DR N-PSDB; AAF83297.
XX
PT Novel composition useful for treating or protecting neural cells, for
PT treating Addison's disease, organ rejection, hyperproliferative
PT disorder, cancer, AIDS, multiple sclerosis, comprises stanniocalcin
PT polypeptide -
XX
PS Claim 1; Fig 1A-C; 253pp; English.
XX
CC The invention relates to a human stanniocalcin (STC) polypeptide. A
CC pharmaceutical composition comprising the STC is useful for treating a
CC patient in need of increased levels of STC activity. STC and its
CC modulators are useful for treating disorders or abnormalities of nervous
CC system, cerebrovascular diseases, dementia, encephalitis, central
CC nervous system infections or neoplasms, demyelinating diseases,
CC encephalomyelitis, spinal cord diseases, mental retardation such as
CC Down's syndrome, Tay-Sachs disease, neuromuscular diseases such as
CC muscular dystrophy, myasthenia gravis, deficiencies or disorders of
CC immune system such as Addison's disease, hemolytic anemia, rheumatoid
CC arthritis, dermatitis, glomerulonephritis, Goodpasture's Syndrome,
CC Grave's disease, multiple sclerosis, autoimmune thyroiditis, systemic
CC lupus erythematosus, insulin dependent diabetes mellitus, allergic
CC reactions and conditions such as asthma, for treating and/or preventing
CC organ rejection or graft-versus-host disease, hyperproliferative diseases
CC such as purpura, Gaucher's disease, cardiovascular disorders such as
CC arrhythmias, telangiectasia, vasculitis, and for treatment of disease or
CC disorders with neovascularization. The composition can be used to treat
CC hemangioma, psoriasis, angiofibroma, atherosclerotic plaques, delayed
CC wound healing, granulations, Osler-Weber syndrome, solid tumors such as
CC Kaposi's sarcoma, cancer, AIDS, neurodegenerative disorders such as
CC Alzheimer's disease, Parkinson's disease, wound healing, and for treating
CC or detecting infectious agents. The present sequence represents the
CC human STC polypeptide.
XX
SQ Sequence 247 AA;

Query Match 100.0%; Score 1268; DB 22; Length 247;
Best Local Similarity 100.0%; Pred. No. 5.9e-124;
Matches 247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 MLQNSAVLLVLVISASATHEAEQNDSVSPRKSRVAAQNSAEVVRCLNSALQVGCGAFACL 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MLQNSAVLLVLVISASATHEAEQNDSVSPRKSRVAAQNSAEVVRCLNSALQVGCGAFACL 60

Qy         61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM 120

Qy        121 IAEVQEECYSKLNVCSIAKRNPEAITEVVQLPNHFSNRYYNRLVRSLLECDEDTVSTIRD 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 IAEVQEECYSKLNVCSIAKRNPEAITEVVQLPNHFSNRYYNRLVRSLLECDEDTVSTIRD 180

Qy        181 SLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRRTNEPQKLKVLLRNLRGEEDSPSHIK 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 SLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRRTNEPQKLKVLLRNLRGEEDSPSHIK 240

Qy        241 RTSHESA 247
              |||||||
Db        241 RTSHESA 247
```

RESULT 8
ABB06259
ID ABB06259 standard; Protein; 247 AA.
XX
AC ABB06259;
XX
DT 23-MAY-2002 (first entry)
XX
DE Human staniocalcin 1 protein.
XX
KW Human; staniocalcin 1; osteopathic; osteogenesis failure; osteoporosis;
KW bone mass reduction; traumatic bone injury; osteomalacia; bone disease;
KW rheumatic bone disease; cancer associated bone disease; rachitis;
KW arthritis deformans.
XX
OS Homo sapiens.
XX
PN WO200204013-A1.
XX
PD 17-JAN-2002.
XX
PF 10-JUL-2001; 2001WO-JP05962.
XX
PR 11-JUL-2000; 2000JP-0209926.
XX
PA (BMLB-) BML INC.
XX
PI Yoshiko Y, Koide Y, Igarashi A, Takano S, Maeda N, Aubin JE;
XX
DR WPI; 2002-164600/21.
DR N-PSDB; ABL40225.
XX
PT Agent used for treating bone diseases e.g. osteoporosis, traumatic bone
PT injury, osteomalacia, rheumatic bone diseases, bone diseases associated
PT with cancer and arthritis deformans containing staniocalcin I -
XX
PS Claim 2; Fig 1; 24pp; Japanese.
XX
CC The present invention describes an agent containing staniocalcin 1,
CC particularly of human origin. Staniocalcin 1 has osteopathic activity.
CC The agent can be used for treating diseases relating to osteogenesis
CC failure or reduction in bone mass e.g. osteoporosis, traumatic bone
CC injury, osteomalacia, rheumatic bone diseases, bone diseases associated
CC with cancer, bone diseases due to phosphorus or calcium metabolic error,
CC rachitis and arthritis deformans. The agent increases bone mass. The
CC present sequence represents human staniocalcin 1.
XX
SQ Sequence 247 AA;

Query Match 100.0%; Score 1268; DB 23; Length 247;
Best Local Similarity 100.0%; Pred. No. 5.9e-124;
Matches 247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 MLQNSAVLLVLVISASATHEAEQNDSVSPRKSRVAAQNSAEVVRCLNSALQVGCGAFACL 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MLQNSAVLLVLVISASATHEAEQNDSVSPRKSRVAAQNSAEVVRCLNSALQVGCGAFACL 60

Qy         61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM 120

Qy        121 IAEVQEECYSKLNVCSIAKRNPEAITEVVQLPNHFSNRYYNRLVRSLLECDEDTVSTIRD 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 IAEVQEECYSKLNVCSIAKRNPEAITEVVQLPNHFSNRYYNRLVRSLLECDEDTVSTIRD 180

Qy        181 SLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRRTNEPQKLKVLLRNLRGEEDSPSHIK 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 SLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRRTNEPQKLKVLLRNLRGEEDSPSHIK 240

Qy        241 RTSHESA 247
              |||||||
Db        241 RTSHESA 247
```

RESULT 9
AAB56848

```
ID   AAB56848 standard; Protein; 276 AA.
XX
AC   AAB56848;
XX
DT   13-MAR-2001  (first entry)
XX
DE   Human prostate cancer antigen protein sequence SEQ ID NO:1426.
XX
KW   Human; prostate cancer; prostate cancer antigen; detection; diagnosis;
KW   neuroprotective; cytostatic; cardioactive; immunomodulatory; muscular;
KW   vulnerary; gastrointestinal; nephrotropic; antiinfective; gynaecological;
KW   antibacterial; gene therapy; neural; immune; reproductive; renal;
KW   gastrointestinal; pulmonary; cardiovascular; proliferative disorder;
KW   wound; infectious disease.
XX
OS   Homo sapiens.
XX
PN   WO200055174-A1.
XX
PD   21-SEP-2000.
XX
PF   08-MAR-2000; 2000WO-US05988.
XX
PR   12-MAR-1999;   99US-0124270.
XX
PA   (HUMA-) HUMAN GENOME SCI INC.
PA   (ROSE/) ROSEN C A.
XX
PI   Rosen CA,  Ruben SM;
XX
DR   WPI; 2000-587513/55.
DR   N-PSDB; AAF16051.
XX
PT   Prostate cancer associated gene sequences, referred to as prostate
PT   cancer antigens, useful for treatment, prevention, and diagnosis of
PT   disorders such as prostate cancer -
XX
PS   Claim 11; Page 1858-1859; 2338pp; English.
XX
CC   AAF15566 to AAF16505 encode the human prostate cancer associated
CC   proteins, called prostate cancer antigens, given in AAB56363 to AAB57302.
CC   The prostate cancer antigens can have neuroprotective, cytostatic,
CC   cardioactive, immunomodulatory, muscular, vulnerary, gastrointestinal,
CC   nephrotropic, antiinfective, gynaecological and antibacterial activities,
CC   and can be used in gene therapy. The prostate cancer antigen
CC   polynucleotides may be used for detection of prostate cancer, chromosome
CC   identification, as chromosome markers, and for numerous other diagnostic
CC   or research purposes. The prostate cancer antigens may be used to treat
CC   disorders such as neural, immune, muscular, reproductive,
CC   gastrointestinal, pulmonary, cardiovascular, renal, and proliferative
CC   disorders, wounds, and infectious diseases. AAF16506 to AAF16514 to
CC   AAB57303 represent sequences used in the exemplification of the present
CC   invention.
XX
SQ   Sequence   276 AA;

  Query Match             73.9%;  Score 937;  DB 21;  Length 276;
  Best Local Similarity   99.5%;  Pred. No. 2.6e-89;
  Matches  185;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 MLQNSAVLLVLVISASATHEAEQNDSVSPRKSRVAAQNSAEVVRCLNSALQVGCGAFACL 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         89 MLQNSAVLLVLVISASATHEAEQNDSVSPRKSRVAAQNSAEVVRCLNSALQVGCGAFACL 148

Qy         61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        149 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM 208

Qy        121 IAEVQEECYSKLNVCSIAKRNPEAITEVVQLPNHFSNRYYNRLVRSLLECDEDTVSTIRD 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        209 IAEVQEECYSKLNVCSIAKRNPEAITEVVQLPNHFSNRYYNRLVRSLLECDEDTVSTIRD 268

Qy        181 SLMEKI 186
              ||||||
Db        269 SLMEXI 274


RESULT 10
AAP82968
ID   AAP82968 standard; protein; 261 AA.
XX
AC   AAP82968;
XX
DT   30-NOV-1990  (first entry)
XX
DE   Corpuscles of Stannius CS protein precursor.
XX
KW   Corpuscles of Stannius; CS protein; cardiovascular disease;
KW   oedema; heart failure; high blood pressure.
XX
OS   Anguilla australis.
XX
FH   Key             Location/Qualifiers
FT   Peptide          1..17
FT                    /label=signal peptide/prohormone
FT   Peptide          18..288
FT                    /label=pro-CS
XX
PN   WO8803949-A.
XX
PD   02-JUN-1988.
XX
PF   19-NOV-1987;   87WO-AU00389.
XX
PR   22-MAY-1987;   87AU-0002086.
PR   22-MAY-1987;   87AU-0009107.
XX
PA   (FLOR-) FLOREY INST EXPER.
XX
PI   Butkus A,  Coghlan JP,  Roche PJ;
XX
DR   WPI; 1988-161619/23.
DR   N-PSDB; AAN80655.
XX
PT   CS protein of corpuscles of stannius - used for treating cardiovascular
PT   disease, renal disease and electrolyte disorders.
XX
PS   Disclosure; ; p; English.
XX
CC   This prepro-CS protein sequence has its signal or pro-hormone fragment
CC   (amino acids -17 to 1) cleaved to yield the pro-CS form which can be
CC   processed to yield the mature form.  Recombinant DNA methods are
CC   utilised in the prodn. of the CS protein.  It is useful as e.g. a
CC   therapeutic agent for the treatment of cardiovascular disease
CC   and oedema.  See also AAN80654.
XX
SQ   Sequence   261 AA;

  Query Match             53.7%;  Score 680.5;  DB 9;  Length 261;
  Best Local Similarity   61.4%;  Pred. No. 1.5e-62;
  Matches  124;  Conservative   41;  Mismatches   36;  Indels    1;  Gaps    1;

Qy          1 MLQNSAVLLVLVISASATHEAEQNDSVSPRKSRVAAQNSAEVVRCLNSALQVGCGAFACL 60
              ||: | ::| ||:  :| :| :::: :||| :| :| : ::| |||| |||||| |||||
Db          1 MLRMSGLILTLVL-VTAAYEQDESEPLSPRTARFSASSPSDVARCLNGALQVGCSAFACL 59

Qy         61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM 120
              :||||:||||::||:|||: |||||||||| ||||||||||||:|||||| |||||:||:|
Db         60 DNSTCNTDGMHEICRSFLHGAAKFDTQGKTFVKESLKCIANGITSKVFLTIRRCSSFQKM 119

Qy        121 IAEVQEECYSKLNVCSIAKRNPEAITEVVQLPNHFSNRYYNRLVRSLLECDEDTVSTIRD 180
              |:||||||||||::||:|: ||||: || |:|: | ||||: |::||| ||||||  :|
Db        120 ISEVQEECYSKLDLCSVAQSNPEAMGEVAQVPSQFPNRYYSTLLQSLLTCDEDTVEQVRA 179

Qy        181 SLMEKIGPNMASLFHILQTDHC 202
              |: :: | |  || :|||  |
```

```
Db        180 GLVSRLEPEMGVLFQLLQTKAC 201
```

RESULT 11
AAB62474
ID AAB62474 standard; Protein; 256 AA.
XX
AC AAB62474;
XX
DT 09-JUL-2001 (first entry)
XX
DE Coho salmon stanniocalcin protein.
XX
KW Stanniocalcin; STC; neuroprotective; antiinflammatory; antianemic;
KW antirheumatic; antiarthritic; dermatological; antiallergic; human;
KW nephrotropic; antithyroid; immunosuppressive; antidiabetic; vulnerary;
KW antiasthmatic; hemostatic; antiarrhythmic; vasotropic; antipsoriatic;
KW antitumor; anti HIV; antiparkinsonian; nootropic; cell proliferation;
KW hemostatic; thrombolytic; coho salmon.
XX
OS Oncorhynchus kisutch.
XX
PN WO200130969-A2.
XX
PD 03-MAY-2001.
XX
PF 20-OCT-2000; 2000WO-US29432.
XX
PR 27-OCT-1999; 99US-0161740.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
PA (UYHE-) UNIV HELSINKI.
XX
PI Olsen HS, Zhang K, Lindsberg P, Tatlisumak T, Kaste M;
PI Andersson LC;
XX
DR WPI; 2001-308626/32.
XX
PT Novel composition useful for treating or protecting neural cells, for
PT treating Addison's disease, organ rejection, hyperproliferative
PT disorder, cancer, AIDS, multiple sclerosis, comprises stanniocalcin
PT polypeptide -
XX
PS Disclosure; Fig 2; 253pp; English.
XX
CC The invention relates to a human stanniocalcin (STC) polypeptide. A
CC pharmaceutical composition comprising the STC is useful for treating a
CC patient in need of increased levels of STC activity. STC and its
CC modulators are useful for treating disorders or abnormalities of nervous
CC system, cerebrovascular diseases, dementia, encephalitis, central
CC nervous system infections or neoplasms, demyelinating diseases,
CC encephalomyelitis, spinal cord diseases, mental retardation such as
CC Down's syndrome, Tay-Sachs disease, neuromuscular diseases such as
CC muscular dystrophy, myasthenia gravis, deficiencies or disorders of
CC immune system such as Addison's disease, hemolytic anemia, rheumatoid
CC arthritis, dermatitis, glomerulonephritis, Goodpasture's Syndrome,
CC Grave's disease, multiple sclerosis, autoimmune thyroiditis, systemic
CC lupus erythematosus, insulin dependent diabetes mellitus, allergic
CC reactions and conditions such as asthma, for treating and/or preventing
CC organ rejection or graft-versus-host disease, hyperproliferative diseases
CC such as purpura, Gaucher's disease, cardiovascular disorders such as
CC arrhythmias, telangiectasia, vasculitis, and for treatment of disease or
CC disorders with neovascularization. The composition can be used to treat
CC hemangioma, psoriasis, angiofibroma, atherosclerotic plaques, delayed
CC wound healing, granulations, Osler-Weber syndrome, solid tumors such as
CC Kaposi's sarcoma, cancer, AIDS, neurodegenerative disorders such as
CC Alzheimer's disease, Parkinson's disease, wound healing, and for treating
CC or detecting infectious agents. The present sequence represents the
CC coho salmon stanniocalcin protein, used in homology studies with the
CC human STC polypeptide.
XX
SQ Sequence 256 AA;

```
  Query Match            52.2%;  Score 662.5;  DB 22;  Length 256;
  Best Local Similarity  53.4%;  Pred. No. 1.1e-60;
  Matches  125;  Conservative   46;  Mismatches   54;  Indels    9;  Gaps    4;

Qy         11 LVISASATHEAEQNDSVSPRKSRVAAQNSAEVVRCLNSALQVGCGAFACLENSTCDTDGM 70
              ||:  :|| : :  :: |||:|| :: : ::| |||| || |||| ||||||||||||||
Db         12 LVLGTAATFDTDPEEA-SPRRARFSSNSPSDVARCLNGALAVGCGTFACLENSTCDTDGM 70

Qy         71 YDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRMIAEVQEECYS 130
              :|||: | ::|| |:|||| ||||||:|||||||||||  ||||  |||||:|||||||
Db         71 HDICQLFFHTAATFNTQGKTFVKESLRCIANGVTSKVFQTIRRCGVFQRMISEVQEECYS 130

Qy        131 KLNVCSIAKRNPEAITEVVQLPNHFSNRYYNRLVRSLLECDEDTVSTIRDSLMEKIGPNM 190
              :|::| :|: ||||| ||||:| || |||| |::||| |||:||: :|  |: ::||:|
Db        131 RLDICGVARSNPEAIGEVVQVPAHFPNRYYSTLLQSLLACDEETVAVVRAGLVARLGPDM 190

Qy        191 ASLFHILQTDHCAQTHPRADFN-----RRRTNEPQKLKVLLRNLRGEEDSPSHI 239
              :|| :||  || |   :   :     |     |   |:   ::|| :  |:|:
Db        191 ETLFQLLQNKHCPQGSNQGPNSAPAGWRWPMGSPPSFKI-QPSMRGRD--PTHL 241
```

RESULT 12
AAY55749
ID AAY55749 standard; Protein; 170 AA.
XX
AC AAY55749;
XX
DT 11-FEB-2000 (first entry)
XX
DE A. australis stanniocalcin polypeptide.
XX
KW Stanniocalcin-alpha polypeptide; teleocalcin; hypocalcin; hypercalcemic;
KW anti-hypercalcemic glycoprotein hormone; corpuscles of stannius; PTH;
KW parathyroid hormone; bone reabsorption; osteoporosis; gene therapy; bone;
KW electrolyte disorder; renal; heart disease; osteopetrosis; human;
KW Paget's disease; hypercalcemia.
XX
OS Anguilla australis.
XX
PN US5994103-A.
XX
PD 30-NOV-1999.
XX
PF 02-JUN-1995; 95US-0460529.
XX
PR 10-NOV-1994; 94WO-US13206.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Fleischmann RD, Olsen HS;
XX
DR WPI; 2000-038260/03.
XX
PT Isolated nucleic acids encoding human stanniocalcin-alpha useful for
PT treating electrolyte disorders which lead to renal, bone and heart
PT diseases, osteoporosis and Paget's disease -
XX
PS Disclosure; Fig 2; 21pp; English.
XX
CC The invention provides a human stanniocalcin-alpha polypeptide (also
CC called teleocalcin and hypocalcin). Stanniocalcin-alpha is an anti-
CC hypercalcemic glycoprotein hormone produced by the corpuscles of
CC stannius. It has a similar reported biological activity to that of
CC parathyroid hormone (PTH) and both these proteins exhibit dual functions
CC in mammals. They exert hypercalcemic activity due to stimulation of bone
CC reabsorption. Further PTH has a biphasic action on bone metabolism (i.e.
CC at low doses it increases bone formation and at high doses it increases
CC bone reabsorption. Accordingly, human stanniocalcin-alpha and antagonists
CC of it (under different circumstances) may be used to treat osteoporosis.
CC The DNA may be used to produce human stanniocalcin-alpha according to
CC standard recombinant DNA methodologies. The human stanniocalcin-alpha may
CC be produced either in vitro in a fermentation culture or in vivo as part
CC of a gene therapy protocol, and may be used to treat electrolyte

```
CC   disorders which lead to renal, bone and heart diseases. Due to the
CC   biphasic nature of stanniocalcin-alpha it may be used to treat
CC   osteoporosis, osteopetrosis and Paget's disease. Alternatively, the
CC   polypeptides may be used as antigens in the production of antibodies to
CC   stanniocalcin-alpha and to assay for agonists and antagonists of its
CC   activity. The antibodies and antagonists may be used to inhibit the
CC   activity of stanniocalcin-alpha and may be used to treat osteoporosis and
CC   hypercalcemia. The present sequence represents a stanniocalcin from
CC   Anguilla austalis.
XX
SQ   Sequence   170 AA;

  Query Match             49.5%;  Score 628;  DB 21;  Length 170;
  Best Local Similarity   66.5%;  Pred. No. 2.4e-57;
  Matches  113;  Conservative   30;  Mismatches   27;  Indels    0;  Gaps    0;

Qy         28 SPRKSRVAAQNSAEVVRCLNSALQVGCGAFACLENSTCDTDGMYDICKSFLYSAAKFDTQ 87
              ||| :| :| : ::| |||| |||||| |||||:||||:||||::||:|||: |||||||
Db          1 SPRTARFSASSPSDVARCLNGALQVGCSAFACLDNSTCNTDGMHEICRSFLHGAAKFDTQ 60

Qy         88 GKAFVKESLKCIANGVTSKVFLAIRRCSTFQRMIAEVQEECYSKLNVCSIAKRNPEAITE 147
              || |||||||||||:|||||| |||||:||:||:||||||||||::||:|:. ||||: |
Db         61 GKTFVKESLKCIANGITSKVFLTIRRCSSFQKMISEVQEECYSKLDLCSVAQSNPEAMGE 120

Qy        148 VVQLPNHFSNRYYNRLVRSLLECDEDTVSTIRDSLMEKIGPNMASLFHIL 197
             | |:|: | |||| |::||| |||||| :|  |: :: | |  || :|
Db        121 VAQVPSQFPNRYYSTLLQSLLTCDEDTVEQVRAGLVSRLEPEMGVLFQLL 170


RESULT 13
ABB31928
ID   ABB31928 standard; Peptide; 70 AA.
XX
AC   ABB31928;
XX
DT   01-FEB-2002  (first entry)
XX
DE   Peptide #4579 encoded by breast cell single exon nucleic acid probe.
XX
KW   Human; microarray; single exon probe; gene expression; breast;
KW   disease; cancer.
XX
OS   Homo sapiens.
XX
PN   WO200157271-A2.
XX
PD   09-AUG-2001.
XX
PF   30-JAN-2001; 2001WO-US00662.
XX
PR   04-FEB-2000; 2000US-0180312.
PR   26-MAY-2000; 2000US-0207456.
PR   30-JUN-2000; 2000US-0608408.
PR   03-AUG-2000; 2000US-0632366.
PR   21-SEP-2000; 2000US-0234687.
PR   27-SEP-2000; 2000US-0236359.
PR   04-OCT-2000; 2000GB-0024263.
XX
PA   (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI   Penn SG,  Hanzel DK,  Chen W,  Rank DR;
XX
DR   WPI; 2001-496933/54.
XX
PT   New spatially-addressable set of single exon nucleic acid probes,
PT   useful for measuring gene expression in sample derived from human
PT   breast, comprises number of single exon nucleic acid probes  -
XX
PS   Claim 27; SEQ ID NO 14896; 327pp + sequence listing; English.
XX
CC   The invention relates to a spatially-addressable set of single exon
CC   nucleic acid probes for measuring gene expression in a sample derived
CC   from human breast and BT 474 cells. The method involves contacting
CC   the probes with a collection of detectably labelled nucleic acids
CC   derived from mRNA of human breast, and then measuring the label
CC   bound to each probe of the microarray. The probes are useful for
CC   verifying the expression of regions of genomic DNA predicted to
CC   encode proteins. They are useful for gene discovery, and for
CC   determining predisposition and/or prognosing breast disease. Gene
CC   expression analysis is useful for assessing the toxicity of chemical
CC   agents on cells. The microarray of this invention presents a far greater
CC   diversity of probes for measuring gene expression, with far less bias
CC   than expressed sequence tag microarrays. The method is suitable for
CC   rapid production of functional information from genomic sequence. The
CC   present sequence is a peptide encoded by a single exon nucleic acid
CC   probe of the invention.
CC   Note: The sequence data for this patent did not form part of the
CC   printed specification, but was obtained in electronic format directly
CC   from WIPO at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence   70 AA;

  Query Match             28.2%;  Score 358;  DB 22;  Length 70;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-29;
  Matches   70;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         88 GKAFVKESLKCIANGVTSKVFLAIRRCSTFQRMIAEVQEECYSKLNVCSIAKRNPEAITE 147
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Qy        148 VVQLPNHFSN 157
              ||||||||||
Db         61 VVQLPNHFSN 70


RESULT 14
ABB37166
ID   ABB37166 standard; Peptide; 70 AA.
XX
AC   ABB37166;
XX
DT   04-FEB-2002  (first entry)
XX
DE   Peptide #4672 encoded by human foetal liver single exon probe.
XX
KW   Human; foetal liver; gene expression; single exon nucleic acid probe.
XX
OS   Homo sapiens.
XX
PN   WO200157277-A2.
XX
PD   09-AUG-2001.
XX
PF   30-JAN-2001; 2001WO-US00669.
XX
PR   04-FEB-2000; 2000US-0180312.
PR   26-MAY-2000; 2000US-0207456.
PR   30-JUN-2000; 2000US-0608408.
PR   03-AUG-2000; 2000US-0632366.
PR   21-SEP-2000; 2000US-0234687.
PR   27-SEP-2000; 2000US-0236359.
PR   04-OCT-2000; 2000GB-0024263.
XX
PA   (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI   Penn SG,  Hanzel DK,  Chen W,  Rank DR;
XX
DR   WPI; 2001-483447/52.
XX
PT   Human genome-derived single exon nucleic acid probes useful for
PT   analyzing gene expression in human fetal liver -
XX
PS   Claim 27; SEQ ID NO 29801; 639pp + sequence listing; English.
XX
CC   The invention relates to a single exon nucleic acid probe for
CC   measuring human gene expression in a sample derived from human foetal
```

```
CC   liver. The single exon nucleic acid probes may be used for predicting,
CC   measuring and displaying gene expression in samples derived from human
CC   fetal liver. The present sequence is a peptide encoded by a single exon
CC   nucleic acid probe of the invention.
CC   Note: The sequence data for this patent did not form part of the
CC   printed specification, but was obtained in electronic format directly
CC   from WIPO at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence   70 AA;

  Query Match             28.2%;  Score 358;  DB 22;  Length 70;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-29;
  Matches   70;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         88 GKAFVKESLKCIANGVTSKVFLAIRRCSTFQRMIAEVQEECYSKLNVCSIAKRNPEAITE 147
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Db          1 GKAFVKESLKCIANGVTSKVFLAIRRCSTFQRMIAEVQEECYSKLNVCSIAKRNPEAITE 60

Qy        148 VVQLPNHFSN 157
              ||||||||||
Db         61 VVQLPNHFSN 70


RESULT 15
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ID   ABB22472 standard; Protein; 70 AA.
XX
AC   ABB22472;
XX
DT   23-JAN-2002  (first entry)
XX
DE   Protein #4471 encoded by probe for measuring heart cell gene expression.
XX
KW   Human; gene expression; heart; microarray; vascular system;
KW   cardiovascular disease; hypertension; cardiac arrhythmia;
KW   congenital heart disease.
XX
OS   Homo sapiens.
XX
PN   WO200157274-A2.
XX
PD   09-AUG-2001.
XX
PF   30-JAN-2001; 2001WO-US00666.
XX
PR   04-FEB-2000; 2000US-0180312.
PR   26-MAY-2000; 2000US-0207456.
PR   30-JUN-2000; 2000US-0608408.
PR   03-AUG-2000; 2000US-0632366.
PR   21-SEP-2000; 2000US-0234687.
PR   27-SEP-2000; 2000US-0236359.
PR   04-OCT-2000; 2000GB-0024263.
XX
PA   (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI   Penn SG,  Hanzel DK,  Chen W,  Rank DR;
XX
DR   WPI; 2001-488899/53.
XX
PT   Single exon nucleic acid probes for analyzing gene expression in human
PT   hearts -
XX
PS   Claim 15; SEQ ID No 24242; 530pp; English.
XX
CC   The present invention relates to single exon nucleic acid probes for
CC   measuring human gene expression in a sample derived from human heart (see
CC   ABA21535-ABA41305). The present sequence is a protein encoded by one such
CC   probe. The probes may be used for predicting, measuring and displaying
CC   gene expression in samples derived from the human heart via microarrays.
CC   By measuring gene expression, the probes are useful for predicting,
CC   diagnosing, grading, staging, monitoring and prognosing diseases of the
CC   human heart and vascular system e.g. cardiovascular disease,
CC   hypertension, cardiac arrhythmias and congenital heart disease.
CC   Note: The sequence data for this patent did not form part of the printed
CC   specification, but was obtained in electronic format directly from WIPO
CC   at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence   70 AA;

  Query Match             28.2%;  Score 358;  DB 22;  Length 70;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-29;
  Matches   70;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         88 GKAFVKESLKCIANGVTSKVFLAIRRCSTFQRMIAEVQEECYSKLNVCSIAKRNPEAITE 147
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Db          1 GKAFVKESLKCIANGVTSKVFLAIRRCSTFQRMIAEVQEECYSKLNVCSIAKRNPEAITE 60

Qy        148 VVQLPNHFSN 157
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Db         61 VVQLPNHFSN 70


Search completed: June 12, 2003, 19:54:53
Job time : 62 secs
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: June 12, 2003, 19:53:58 ; Search time 35 Seconds
(without alignments)
207.642 Million cell updates/sec

Title: US-09-705-500A-3
Perfect score: 1268
Sequence: 1 MLQNSAVLLVLVISASATHE.....NLRGEEDSPSHIKRTSHESA 247

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1268	100.0	247	2	US-08-208-005C-2	Sequence 2, Appli
2	1268	100.0	247	2	US-09-038-597A-2	Sequence 2, Appli
3	1268	100.0	247	2	US-08-460-529B-10	Sequence 10, Appl
4	1268	100.0	247	2	US-08-431-117A-2	Sequence 2, Appli
5	660.5	52.1	204	2	US-08-208-005C-5	Sequence 5, Appli
6	660.5	52.1	204	2	US-09-038-597A-5	Sequence 5, Appli
7	628	49.5	170	2	US-08-460-529B-9	Sequence 9, Appli
8	354.5	28.0	296	3	US-08-831-132-14	Sequence 14, Appl
9	354.5	28.0	296	4	US-09-416-150-14	Sequence 14, Appl
10	354	27.9	302	3	US-08-831-132-2	Sequence 2, Appli
11	354	27.9	302	4	US-09-416-150-2	Sequence 2, Appli
12	333.5	26.3	251	2	US-08-460-529B-2	Sequence 2, Appli
13	89.5	7.1	10182	4	US-09-134-001C-3159	Sequence 3159, Ap
14	85.5	6.7	656	4	US-09-134-001C-4322	Sequence 4322, Ap
15	83	6.5	417	4	US-09-134-001C-3810	Sequence 3810, Ap
16	82	6.5	362	4	US-09-134-001C-4670	Sequence 4670, Ap
17	81	6.4	680	4	US-09-298-924-4	Sequence 4, Appli
18	81	6.4	720	2	US-08-840-236-1	Sequence 1, Appli
19	81	6.4	720	2	US-08-505-448A-1	Sequence 1, Appli
20	79.5	6.3	708	1	US-08-145-681-4	Sequence 4, Appli
21	79.5	6.3	708	1	US-08-453-703-4	Sequence 4, Appli
22	79.5	6.3	708	2	US-08-456-106-4	Sequence 4, Appli
23	79.5	6.3	708	3	US-08-456-108-4	Sequence 4, Appli
24	79.5	6.3	708	4	US-09-265-577-4	Sequence 4, Appli
25	78	6.2	315	4	US-09-184-964-4	Sequence 4, Appli
26	77.5	6.1	467	2	US-08-686-599A-17	Sequence 17, Appl
27	76.5	6.0	315	4	US-09-615-192A-378	Sequence 378, App
28	76	6.0	2802	4	US-09-542-331-1	Sequence 1, Appli
29	76	6.0	2802	4	US-09-510-791-1	Sequence 1, Appli
30	75.5	6.0	452	2	US-08-686-599A-18	Sequence 18, Appl
31	75.5	6.0	493	2	US-08-686-599A-5	Sequence 5, Appli
32	75.5	6.0	493	2	US-08-686-599A-16	Sequence 16, Appl
33	75.5	6.0	733	3	US-08-725-459B-29	Sequence 29, Appl
34	75	5.9	1257	4	US-09-220-641-3	Sequence 3, Appli
35	75	5.9	3696	4	US-09-134-001C-5080	Sequence 5080, Ap
36	74.5	5.9	323	6	5185254-4	Patent No. 5185254
37	74.5	5.9	533	2	US-08-770-544-4	Sequence 4, Appli
38	74	5.8	341	4	US-09-134-001C-4268	Sequence 4268, Ap
39	73.5	5.8	861	1	US-08-484-105-18	Sequence 18, Appl
40	73.5	5.8	861	1	US-08-484-106-18	Sequence 18, Appl
41	73.5	5.8	920	1	US-08-451-715A-2	Sequence 2, Appli
42	73	5.8	511	3	US-09-105-039A-2	Sequence 2, Appli
43	73	5.8	530	3	US-09-105-039A-4	Sequence 4, Appli
44	73	5.8	1093	5	PCT-US93-03077-1	Sequence 1, Appli
45	72.5	5.7	334	1	US-08-287-442-9	Sequence 9, Appli

ALIGNMENTS

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RESULT 1
US-08-208-005C-2
; Sequence 2, Application US/08208005C
; Patent No. 5837498
;  GENERAL INFORMATION:
;    APPLICANT:  OLSEN, ET AL.
;    TITLE OF INVENTION:  Corpuscles of Stannius Protein, Stanniocalcin
;    NUMBER OF SEQUENCES:  5
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  CARELLA, BYRNE, BAIN, GILFILLAN,
;      ADDRESSEE:  CECCHI, STEWART & OLSTEIN
;      STREET:  6 BECKER FARM ROAD
;      CITY:  ROSELAND
;      STATE:  NEW JERSEY
;      COUNTRY:  USA
;      ZIP:  07068
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5 INCH DISKETTE
;      COMPUTER:  IBM PS/2
;      OPERATING SYSTEM:  MS-DOS
;      SOFTWARE:  WORD PERFECT 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/208,005C
;      FILING DATE:  8 MARCH 1994
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  FERRARO, GREGORY D.
;      REGISTRATION NUMBER:  36,134
;      REFERENCE/DOCKET NUMBER:  325800-78
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  201-994-1700
;      TELEFAX:  201-994-1744
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  247 AMINO ACIDS
;      TYPE:  AMINO ACID
;      STRANDEDNESS:
;      TOPOLOGY:  LINEAR
;    MOLECULE TYPE:  PROTEIN
US-08-208-005C-2

  Query Match           100.0%;  Score 1268;  DB 2;  Length 247;
  Best Local Similarity  100.0%;  Pred. No. 1.6e-136;
  Matches  247;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MLQNSAVLLVLVISASATHEAEQNDSVSPRKSRVAAQNSAEVVRCLNSALQVGCGAFACL 60
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Db          1 MLQNSAVLLVLVISASATHEAEQNDSVSPRKSRVAAQNSAEVVRCLNSALQVGCGAFACL 60

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Qy        241 RTSHESA 247
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RESULT 2
US-09-038-597A-2
; Sequence 2, Application US/09038597A
; Patent No. 5877290
;  GENERAL INFORMATION:
;    APPLICANT:  OLSEN, ET AL.
;    TITLE OF INVENTION:  Corpuscles of Stannius Protein,
;    TITLE OF INVENTION:  Stanniocalcin
;    NUMBER OF SEQUENCES:  5
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  CARELLA, BYRNE, BAIN, GILFILLAN,
;      ADDRESSEE:  CECCHI, STEWART & OLSTEIN
;      STREET:  6 BECKER FARM ROAD
;      CITY:  ROSELAND
;      STATE:  NEW JERSEY
;      COUNTRY:  USA
;      ZIP:  07068
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5 INCH DISKETTE
;      COMPUTER:  IBM PS/2
;      OPERATING SYSTEM:  MS-DOS
;      SOFTWARE:  WORD PERFECT 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/038,597A
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/208,005
;      FILING DATE:  8-MARCH-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  FERRARO, GREGORY D.
;      REGISTRATION NUMBER:  36,134
;      REFERENCE/DOCKET NUMBER:  325800-78
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  201-994-1700
;      TELEFAX:  201-994-1744
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  247 AMINO ACIDS
;      TYPE:  AMINO ACID
;      STRANDEDNESS:
;      TOPOLOGY:  LINEAR
;    MOLECULE TYPE:  PROTEIN
US-09-038-597A-2

  Query Match           100.0%;  Score 1268;  DB 2;  Length 247;
  Best Local Similarity  100.0%;  Pred. No. 1.6e-136;
  Matches  247;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MLQNSAVLLVLVISASATHEAEQNDSVSPRKSRVAAQNSAEVVRCLNSALQVGCGAFACL 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy         61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM 120
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Db         61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM 120

Qy        121 IAEVQEECYSKLNVCSIAKRNPEAITEVVQLPNHFSNRYYNRLVRSLLECDEDTVSTIRD 180
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Qy        241 RTSHESA 247
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Db        241 RTSHESA 247


RESULT 3
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; Sequence 10, Application US/08460529B
; Patent No. 5994103
;  GENERAL INFORMATION:
;    APPLICANT:  OLSEN, ET AL.
;    TITLE OF INVENTION:  Human Stanniocalcin-alpha
;    NUMBER OF SEQUENCES:  10
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  CARELLA, BYRNE, BAIN, GILFILLAN,
;      ADDRESSEE:  CECCHI, STEWART & OLSTEIN
;      STREET:  6 BECKER FARM ROAD
;      CITY:  ROSELAND
;      STATE:  NEW JERSEY
;      COUNTRY:  USA
;      ZIP:  07068
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5 INCH DISKETTE
;      COMPUTER:  IBM PS/2
;      OPERATING SYSTEM:  MS-DOS
;      SOFTWARE:  WORD PERFECT 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/460,529B
;      FILING DATE:  June 2, 1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US94/13206
;      FILING DATE:  10 NOV 1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  MULLINS, J.G.
;      REGISTRATION NUMBER:  33,073
;      REFERENCE/DOCKET NUMBER:  325800-334  (PF143)
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  201-994-1700
;      TELEFAX:  201-994-1744
;  INFORMATION FOR SEQ ID NO:  10:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  247 AMINO ACIDS
;      TYPE:  AMINO ACID
;      STRANDEDNESS:
;      TOPOLOGY:  LINEAR
;    MOLECULE TYPE:  PROTEIN
US-08-460-529B-10

  Query Match           100.0%;  Score 1268;  DB 2;  Length 247;
  Best Local Similarity  100.0%;  Pred. No. 1.6e-136;
  Matches  247;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MLQNSAVLLVLVISASATHEAEQNDSVSPRKSRVAAQNSAEVVRCLNSALQVGCGAFACL 60
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Qy        241 RTSHESA 247
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Db        241 RTSHESA 247
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Db        121 IAEVQEECYSKLNVCSIAKRNPEAITEVVQLPNHFSNRYYNRLVRSLLECDEDTVSTIRD 180

Qy        181 SLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRRTNEPQKLKVLLRNLRGEEDSPSHIK 240
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Qy        241 RTSHESA 247
                    |||||||
Db        241 RTSHESA 247


RESULT 4
US-08-431-117A-2
; Sequence 2, Application US/08431117A
; Patent No. 5994301
;  GENERAL INFORMATION:
;    APPLICANT:  OLSEN, ET AL.
;    TITLE OF INVENTION:  Corpuscles of Stannius Protein, Stanniocalcin
;    NUMBER OF SEQUENCES:  8
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  CARELLA, BYRNE, BAIN, GILFILLAN,
;      ADDRESSEE:  CECCHI, STEWART & OLSTEIN
;      STREET:  6 BECKER FARM ROAD
;      CITY:  ROSELAND
;      STATE:  NEW JERSEY
;      COUNTRY:  USA
;      ZIP:  07068
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5 INCH DISKETTE
;      COMPUTER:  IBM PS/2
;      OPERATING SYSTEM:  MS-DOS
;      SOFTWARE:  WORD PERFECT 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/431,117A
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/208,005
;      FILING DATE:  8 MARCH 1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  FERRARO, GREGORY D.
;      REGISTRATION NUMBER:  36,134
;      REFERENCE/DOCKET NUMBER:  325800-296
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  201-994-1700
;      TELEFAX:  201-994-1744
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  247 AMINO ACIDS
;      TYPE:  AMINO ACID
;      STRANDEDNESS:
;      TOPOLOGY:  LINEAR
;    MOLECULE TYPE:  PROTEIN
US-08-431-117A-2

  Query Match           100.0%;  Score 1268;  DB 2;  Length 247;
  Best Local Similarity  100.0%;  Pred. No. 1.6e-136;
  Matches  247;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MLQNSAVLLVLVISASATHEAEQNDSVSPRKSRVAAQNSAEVVRCLNSALQVGCGAFACL 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MLQNSAVLLVLVISASATHEAEQNDSVSPRKSRVAAQNSAEVVRCLNSALQVGCGAFACL 60

Qy         61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM 120

Qy        121 IAEVQEECYSKLNVCSIAKRNPEAITEVVQLPNHFSNRYYNRLVRSLLECDEDTVSTIRD 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 IAEVQEECYSKLNVCSIAKRNPEAITEVVQLPNHFSNRYYNRLVRSLLECDEDTVSTIRD 180

Qy        181 SLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRRTNEPQKLKVLLRNLRGEEDSPSHIK 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 SLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRRTNEPQKLKVLLRNLRGEEDSPSHIK 240

Qy        241 RTSHESA 247
              |||||||
Db        241 RTSHESA 247


RESULT 5
US-08-208-005C-5
; Sequence 5, Application US/08208005C
; Patent No. 5837498
;  GENERAL INFORMATION:
;    APPLICANT:  OLSEN, ET AL.
;    TITLE OF INVENTION:  Corpuscles of Stannius Protein, Stanniocalcin
;    NUMBER OF SEQUENCES:  5
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  CARELLA, BYRNE, BAIN, GILFILLAN,
;      ADDRESSEE:  CECCHI, STEWART & OLSTEIN
;      STREET:  6 BECKER FARM ROAD
;      CITY:  ROSELAND
;      STATE:  NEW JERSEY
;      COUNTRY:  USA
;      ZIP:  07068
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5 INCH DISKETTE
;      COMPUTER:  IBM PS/2
;      OPERATING SYSTEM:  MS-DOS
;      SOFTWARE:  WORD PERFECT 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/208,005C
;      FILING DATE:  8 MARCH 1994
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  FERRARO, GREGORY D.
;      REGISTRATION NUMBER:  36,134
;      REFERENCE/DOCKET NUMBER:  325800-78
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  201-994-1700
;      TELEFAX:  201-994-1744
;  INFORMATION FOR SEQ ID NO:  5:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  204 AMINO ACIDS
;      TYPE:  AMINO ACID
;      STRANDEDNESS:
;      TOPOLOGY:  LINEAR
;    MOLECULE TYPE:  PROTEIN
US-08-208-005C-5

  Query Match           52.1%;  Score 660.5;  DB 2;  Length 204;
  Best Local Similarity  60.8%;  Pred. No. 2.4e-67;
  Matches  118;  Conservative   38;  Mismatches   37;  Indels    1;  Gaps    1;

Qy         11 LVISASATHEAEQNDSVSPRKSRVAAQNSAEVVRCLNSALQVGCGAFACLENSTCDTDGM 70
              ||: :|| : :  :: |||::| :: : ::| |||| || |||| ||||||||||||||
Db         12 LVLGTAATFDTDPEEA-SPRRARFSSNSPSDVARCLNGALAVGCGTFACLENSTCDTDGM 70

Qy         71 YDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRMIAEVQEECYS 130
              :|||: | ::|| |:|||| |||||:|||||||||  |||| |||||:||||||||
Db         71 HDICQLFFHTAATFNTQGKTFVKESLRCIANGVTSKVFQTIRRCGVFQRMISEVQEECYS 130

Qy        131 KLNVCSIAKRNPEAITEVVQLPNHFSNRYYNRLVRSLLECDEDTVSTIRDSLMEKIGPNM 190
              :|::| :|: ||||| ||||:| || |||| |::||| |||:||: :|  |: ::||:|
Db        131 RLDICGVARSNPEAIGEVVQVPAHFPNRYYSTLLQSLLACDEETVAVVRAGLVARLGPDM 190

Qy        191 ASLFHILQTDHCAQ 204
              :|| :||  || |
Db        191 ETLFQLLQNKHCPQ 204
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RESULT 6
US-09-038-597A-5
; Sequence 5, Application US/09038597A
; Patent No. 5877290
;  GENERAL INFORMATION:
;    APPLICANT:  OLSEN, ET AL.
;    TITLE OF INVENTION:  Corpuscles of Stannius Protein,
;    TITLE OF INVENTION:  Stanniocalcin
;    NUMBER OF SEQUENCES:  5
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  CARELLA, BYRNE, BAIN, GILFILLAN,
;      ADDRESSEE:  CECCHI, STEWART & OLSTEIN
;      STREET:  6 BECKER FARM ROAD
;      CITY:  ROSELAND
;      STATE:  NEW JERSEY
;      COUNTRY:  USA
;      ZIP:  07068
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5 INCH DISKETTE
;      COMPUTER:  IBM PS/2
;      OPERATING SYSTEM:  MS-DOS
;      SOFTWARE:  WORD PERFECT 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/038,597A
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/208,005
;      FILING DATE:  8-MARCH-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  FERRARO, GREGORY D.
;      REGISTRATION NUMBER:  36,134
;      REFERENCE/DOCKET NUMBER:  325800-78
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  201-994-1700
;      TELEFAX:  201-994-1744
;  INFORMATION FOR SEQ ID NO:  5:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  204 AMINO ACIDS
;      TYPE:  AMINO ACID
;      STRANDEDNESS:
;      TOPOLOGY:  LINEAR
;    MOLECULE TYPE:  PROTEIN
US-09-038-597A-5

  Query Match           52.1%;  Score 660.5;  DB 2;  Length 204;
  Best Local Similarity  60.8%;  Pred. No. 2.4e-67;
  Matches  118;  Conservative   38;  Mismatches   37;  Indels    1;  Gaps    1;

Qy         11 LVISASATHEAEQNDSVSPRKSRVAAQNSAEVVRCLNSALQVGCGAFACLENSTCDTDGM 70
              ||:  :|| : :  :: |||:| :: : ::| |||| || |||| ||||||||||||||
Db         12 LVLGTAATFDTDPEEA-SPRRARFSSNSPSDVARCLNGALAVGCGTFACLENSTCDTDGM 70

Qy         71 YDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRMIAEVQEECYS 130
              :|||: | ::|| |:|||| ||||||:||||||||||  |||| |||||:||||||||
Db         71 HDICQLFFHTAATFNTQGKTFVKESLRCIANGVTSKVFQTIRRCGVFQRMISEVQEECYS 130

Qy        131 KLNVCSIAKRNPEAITEVVQLPNHFSNRYYNRLVRSLLECDEDTVSTIRDSLMEKIGPNM 190
              :|::| :|: ||||| ||||:| || |||| |::||| |||:||: :|  |: ::||:|
Db        131 RLDICGVARSNPEAIGEVVQVPAHFPNRYYSTLLQSLLACDEETVAVVRAGLVARLGPDM 190

Qy        191 ASLFHILQTDHCAQ 204
              :|| :||  || |
Db        191 ETLFQLLQNKHCPQ 204


RESULT 7
US-08-460-529B-9
; Sequence 9, Application US/08460529B
; Patent No. 5994103
;  GENERAL INFORMATION:
;    APPLICANT:  OLSEN, ET AL.
;    TITLE OF INVENTION:  Human Stanniocalcin-alpha
;    NUMBER OF SEQUENCES:  10
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  CARELLA, BYRNE, BAIN, GILFILLAN,
;      ADDRESSEE:  CECCHI, STEWART & OLSTEIN
;      STREET:  6 BECKER FARM ROAD
;      CITY:  ROSELAND
;      STATE:  NEW JERSEY
;      COUNTRY:  USA
;      ZIP:  07068
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5 INCH DISKETTE
;      COMPUTER:  IBM PS/2
;      OPERATING SYSTEM:  MS-DOS
;      SOFTWARE:  WORD PERFECT 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/460,529B
;      FILING DATE:  June 2, 1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US94/13206
;      FILING DATE:  10 NOV 1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  MULLINS, J.G.
;      REGISTRATION NUMBER:  33,073
;      REFERENCE/DOCKET NUMBER:  325800-334  (PF143)
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  201-994-1700
;      TELEFAX:  201-994-1744
;  INFORMATION FOR SEQ ID NO:  9:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  170 AMINO ACIDS
;      TYPE:  AMINO ACID
;      STRANDEDNESS:
;      TOPOLOGY:  LINEAR
;    MOLECULE TYPE:  PROTEIN
US-08-460-529B-9

  Query Match           49.5%;  Score 628;  DB 2;  Length 170;
  Best Local Similarity  66.5%;  Pred. No. 9.5e-64;
  Matches  113;  Conservative   30;  Mismatches   27;  Indels    0;  Gaps    0;

Qy         28 SPRKSRVAAQNSAEVVRCLNSALQVGCGAFACLENSTCDTDGMYDICKSFLYSAAKFDTQ 87
              ||| :| :| : ::| |||| |||||| |||||:||||:||||::||:|||: |||||||
Db          1 SPRTARFSASSPSDVARCLNGALQVGCSAFACLDNSTCNTDGMHEICRSFLHGAAKFDTQ 60

Qy         88 GKAFVKESLKCIANGVTSKVFLAIRRCSTFQRMIAEVQEECYSKLNVCSIAKRNPEAITE 147
              || |||||||||||:|||||| |||||:||:||:||||||||::||:|: ||||: |
Db         61 GKTFVKESLKCIANGITSKVFLTIRRCSSFQKMISEVQEECYSKLDLCSVAQSNPEAMGE 120

Qy        148 VVQLPNHFSNRYYNRLVRSLLECDEDTVSTIRDSLMEKIGPNMASLFHIL 197
              | |:|: | ||||: |::||| ||||||  :|  |: :: | |  || :|
Db        121 VAQVPSQFPNRYYSTLLQSLLTCDEDTVEQVRAGLVSRLEPEMGVLFQLL 170


RESULT 8
US-08-831-132-14
; Sequence 14, Application US/08831132
; Patent No. 6008322
;  GENERAL INFORMATION:
;    APPLICANT:  Kuestner, Rolf E.
;    APPLICANT:  Conklin, Darrell C.
;    APPLICANT:  Lok, Si
;    APPLICANT:  Buddle, Michele
;    APPLICANT:  Downey, William
;    TITLE OF INVENTION:  STANNIOCALCIN-2
;    NUMBER OF SEQUENCES:  22
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  ZymoGenetics, Inc.
;      STREET:  1201 Eastlake Avenue East
;      CITY:  Seattle
;      STATE:  WA
;      COUNTRY:  USA
;      ZIP:  98102
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;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/831,132
;      FILING DATE:
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Sawislak, Deborah A.
;      REGISTRATION NUMBER:  37,438
;      REFERENCE/DOCKET NUMBER:  96-01
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  206-442-6672
;      TELEFAX:  206-442-6678
;  INFORMATION FOR SEQ ID NO:  14:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  296 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-831-132-14

  Query Match             28.0%;  Score 354.5;  DB 3;  Length 296;
  Best Local Similarity   31.7%;  Pred. No. 3.6e-32;
  Matches   85;  Conservative   45;  Mismatches  109;  Indels   29;  Gaps    5;

Qy          7 VLLVLVISASATHEAEQNDSVSP----------RKSRVAAQNSAEVVRCLNSALQVGCGA 56
              | | ||   :    |:  || :|          :| |:: ||:||:  || :|  ||||
Db         10 VTLALVF--ATLDPAQGTDSTNPPEGPQDRSSQQKGRLSLQNTAEIQHCLVNAGDVGCGV 67

Qy         57 FACLENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCST 116
              | | ||::|:  |:: || :||::| ||| |||:|:|::|:| |: :  |      |:|
Db         68 FECFENNSCEIQGLHGICMTFLHNAGKFDAQGKSFIKDALRCKAHALRHKFGCISRKCPA 127

Qy        117 FQRMIAEVQEECYSKLNVCSIAKRNPEAITEVVQLPNHFSNRYYNRLVRSLLECDEDTVS 176
              : |: ::| ||| | ::|| |: |   | |::   :   :  |  ||  || | ||
Db        128 IREMVFQLQRECYLKHDLCSAAQENVGVIVEMIHFKDLLLHEPYVDLVNLLLTCGEDVKE 187

Qy        177 TIRDSLMEKIGPNMASLFHIL--------QTDHCAQTH----PRADFNRRRTNEPQKLKV 224
              :  |:  :   :   |  ||        :   |  |     ||  :|    :
Db        188 AVTRSVQAQCEQSWGGLCSILSFCTSNIQRPPTAAPEHQPLADRAQLSRPHHRDTDHHLT 247

Qy        225 LLRNLRGEEDSPSHIK-----RTSHESA 247
                |  :||  | ||       ||  :||
Db        248 ANRGAKGERGSKSHPNAHARGRTGGQSA 275


RESULT 9
US-09-416-150-14
; Sequence 14, Application US/09416150
; Patent No. 6171822
;   GENERAL INFORMATION:
;        APPLICANT: Kuestner, Rolf E.
;                   Conklin, Darrell C.
;                   Lok, Si
;                   Buddle, Michele
;                   Downey, William
;        TITLE OF INVENTION: STANNIOCALCIN-2
;        NUMBER OF SEQUENCES: 22
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: ZymoGenetics, Inc.
;             STREET: 1201 Eastlake Avenue East
;             CITY: Seattle
;             STATE: WA
;             COUNTRY: USA
;             ZIP: 98102
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.25
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/416,150
;             FILING DATE: 11-Oct-1999
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 08/831,132
;             FILING DATE: <Unknown>
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Sawislak, Deborah A.
;             REGISTRATION NUMBER: 37,438
;             REFERENCE/DOCKET NUMBER: 96-01
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 206-442-6672
;             TELEFAX: 206-442-6678
;   INFORMATION FOR SEQ ID NO: 14:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 296 amino acids
;             TYPE: amino acid
;             TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-09-416-150-14

  Query Match             28.0%;  Score 354.5;  DB 4;  Length 296;
  Best Local Similarity   31.7%;  Pred. No. 3.6e-32;
  Matches   85;  Conservative   45;  Mismatches  109;  Indels   29;  Gaps    5;

Qy          7 VLLVLVISASATHEAEQNDSVSP----------RKSRVAAQNSAEVVRCLNSALQVGCGA 56
              | | ||   :    |:  || :|          :| |:: ||:||:  || :|  ||||
Db         10 VTLALVF--ATLDPAQGTDSTNPPEGPQDRSSQQKGRLSLQNTAEIQHCLVNAGDVGCGV 67

Qy         57 FACLENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCST 116
              | | ||::|:  |:: || :||::| ||| |||:|:|::|:| |: :  |      |:|
Db         68 FECFENNSCEIQGLHGICMTFLHNAGKFDAQGKSFIKDALRCKAHALRHKFGCISRKCPA 127

Qy        117 FQRMIAEVQEECYSKLNVCSIAKRNPEAITEVVQLPNHFSNRYYNRLVRSLLECDEDTVS 176
              : |: ::| ||| | ::|| |: |   | |::   :   :  |  ||  || | ||
Db        128 IREMVFQLQRECYLKHDLCSAAQENVGVIVEMIHFKDLLLHEPYVDLVNLLLTCGEDVKE 187

Qy    -   177 TIRDSLMEKIGPNMASLFHIL--------QTDHCAQTH----PRADFNRRRTNEPQKLKV 224
              :  |:  :   :   |  ||        :   |  |     ||  :|    :
Db        188 AVTRSVQAQCEQSWGGLCSILSFCTSNIQRPPTAAPEHQPLADRAQLSRPHHRDTDHHLT 247

Qy        225 LLRNLRGEEDSPSHIK-----RTSHESA 247
                |  :||  | ||       ||  :||
Db        248 ANRGAKGERGSKSHPNAHARGRTGGQSA 275


RESULT 10
US-08-831-132-2
; Sequence 2, Application US/08831132
; Patent No. 6008322
;  GENERAL INFORMATION:
;    APPLICANT:  Kuestner, Rolf E.
;    APPLICANT:  Conklin, Darrell C.
;    APPLICANT:  Lok, Si
;    APPLICANT:  Buddle, Michele
;    APPLICANT:  Downey, William
;    TITLE OF INVENTION:  STANNIOCALCIN-2
;    NUMBER OF SEQUENCES:  22
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  ZymoGenetics, Inc.
;      STREET:  1201 Eastlake Avenue East
;      CITY:  Seattle
;      STATE:  WA
;      COUNTRY:  USA
;      ZIP:  98102
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
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;       APPLICATION NUMBER:  US/08/831,132
;       FILING DATE:
;       CLASSIFICATION:  424
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Sawislak, Deborah A.
;       REGISTRATION NUMBER:  37,438
;       REFERENCE/DOCKET NUMBER:  96-01
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  206-442-6672
;       TELEFAX:  206-442-6678
;   INFORMATION FOR SEQ ID NO:  2:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  302 amino acids
;       TYPE:  amino acid
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  protein
US-08-831-132-2

  Query Match             27.9%;  Score 354;  DB 3;  Length 302;
  Best Local Similarity   32.4%;  Pred. No. 4.2e-32;
  Matches   83;  Conservative   45;  Mismatches  102;  Indels   26;  Gaps    4;

Qy          9 LVLVIS-------ASATHEAE-QNDSVSPRKSRVAAQNSAEVVRCLNSALQVGCGAFACL 60
              | ||::         ||:  |   |  | :| |:: ||:||:  || :|  |||| | |
Db         12 LALVLATFDPARGTDATNPPEGPQDRSSQQKGRLSLQNTAEIQHCLVNAGDVGCGVFECF 71

Qy         61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM 120
              ||::|:  |:: || :||::| ||| |||:|:|::||| |: :  :      |:|   : |
Db         72 ENNSCEIRGLHGICMTFLHNAGKFDAQGKSFIKDALKCKAHALRHRFGCISRKCPAIREM 131

Qy        121 IAEVQEECYSKLNVCSIAKRNPEAITEVVQLPNHFSNRYYNRLVRSLLECDEDTVSTIRD 180
              ::::| ||| | ::|: |: |  | |::   :   :  |  ||  || | |:    |
Db        132 VSQLQRECYLKHDLCAAAQENTRVIVEMIHFKDLLLHEPYVDLVNLLLTCGEEVKEAITH 191

Qy        181 SLMEKIGPNMASLFHILQ-TDHCAQTHPRADFNRRRTNEPQKL---------------- 222
              |:  :   |  ||  ||       |  | |   |:   : ||
Db        192 SVQVQCEQNWGSLCSILSFCTSAIQKPPTAPPERQPQVDRTKLSRAHHGEAGHHLPEPSS 251

Qy        223 KVLLRNLRGEEDSPSH 238
              :   |  :||  | ||
Db        252 RETGRGAKGERGSKSH 267


RESULT 11
US-09-416-150-2
; Sequence 2, Application US/09416150
; Patent No. 6171822
;   GENERAL INFORMATION:
;       APPLICANT: Kuestner, Rolf E.
;                  Conklin, Darrell C.
;                  Lok, Si
;                  Buddle, Michele
;                  Downey, William
;       TITLE OF INVENTION: STANNIOCALCIN-2
;       NUMBER OF SEQUENCES: 22
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: ZymoGenetics, Inc.
;            STREET: 1201 Eastlake Avenue East
;            CITY: Seattle
;            STATE: WA
;            COUNTRY: USA
;            ZIP: 98102
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.25
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/416,150
;            FILING DATE: 11-Oct-1999
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: 08/831,132
;            FILING DATE: <Unknown>
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Sawislak, Deborah A.
;            REGISTRATION NUMBER: 37,438
;            REFERENCE/DOCKET NUMBER: 96-01
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: 206-442-6672
;            TELEFAX: 206-442-6678
;   INFORMATION FOR SEQ ID NO: 2:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 302 amino acids
;            TYPE: amino acid
;            TOPOLOGY: linear
;       MOLECULE TYPE: protein
;       SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-416-150-2

  Query Match             27.9%;  Score 354;  DB 4;  Length 302;
  Best Local Similarity   32.4%;  Pred. No. 4.2e-32;
  Matches   83;  Conservative   45;  Mismatches  102;  Indels   26;  Gaps    4;

Qy          9 LVLVIS-------ASATHEAE-QNDSVSPRKSRVAAQNSAEVVRCLNSALQVGCGAFACL 60
              | ||::         ||:  |   |  | :| |:: ||:||:  || :|  |||| | |
Db         12 LALVLATFDPARGTDATNPPEGPQDRSSQQKGRLSLQNTAEIQHCLVNAGDVGCGVFECF 71

Qy         61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM 120
              ||::|:  |:: || :||::| ||| |||:|:|::||| |: :  :      |:|   : |
Db         72 ENNSCEIRGLHGICMTFLHNAGKFDAQGKSFIKDALKCKAHALRHRFGCISRKCPAIREM 131

Qy        121 IAEVQEECYSKLNVCSIAKRNPEAITEVVQLPNHFSNRYYNRLVRSLLECDEDTVSTIRD 180
              ::::| ||| | ::|: |: |  | |::   :   :  |  ||  || | |:    |
Db        132 VSQLQRECYLKHDLCAAAQENTRVIVEMIHFKDLLLHEPYVDLVNLLLTCGEEVKEAITH 191

Qy        181 SLMEKIGPNMASLFHILQ-TDHCAQTHPRADFNRRRTNEPQKL---------------- 222
              |:  :   |  ||  ||       |  | |   |:   : ||
Db        192 SVQVQCEQNWGSLCSILSFCTSAIQKPPTAPPERQPQVDRTKLSRAHHGEAGHHLPEPSS 251

Qy        223 KVLLRNLRGEEDSPSH 238
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Db        252 RETGRGAKGERGSKSH 267


RESULT 12
US-08-460-529B-2
; Sequence 2, Application US/08460529B
; Patent No. 5994103
;  GENERAL INFORMATION:
;    APPLICANT:  OLSEN, ET AL.
;    TITLE OF INVENTION:  Human Stanniocalcin-alpha
;    NUMBER OF SEQUENCES:  10
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  CARELLA, BYRNE, BAIN, GILFILLAN,
;      ADDRESSEE:  CECCHI, STEWART & OLSTEIN
;      STREET:  6 BECKER FARM ROAD
;      CITY:  ROSELAND
;      STATE:  NEW JERSEY
;      COUNTRY:  USA
;      ZIP:  07068
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5 INCH DISKETTE
;      COMPUTER:  IBM PS/2
;      OPERATING SYSTEM:  MS-DOS
;      SOFTWARE:  WORD PERFECT 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/460,529B
;      FILING DATE:  June 2, 1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US94/13206
;      FILING DATE:  10 NOV 1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  MULLINS, J.G.
;      REGISTRATION NUMBER:  33,073
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;      REFERENCE/DOCKET NUMBER:  325800-334  (PF143).
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  201-994-1700
;      TELEFAX:  201-994-1744
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  251 AMINO ACIDS
;      TYPE:  AMINO ACID
;      STRANDEDNESS:
;      TOPOLOGY:  LINEAR
;    MOLECULE TYPE:  PROTEIN
US-08-460-529B-2

  Query Match             26.3%;  Score 333.5;  DB 2;  Length 251;
  Best Local Similarity   32.6%;  Pred. No. 6.9e-30;
  Matches   78;  Conservative   43;  Mismatches   89;  Indels   29;  Gaps    5;

Qy          9 LVLVIS-------ASATHEAE-QNDSVSPRKSRVAAQNSAEVVRCLNSALQVGCGAFACL 60
              | ||::          ||:  |   |  | :| |:: ||:||:  || :|  |||| | |
Db         12 LALVLATFDPARGTDATNPPEGPQDRSSQQKGRLSLQNTAEIQHCLVNAGDVGCGVFECF 71

Qy         61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM 120
              ||::|:  |:: || :||::| ||| |||:|:|::||| |: :  :     |:|   : |
Db         72 ENNSCEIRGLHGICMTFLHNAGKFDAQGKSFIKDALKCKAHALRHRFGCISRKCPAIREM 131

Qy        121 IAEVQEECYSKLNVCSIAKRNPEAITEVVQLPNHFSNRYYNRLVRSLLECDEDTVSTIRD 180
              ::::|  |  | ::|: |: |   | |::   :   :  |  ||  || | |:    |
Db        132 VSQLQRGCTLKHDLCAAAQENTRVIVEMIHFKDLLLHGPYVDLVNLLLTCGEEVKEAITH 191

Qy        181 SLMEKIGPNMASLFHILQTDHCAQ------THP-------------RADFNRRRTNEPQ 220
              |:  :   |  ||  ||     |       | |             ||    |||: |:
Db        192 SVQVQCEQNWGSLCSIL--SFCTSDIQKPPTAPPERQPQVDRTKLSRAHHGGRRTSPPR 248


RESULT 13
US-09-134-001C-3159
; Sequence 3159, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
;  APPLICANT: Lynn Doucette-Stamm et al
;  TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
;  TITLE OF INVENTION:  EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
;  FILE REFERENCE: GTC-007
;  CURRENT APPLICATION NUMBER: US/09/134,001C
;  CURRENT FILING DATE:  1998-08-13
;  PRIOR APPLICATION NUMBER: US 60/064,964
;  PRIOR FILING DATE: 1997-11-08
;  PRIOR APPLICATION NUMBER: US 60/055,779
;  PRIOR FILING DATE: 1997-08-14
;  NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 3159
;   LENGTH: 10182
;   TYPE: PRT
;   ORGANISM: Staphylococcus epidermidis
US-09-134-001C-3159

  Query Match             7.1%;  Score 89.5;  DB 4;  Length 10182;
  Best Local Similarity   22.0%;  Pred. No. 13;
  Matches   50;  Conservative   38;  Mismatches   78;  Indels   61;  Gaps   11;

Qy         17 ATHEAEQ---NDSVSPRKSRVA----------------------AQNSAEVVRCLNSALQ 51
              | :|||:   ||  :|: |:|                      :|: |:|   |
Db       2954 AKNEAERILGND--NPQVSQVTQALNKIKAIQPKLTEAINMLQNKENNTELVNAKNR--- 3008

Qy         52 VGCGAFACLENSTCDTDGMYDICKSFL--YSAAKFDTQGKAFVKESLKCIANG------- 102
                  |||:  |||  : : :  :  |:| | : | :  ::::   | ||
Db       3009 --------LENAVNDTDPTHGMTQETINNYNAKKREAQNE--IQKANMIINNGDATAQDI 3058

Qy        103 -----VTSKVFLAIRRCSTFQRMIAEVQEECYSKL--NVCSIAKRNPEAITEVVQLPNHF 155
                  :|  |::       |      : .|:||  || :  |: | :|       :
Db       3059 SSEKSKVEQVLQALQNAKNDLRADKRELQTAYNKLIQNVNTNGKK-PSSIQNYKSARRNI 3117

Qy        156 SNRY--YNRLVRSLLECDEDTVSTIRDSL--MEKIGPNMASLFHILQ 198
                |:|       ::||    ||: : |:|  :  | | :    :|||
Db       3118 ENQYNTAKNEAHNVLENTNPTVNAVEDALRKINAIQPEVTKAINILQ 3164


RESULT 14
US-09-134-001C-4322
; Sequence 4322, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
;  APPLICANT: Lynn Doucette-Stamm et al
;  TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
;  TITLE OF INVENTION:  EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
;  FILE REFERENCE: GTC-007
;  CURRENT APPLICATION NUMBER: US/09/134,001C
;  CURRENT FILING DATE:  1998-08-13
;  PRIOR APPLICATION NUMBER: US 60/064,964
;  PRIOR FILING DATE: 1997-11-08
;  PRIOR APPLICATION NUMBER: US 60/055,779
;  PRIOR FILING DATE: 1997-08-14
;  NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 4322
;   LENGTH: 656
;   TYPE: PRT
;   ORGANISM: Staphylococcus epidermidis
US-09-134-001C-4322

  Query Match             6.7%;  Score 85.5;  DB 4;  Length 656;
  Best Local Similarity   25.6%;  Pred. No. 0.6;
  Matches   42;  Conservative   21;  Mismatches   70;  Indels   31;  Gaps    6;

Qy         35 AAQNSAEVVRCLNSALQVGCGAFACLENSTCDTDGMY-----------------DICK 75
              :|:  |  :  | | |::  |     |:   |  | |                 || |
Db         25 SAEKLATEIINLESILELPKGT----EHFVSDLHGEYESFQHVLRNGSGNVRAKINDIFK 80

Qy         76 SFLYSAAKFDTQGKAFV-KESLKCIANGVTSKVFLAIRRCSTFQRMIAEVQEECYSKLNV 134
                 |      |     :  :| || : |   |   | |   :| ||:| ::   | ||
Db         81 DKLSQQEINDLAALVYYPEEKLKLVKNNFDSIGTLNIWYITTIQRLI-DLITYCSSKYTR 139

Qy        135 CSIAKRNPE----AITEVVQLPNHFSNR--YYNRLVRSLLECDE 172
                : |  ||     | |::   | | |:  ||  ||  ::| :
Db        140 SKLRKALPEQYVYIIEELLYKSNEFHNKKPYYETLVNQIIELEQ 183


RESULT 15
US-09-134-001C-3810
; Sequence 3810, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
;  APPLICANT: Lynn Doucette-Stamm et al
;  TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
;  TITLE OF INVENTION:  EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
;  FILE REFERENCE: GTC-007
;  CURRENT APPLICATION NUMBER: US/09/134,001C
;  CURRENT FILING DATE:  1998-08-13
;  PRIOR APPLICATION NUMBER: US 60/064,964
;  PRIOR FILING DATE: 1997-11-08
;  PRIOR APPLICATION NUMBER: US 60/055,779
;  PRIOR FILING DATE: 1997-08-14
;  NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 3810
;   LENGTH: 417
;   TYPE: PRT
;   ORGANISM: Staphylococcus epidermidis
US-09-134-001C-3810

  Query Match             6.5%;  Score 83;  DB 4;  Length 417;
  Best Local Similarity   22.6%;  Pred. No. 0.58;
  Matches   44;  Conservative   32;  Mismatches   57;  Indels   62;  Gaps   11;

Qy         57 FACLENSTCDTD-----GMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAI 111
              |   | :| :||     |:||: :||     | :|:||:| : :::     : |:  :|
Db        266 FIKFEEATIETDHTSKQGLYDVIQSF---KDKVRTEGKSFYRLNVR-----INSEDIIAP 317
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Qy        112 RRCSTFQRMIAEVQEECYSKLNVCSIAKRNPEAITEVVQLPNHFSNRYYNRLVRSLLECD 171
              :     : || | :|                          | |   :   |    :: |
Db        318 QDLIQLKEMITEFEEN----------------------ENQFV--FIEDLNLQYVQND 351

Qy        172 EDTVSTIRDSLMEKIGPNM---ASLFHILQTDHCAQTHPRA-----DFNR----RRTNEP 219
              |  :       :::  | :   ||||    ||     :|||     |:|       |
Db        352 EMPI-------VKEFSPELLDDASLFDSAMTD--LYLNPRASKFLDDYNEFDKVELVNHA 402

Qy        220 QKLKVLLRNLRGEED 234
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Db        403 ERL--LKDEMRGEQN 415
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Search completed: June 12, 2003, 19:58:38
Job time : 36 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: June 12, 2003, 19:56:59 ; Search time 55 Seconds
(without alignments)
463.643 Million cell updates/sec

Title: US-09-705-500A-3
Perfect score: 1268
Sequence: 1 MLQNSAVLLVLVISASATHE.....NLRGEEDSPSHIKRTSHESA 247

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 392085 seqs, 103240269 residues

Total number of hits satisfying chosen parameters: 392085

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA:*
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2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
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11: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
12: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep:*
13: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
14: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1268	100.0	247	10	US-09-840-989A-2	Sequence 2, Appli
2	1268	100.0	247	10	US-09-361-736-10	Sequence 10, Appl
3	1268	100.0	247	12	US-10-116-051-2	Sequence 2, Appli
4	937	73.9	276	10	US-09-925-300-1426	Sequence 1426, Ap
5	662.5	52.2	256	10	US-09-840-989A-3	Sequence 3, Appli
6	660.5	52.1	204	12	US-10-116-051-10	Sequence 10, Appl
7	628	49.5	170	10	US-09-361-736-9	Sequence 9, Appli
8	358	28.2	70	10	US-09-864-761-37770	Sequence 37770, A
9	333.5	26.3	251	10	US-09-361-736-2	Sequence 2, Appli
10	303	23.9	118	12	US-10-116-051-9	Sequence 9, Appli
11	91	7.2	901	9	US-09-828-062-8	Sequence 8, Appli
12	81	6.4	720	10	US-09-419-305-1	Sequence 1, Appli
13	80	6.3	2180	9	US-09-736-968A-110	Sequence 110, App
14	80	6.3	2180	10	US-09-736-969A-96	Sequence 96, Appl
15	80	6.3	2180	10	US-09-736-960-93	Sequence 93, Appl
16	78.5	6.2	1288	9	US-09-736-968A-13	Sequence 13, Appl
17	78.5	6.2	1288	10	US-09-736-969A-13	Sequence 13, Appl
18	78.5	6.2	1288	10	US-09-736-960-13	Sequence 13, Appl
19	76	6.0	822	10	US-09-826-312-12	Sequence 12, Appl
20	76	6.0	1501	10	US-09-924-154-17	Sequence 17, Appl
21	76	6.0	26926	9	US-09-759-508B-2	Sequence 2, Appli
22	75.5	6.0	1338	10	US-09-402-100-4	Sequence 4, Appli
23	75	5.9	454	9	US-09-963-339-2	Sequence 2, Appli
24	75	5.9	1336	9	US-10-278-173-128	Sequence 128, App
25	74.5	5.9	211	10	US-09-861-451A-38	Sequence 38, Appl
26	74.5	5.9	323	9	US-10-097-340-314	Sequence 314, App
27	74.5	5.9	581	12	US-10-074-527-2	Sequence 2, Appli
28	74.5	5.9	903	9	US-10-087-464-52	Sequence 52, Appl
29	73.5	5.8	301	9	US-09-971-536-55	Sequence 55, Appl
30	73.5	5.8	302	9	US-09-764-868-1069	Sequence 1069, Ap
31	73.5	5.8	302	9	US-09-955-999-94	Sequence 94, Appl
32	73.5	5.8	947	10	US-09-801-574-4	Sequence 4, Appli
33	72.5	5.7	305	9	US-09-764-868-643	Sequence 643, App
34	72.5	5.7	362	10	US-09-815-242-11352	Sequence 11352, A
35	72.5	5.7	1530	9	US-10-118-513A-6	Sequence 6, Appli
36	72.5	5.7	1765	9	US-10-037-182-8	Sequence 8, Appli
37	72.5	5.7	1786	9	US-10-037-182-6	Sequence 6, Appli
38	72.5	5.7	1786	10	US-09-873-676-113	Sequence 113, App
39	72.5	5.7	1786	10	US-09-938-275-6	Sequence 6, Appli
40	72.5	5.7	2266	9	US-10-118-513A-14	Sequence 14, Appl
41	72	5.7	256	9	US-09-925-299-992	Sequence 992, App
42	72	5.7	256	10	US-09-925-299-992	Sequence 992, App
43	72	5.7	583	9	US-10-176-847-64	Sequence 64, Appl
44	71.5	5.6	1481	10	US-09-371-900-40	Sequence 40, Appl
45	71.5	5.6	1481	10	US-09-924-417-60	Sequence 60, Appl

ALIGNMENTS

RESULT 1
US-09-840-989A-2
; Sequence 2, Application US/09840989A
; Patent No. US20020042372A1
; GENERAL INFORMATION:
; APPLICANT: Olsen et al.
; TITLE OF INVENTION: Stanniocalcin Polynucleotides, Polypeptides, and Methods Based The
; FILE REFERENCE: PF108P2
; CURRENT APPLICATION NUMBER: US/09/840,989A
; CURRENT FILING DATE: 2001-04-25
; PRIOR APPLICATION NUMBER: PCT/US00/29432
; PRIOR FILING DATE: 2000-10-26
; PRIOR APPLICATION NUMBER: US 60/161,740
; PRIOR FILING DATE: 1999-10-27
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 247
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-840-989A-2

Query Match 100.0%; Score 1268; DB 10; Length 247;
Best Local Similarity 100.0%; Pred. No. 1.2e-119;
Matches 247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 MLQNSAVLLVLVISASATHEAEQNDSVSPRKSRVAAQNSAEVVRCLNSALQVGCGAFACL 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MLQNSAVLLVLVISASATHEAEQNDSVSPRKSRVAAQNSAEVVRCLNSALQVGCGAFACL 60

Qy         61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM 120

Qy        121 IAEVQEECYSKLNVCSIAKRNPEAITEVVQLPNHFSNRYYNRLVRSLLECDEDTVSTIRD 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 IAEVQEECYSKLNVCSIAKRNPEAITEVVQLPNHFSNRYYNRLVRSLLECDEDTVSTIRD 180

Qy        181 SLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRRTNEPQKLKVLLRNLRGEEDSPSHIK 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 SLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRRTNEPQKLKVLLRNLRGEEDSPSHIK 240
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Qy        241 RTSHESA 247
              |||||||
Db        241 RTSHESA 247


RESULT 2
US-09-361-736-10
; Sequence 10, Application US/09361736
; Patent No. US20020102634A1
;  GENERAL INFORMATION:
;    APPLICANT:  OLSEN, ET AL.
;    TITLE OF INVENTION:  Human Stanniocalcin-alpha
;    NUMBER OF SEQUENCES:  10
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  CARELLA, BYRNE, BAIN, GILFILLAN,
;      ADDRESSEE:  CECCHI, STEWART & OLSTEIN
;      STREET:  6 BECKER FARM ROAD
;      CITY:  ROSELAND
;      STATE:  NEW JERSEY
;      COUNTRY:  USA
;      ZIP:  07068
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5 INCH DISKETTE
;      COMPUTER:  IBM PS/2
;      OPERATING SYSTEM:  MS-DOS
;      SOFTWARE:  WORD PERFECT 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/361,736
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/460,529
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  MULLINS, J.G.
;      REGISTRATION NUMBER:  33,073
;      REFERENCE/DOCKET NUMBER:  325800-334  (PF143)
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  201-994-1700
;      TELEFAX:  201-994-1744
;  INFORMATION FOR SEQ ID NO:  10:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  247 AMINO ACIDS
;      TYPE:  AMINO ACID
;      STRANDEDNESS:
;      TOPOLOGY:  LINEAR
;    MOLECULE TYPE:  PROTEIN
US-09-361-736-10

  Query Match             100.0%;  Score 1268;  DB 10;  Length 247;
  Best Local Similarity   100.0%;  Pred. No. 1.2e-119;
  Matches  247;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MLQNSAVLLVLVISASATHEAEQNDSVSPRKSRVAAQNSAEVVRCLNSALQVGCGAFACL 60
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Qy         61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM 120
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM 120

Qy        121 IAEVQEECYSKLNVCSIAKRNPEAITEVVQLPNHFSNRYYNRLVRSLLECDEDTVSTIRD 180
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 IAEVQEECYSKLNVCSIAKRNPEAITEVVQLPNHFSNRYYNRLVRSLLECDEDTVSTIRD 180

Qy        181 SLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRRTNEPQKLKVLLRNLRGEEDSPSHIK 240
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 SLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRRTNEPQKLKVLLRNLRGEEDSPSHIK 240

Qy        241 RTSHESA 247
              |||||||
Db        241 RTSHESA 247


RESULT 3
US-10-116-051-2
; Sequence 2, Application US/10116051
; Patent No. US20020146791A1
; GENERAL INFORMATION:
;  APPLICANT: Olsen et al.
;  TITLE OF INVENTION: CORPUSCLES OF STANNIUS PROTEIN, STANNIOCALCIN
;  FILE REFERENCE: PF108P1D1C1
;  CURRENT APPLICATION NUMBER: US/10/116,051
;  CURRENT FILING DATE:  2002-04-05
;  PRIOR APPLICATION NUMBER: 09/312,610
;  PRIOR FILING DATE: 1999-05-17
;  PRIOR APPLICATION NUMBER: 08/431,117
;  PRIOR FILING DATE: 1995-04-28
;  PRIOR APPLICATION NUMBER: 08/208,005
;  PRIOR FILING DATE: 1994-03-08
;  NUMBER OF SEQ ID NOS: 10
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
;   LENGTH: 247
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-116-051-2

  Query Match             100.0%;  Score 1268;  DB 12;  Length 247;
  Best Local Similarity   100.0%;  Pred. No. 1.2e-119;
  Matches  247;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MLQNSAVLLVLVISASATHEAEQNDSVSPRKSRVAAQNSAEVVRCLNSALQVGCGAFACL 60
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MLQNSAVLLVLVISASATHEAEQNDSVSPRKSRVAAQNSAEVVRCLNSALQVGCGAFACL 60

Qy         61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM 120
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM 120

Qy        121 IAEVQEECYSKLNVCSIAKRNPEAITEVVQLPNHFSNRYYNRLVRSLLECDEDTVSTIRD 180
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 IAEVQEECYSKLNVCSIAKRNPEAITEVVQLPNHFSNRYYNRLVRSLLECDEDTVSTIRD 180

Qy        181 SLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRRTNEPQKLKVLLRNLRGEEDSPSHIK 240
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 SLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRRTNEPQKLKVLLRNLRGEEDSPSHIK 240

Qy        241 RTSHESA 247
              |||||||
Db        241 RTSHESA 247


RESULT 4
US-09-925-300-1426
; Sequence 1426, Application US/09925300
; Patent No. US20020151681A1
; GENERAL INFORMATION:
;  APPLICANT: Craig Rosen,
;  APPLICANT:  Steve Ruben
;  TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
;  FILE REFERENCE: PA101
;  CURRENT APPLICATION NUMBER: US/09/925,300
;  CURRENT FILING DATE:  2001-08-10
;  PRIOR APPLICATION NUMBER: PCT/US00/05988
;  PRIOR FILING DATE: 2000-03-08
;  PRIOR APPLICATION NUMBER: 60/124,270
;  PRIOR FILING DATE: 1999-03-12
;  NUMBER OF SEQ ID NOS: 1890
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1426
;   LENGTH: 276
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: SITE
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;   LOCATION: (43)
;   OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
;   NAME/KEY: SITE
;   LOCATION: (273)
;   OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
;   NAME/KEY: SITE
;   LOCATION: (275)
;   OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-925-300-1426

  Query Match             73.9%;  Score 937;  DB 10;  Length 276;
  Best Local Similarity   99.5%;  Pred. No. 2.8e-86;
  Matches  185;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 MLQNSAVLLVLVISASATHEAEQNDSVSPRKSRVAAQNSAEVVRCLNSALQVGCGAFACL 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         89 MLQNSAVLLVLVISASATHEAEQNDSVSPRKSRVAAQNSAEVVRCLNSALQVGCGAFACL 148

Qy         61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        149 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM 208

Qy        121 IAEVQEECYSKLNVCSIAKRNPEAITEVVQLPNHFSNRYYNRLVRSLLECDEDTVSTIRD 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        209 IAEVQEECYSKLNVCSIAKRNPEAITEVVQLPNHFSNRYYNRLVRSLLECDEDTVSTIRD 268

Qy        181 SLMEKI 186
              ||||  |
Db        269 SLMEXI 274


RESULT 5
US-09-840-989A-3
; Sequence 3, Application US/09840989A
; Patent No. US20020042372A1
; GENERAL INFORMATION:
;  APPLICANT: Olsen et al.
;  TITLE OF INVENTION: Stanniocalcin Polynucleotides, Polypeptides, and Methods Based Th
;  FILE REFERENCE: PF108P2
;  CURRENT APPLICATION NUMBER: US/09/840,989A
;  CURRENT FILING DATE:  2001-04-25
;  PRIOR APPLICATION NUMBER: PCT/US00/29432
;  PRIOR FILING DATE: 2000-10-26
;  PRIOR APPLICATION NUMBER: US 60/161,740
;  PRIOR FILING DATE: 1999-10-27
;  NUMBER OF SEQ ID NOS: 12
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
;   LENGTH: 256
;   TYPE: PRT
;   ORGANISM: Oncorhynchus kisutch
US-09-840-989A-3

  Query Match             52.2%;  Score 662.5;  DB 10;  Length 256;
  Best Local Similarity   53.4%;  Pred. No. 1.1e-58;
  Matches  125;  Conservative   46;  Mismatches   54;  Indels    9;  Gaps    4;

Qy         11 LVISASATHEAEQNDSVSPRKSRVAAQNSAEVVRCLNSALQVGCGAFACLENSTCDTDGM 70
              ||:  :|| : :  :: |||::| :: : ::| |||| || |||| ||||||||||||||
Db         12 LVLGTAATFDTDPEEA-SPRRARFSSNSPSDVARCLNGALAVGCGTFACLENSTCDTDGM 70

Qy         71 YDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRMIAEVQEECYS 130
              :|||: | ::|| |:|||| ||||||:|||||||||||  ||||  |||||:||||||||
Db         71 HDICQLFFHTAATFNTQGKTFVKESLRCIANGVTSKVFQTIRRCGVFQRMISEVQEECYS 130

Qy        131 KLNVCSIAKRNPEAITEVVQLPNHFSNRYYNRLVRSLLECDEDTVSTIRDSLMEKIGPNM 190
              :|::| :|: ||||| ||||:| || ||||: |::||| |||:||: :|  |: ::||:|
Db        131 RLDICGVARSNPEAIGEVVQVPAHFPNRYYSTLLQSLLACDEETVAVVRAGLVARLGPDM 190

Qy        191 ASLFHILQTDHCAQTHPRADFN-----RRRTNEPQKLKVLLRNLRGEEDSPSHI 239
              :|| :||  || |   :   :     |     |   |:   ::|| :  |:|:
Db        191 ETLFQLLQNKHCPQGSNQGPNSAPAGWRWPMGSPPSFKI-QPSMRGRD--PTHL 241


RESULT 6
US-10-116-051-10
; Sequence 10, Application US/10116051
; Patent No. US20020146791A1
; GENERAL INFORMATION:
;  APPLICANT: Olsen et al.
;  TITLE OF INVENTION: CORPUSCLES OF STANNIUS PROTEIN, STANNIOCALCIN
;  FILE REFERENCE: PF108P1D1C1
;  CURRENT APPLICATION NUMBER: US/10/116,051
;  CURRENT FILING DATE:  2002-04-05
;  PRIOR APPLICATION NUMBER: 09/312,610
;  PRIOR FILING DATE: 1999-05-17
;  PRIOR APPLICATION NUMBER: 08/431,117
;  PRIOR FILING DATE: 1995-04-28
;  PRIOR APPLICATION NUMBER: 08/208,005
;  PRIOR FILING DATE: 1994-03-08
;  NUMBER OF SEQ ID NOS: 10
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
;   LENGTH: 204
;   TYPE: PRT
;   ORGANISM: Oncorhynchus kisutch
US-10-116-051-10

  Query Match             52.1%;  Score 660.5;  DB 12;  Length 204;
  Best Local Similarity   60.8%;  Pred. No. 1.2e-58;
  Matches  118;  Conservative   38;  Mismatches   37;  Indels    1;  Gaps    1;

Qy         11 LVISASATHEAEQNDSVSPRKSRVAAQNSAEVVRCLNSALQVGCGAFACLENSTCDTDGM 70
              ||:  :|| : :  :: |||::| :: : ::| |||| || |||| ||||||||||||||
Db         12 LVLGTAATFDTDPEEA-SPRRARFSSNSPSDVARCLNGALAVGCGTFACLENSTCDTDGM 70

Qy         71 YDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRMIAEVQEECYS 130
              :|||: | ::|| |:|||| ||||||:|||||||||||  ||||  |||||:||||||||
Db         71 HDICQLFFHTAATFNTQGKTFVKESLRCIANGVTSKVFQTIRRCGVFQRMISEVQEECYS 130

Qy        131 KLNVCSIAKRNPEAITEVVQLPNHFSNRYYNRLVRSLLECDEDTVSTIRDSLMEKIGPNM 190
              :|::| :|: ||||| ||||:| || ||||: |::||| |||:||: :|  |: ::||:|
Db        131 RLDICGVARSNPEAIGEVVQVPAHFPNRYYSTLLQSLLACDEETVAVVRAGLVARLGPDM 190

Qy        191 ASLFHILQTDHCAQ 204
              :|| :||  || |
Db        191 ETLFQLLQNKHCPQ 204


RESULT 7
US-09-361-736-9
; Sequence 9, Application US/09361736
; Patent No. US20020102634A1
;  GENERAL INFORMATION:
;    APPLICANT:  OLSEN, ET AL.
;    TITLE OF INVENTION:  Human Stanniocalcin-alpha
;    NUMBER OF SEQUENCES:  10
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  CARELLA, BYRNE, BAIN, GILFILLAN,
;      ADDRESSEE:  CECCHI, STEWART & OLSTEIN
;      STREET:  6 BECKER FARM ROAD
;      CITY:  ROSELAND
;      STATE:  NEW JERSEY
;      COUNTRY:  USA
;      ZIP:  07068
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5 INCH DISKETTE
;      COMPUTER:  IBM PS/2
;      OPERATING SYSTEM:  MS-DOS
;      SOFTWARE:  WORD PERFECT 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/361,736
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/460,529
```

```
;       FILING DATE:
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  MULLINS, J.G.
;       REGISTRATION NUMBER:  33,073
;       REFERENCE/DOCKET NUMBER:  325800-334  (PF143)
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  201-994-1700
;       TELEFAX:  201-994-1744
;   INFORMATION FOR SEQ ID NO:  9:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  170 AMINO ACIDS
;       TYPE:  AMINO ACID
;       STRANDEDNESS:
;       TOPOLOGY:  LINEAR
;     MOLECULE TYPE:  PROTEIN
US-09-361-736-9

  Query Match             49.5%;  Score 628;  DB 10;  Length 170;
  Best Local Similarity   66.5%;  Pred. No. 1.8e-55;
  Matches  113;  Conservative   30;  Mismatches   27;  Indels    0;  Gaps    0;

Qy         28 SPRKSRVAAQNSAEVVRCLNSALQVGCGAFACLENSTCDTDGMYDICKSFLYSAAKFDTQ 87
              ||| :| :| : ::| |||| |||||| |||||:||||:||||::||:|||: |||||||
Db          1 SPRTARFSASSPSDVARCLNGALQVGCSAFACLDNSTCNTDGMHEICRSFLHGAAKFDTQ 60

Qy         88 GKAFVKESLKCIANGVTSKVFLAIRRCSTFQRMIAEVQEECYSKLNVCSIAKRNPEAITE 147
              || |||||||||||||:|||||| |||||:||:||:||||||||||::||:|: |||||: |
Db         61 GKTFVKESLKCIANGITSKVFLTIRRCSSFQKMISEVQEECYSKLDLCSVAQSNPEAMGE 120

Qy        148 VVQLPNHFSNRYYNRLVRSLLECDEDTVSTIRDSLMEKIGPNMASLFHIL 197
              | |:|: | ||||: |::||| ||||||  :|  |: :: | |  || :|
Db        121 VAQVPSQFPNRYYSTLLQSLLTCDEDTVEQVRAGLVSRLEPEMGVLFQLL 170


RESULT 8
US-09-864-761-37770
; Sequence 37770, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
;  APPLICANT: Penn, Sharron G.
;  APPLICANT:  Rank, David R.
;  APPLICANT:  Hanzel, David K.
;  APPLICANT:  Chen, Wensheng
;  TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
;  TITLE OF INVENTION:  GENE EXPRESSION ANALYSIS BY MICROARRAY
;  FILE REFERENCE: Aeomica-X-1
;  CURRENT APPLICATION NUMBER: US/09/864,761
;  CURRENT FILING DATE:  2001-05-23
;  PRIOR APPLICATION NUMBER: US 60/180,312
;  PRIOR FILING DATE: 2000-02-04
;  PRIOR APPLICATION NUMBER: US 60/207,456
;  PRIOR FILING DATE: 2000-05-26
;  PRIOR APPLICATION NUMBER: US 09/632,366
;  PRIOR FILING DATE: 2000-08-03
;  PRIOR APPLICATION NUMBER: GB 24263.6
;  PRIOR FILING DATE: 2000-10-04
;  PRIOR APPLICATION NUMBER: US 60/236,359
;  PRIOR FILING DATE: 2000-09-27
;  PRIOR APPLICATION NUMBER: PCT/US01/00666
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00667
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00664
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00669
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00665
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00668
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00663
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00662
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00661
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00670
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: US 60/234,687
;  PRIOR FILING DATE: 2000-09-21
;  PRIOR APPLICATION NUMBER: US 09/608,408
;  PRIOR FILING DATE: 2000-06-30
;  PRIOR APPLICATION NUMBER: US 09/774,203
;  PRIOR FILING DATE: 2001-01-29
;  NUMBER OF SEQ ID NOS: 49117
;  SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 37770
;   LENGTH: 70
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: MAP TO AC012119.1
;   OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.7
;   OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 2.4
;   OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 2.8
;   OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 2.8
;   OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 2.4
;   OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 3.1
;   OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 1.8
;   OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.7
;   OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 2.2
;   OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 2.7
;   OTHER INFORMATION: SWISSPROT HIT: P52823, EVALUE 3.00e-35
;   OTHER INFORMATION: EST_HUMAN HIT: AW954342.1, EVALUE 3.00e-34
US-09-864-761-37770

  Query Match             28.2%;  Score 358;  DB 10;  Length 70;
  Best Local Similarity   100.0%;  Pred. No. 7.8e-29;
  Matches   70;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         88 GKAFVKESLKCIANGVTSKVFLAIRRCSTFQRMIAEVQEECYSKLNVCSIAKRNPEAITE 147
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GKAFVKESLKCIANGVTSKVFLAIRRCSTFQRMIAEVQEECYSKLNVCSIAKRNPEAITE 60

Qy        148 VVQLPNHFSN 157
              ||||||||||
Db         61 VVQLPNHFSN 70


RESULT 9
US-09-361-736-2
; Sequence 2, Application US/09361736
; Patent No. US20020102634A1
;  GENERAL INFORMATION:
;    APPLICANT:  OLSEN, ET AL.
;    TITLE OF INVENTION:  Human Stanniocalcin-alpha
;    NUMBER OF SEQUENCES:  10
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  CARELLA, BYRNE, BAIN, GILFILLAN,
;      ADDRESSEE:  CECCHI, STEWART & OLSTEIN
;      STREET:  6 BECKER FARM ROAD
;      CITY:  ROSELAND
;      STATE:  NEW JERSEY
;      COUNTRY:  USA
;      ZIP:  07068
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5 INCH DISKETTE
;      COMPUTER:  IBM PS/2
;      OPERATING SYSTEM:  MS-DOS
;      SOFTWARE:  WORD PERFECT 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/361,736
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/460,529
```

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;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  MULLINS, J.G.
;      REGISTRATION NUMBER:  33,073
;      REFERENCE/DOCKET NUMBER:  325800-334  (PF143)
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  201-994-1700
;      TELEFAX:  201-994-1744
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  251 AMINO ACIDS
;      TYPE:  AMINO ACID
;      STRANDEDNESS:
;      TOPOLOGY:  LINEAR
;    MOLECULE TYPE:  PROTEIN
US-09-361-736-2

  Query Match             26.3%;  Score 333.5;  DB 10;  Length 251;
  Best Local Similarity   32.6%;  Pred. No. 1.3e-25;
  Matches   78;  Conservative   43;  Mismatches   89;  Indels   29;  Gaps    5;

Qy          9 LVLVIS-------ASATHEAE-QNDSVSPRKSRVAAQNSAEVVRCLNSALQVGCGAFACL 60
              | ||::       ||:  |   |  | :| |:: ||:||:  || :|  |||| | |
Db         12 LALVLATFDPARGTDATNPPEGPQDRSSQQKGRLSLQNTAEIQHCLVNAGDVGCGVFECF 71

Qy         61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM 120
              ||::|:  |:: || :||::| ||| |||:|:|::||| |: :  :     |:|   : |
Db         72 ENNSCEIRGLHGICMTFLHNAGKFDAQGKSFIKDALKCKAHALRHRFGCISRKCPAIREM 131

Qy        121 IAEVQEECYSKLNVCSIAKRNPEAITEVVQLPNHFSNRYYNRLVRSLLECDEDTVSTIRD 180
              ::::|  |  | ::|: |: |   | |::   :   :  |  ||  || | |:    |
Db        132 VSQLQRGCTLKHDLCAAAQENTRVIVEMIHFKDLLLHGPYVDLVNLLLTCGEEVKEAITH 191

Qy        181 SLMEKIGPNMASLFHILQTDHCAQ------THP-------------RADFNRRRTNEPQ 220
              |:  :   |  ||  ||    |       | |             ||    |||: |:
Db        192 SVQVQCEQNWGSLCSIL--SFCTSDIQKPPTAPPERQPQVDRTKLSRAHHGGRRTSPPR 248


RESULT 10
US-10-116-051-9
; Sequence 9, Application US/10116051
; Patent No. US20020146791A1
; GENERAL INFORMATION:
;  APPLICANT: Olsen et al.
;  TITLE OF INVENTION: CORPUSCLES OF STANNIUS PROTEIN, STANNIOCALCIN
;  FILE REFERENCE: PF108P1D1C1
;  CURRENT APPLICATION NUMBER: US/10/116,051
;  CURRENT FILING DATE:  2002-04-05
;  PRIOR APPLICATION NUMBER: 09/312,610
;  PRIOR FILING DATE: 1999-05-17
;  PRIOR APPLICATION NUMBER: 08/431,117
;  PRIOR FILING DATE: 1995-04-28
;  PRIOR APPLICATION NUMBER: 08/208,005
;  PRIOR FILING DATE: 1994-03-08
;  NUMBER OF SEQ ID NOS: 10
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
;   LENGTH: 118
;   TYPE: PRT
;   ORGANISM: Oncorhynchus kisutch
US-10-116-051-9

  Query Match             23.9%;  Score 303;  DB 12;  Length 118;
  Best Local Similarity   54.9%;  Pred. No. 5.5e-23;
  Matches   96;  Conservative    8;  Mismatches    9;  Indels   62;  Gaps   20;

Qy         28 SPRKSRVAAQNSAEVVRCLNSALQVGCGAFACLENSTCDTDGMYDICKSFLYSAAKFDTQ 87
              |||:          |||||:   |||| |||||||||||||| |||       | | ||
Db          5 SPRR----------VRCLNAL--VGCG-FACLENSTCDTDGM-DIC------FAAF-TQ 42

Qy         88 GKAFVKESLKCIANGVTSKVFLAIRRCSTFQRMIAEVQEECYSKLNVCSIAKRNPEAITE 147
              || |||||| |||||||||||  ||||  ||||| ||||||||   :|:    ||||| |
Db         43 GK-FVKESL-CIANGVTSKVF--IRRC--FQRMI-EVQEECYS---LCA----NPEAI-E 87

Qy        148 VVQLPNHFSNRYYNRLVRSLLECDEDTVSTIRDSLMEKIGPNMASLFHILQTDHC 202
              |||   || ||||  |:     |||    |:|      :||       :|   ||
Db         88 VVQ--PHF-NRYYLSLL-----CDE----TVR------LGP-------MLFLQHC 117


RESULT 11
US-09-828-062-8
; Sequence 8, Application US/09828062
; Publication No. US20030097675A1
; GENERAL INFORMATION:
;  APPLICANT: COSTA E SILVA, OSWALDO DA
;  APPLICANT:  BOHNERT, HANS J.
;  APPLICANT:  VAN THIELEN, NOCHA
;  APPLICANT:  CHEN, ROUYING
;  APPLICANT:  SARRIA-MILLAN, RODRIGO
;  TITLE OF INVENTION: CELL CYCLE STRESS-RELATED PROTEINS AND METHODS OF USE
;  TITLE OF INVENTION:  IN PLANTS
;  FILE REFERENCE: 16313-0031
;  CURRENT APPLICATION NUMBER: US/09/828,062
;  CURRENT FILING DATE:  2001-08-20
;  PRIOR APPLICATION NUMBER: 60/196,001
;  PRIOR FILING DATE: 2000-04-07
;  NUMBER OF SEQ ID NOS: 34
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
;   LENGTH: 901
;   TYPE: PRT
;   ORGANISM: Physcomitrella patens
US-09-828-062-8

  Query Match              7.2%;  Score 91;  DB 9;  Length 901;
  Best Local Similarity   20.2%;  Pred. No. 1.9;
  Matches   47;  Conservative   40;  Mismatches   98;  Indels   48;  Gaps    7;

Qy         16 SATHEAEQNDSVSPRKSRVAAQNSAEVVRCLNSALQVGCGAFACLENSTCDTDGMYDICK 75
              :: |  | | |   :   |       |:|| :   ::    | ||           :|
Db        282 ASVHMRELNPSDIDKLVSVKGM----VIRCSSIIPEIKGAFFKCL-----------VCG 325

Qy         76 SFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAI--RRCSTFQRMIAEVQEECYSKLN 133
                 :   |  |  |:|  :|      ::  :::   ||:   : |  :||
Db        326 ----HSPPLVTVVKGRVEEPTRCEKPECAARNAMSLIHNRCTFANKQIVRLQE------- 374

Qy        134 VCSIAKRNPEAITEVVQLPNHFSNRYYNRLVRSLLECDEDTVSTIRDSLMEKIGPNMASL 193
                    |:|| |  : |:  |    || :| ::    |    |: :  ::  ::|||  :|
Db        375 -------TPDAIPE-GETPHTVSMCLYNTMVDAVKPGDRIEVTGVFKAMAVRVGPNQRTL 426

Qy        194 FHILQTDHCAQTHPRADFNRRRTNEPQKLKVLLRNLRGEEDSPSHIKRTSHES 246
              : :|         ::|  | :| :|           | |  : :    |||
Db        427 RALYKTYIDCVHVKKSDRGRLQTEDPM----------EMDKENDMYAGYHES 468


RESULT 12
US-09-419-305-1
; Sequence 1, Application US/09419305
; Patent No. US20020102696A1
;  GENERAL INFORMATION:
;    APPLICANT:  MARUTA, Kazuhiko
;    APPLICANT:  KUBOTA, Michio
;    APPLICANT:  SUGIMOTO, Toshiyuki
;    TITLE OF INVENTION:  RECOMBINANT THERMOSTABLE ENZYME WHICH
;    TITLE OF INVENTION:  FORMS NON-REDUCING SACCHARIDE FROM REDUCING AMYLACEOUS
;    TITLE OF INVENTION:  SACCHARIDE
;    NUMBER OF SEQUENCES:  19
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Browdy and Neimark
;      STREET:  419 Seventh Street N.W. Ste. 300
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  U.S.A.
;      ZIP:  20004
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
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;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.30
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/09/419,305
;       FILING DATE:
;       CLASSIFICATION:
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/505,448
;       FILING DATE:  21-JUL-1994
;       APPLICATION NUMBER:  JP 190183/1994
;       FILING DATE:  21-JUL-1994
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  JP 189706/1995
;       FILING DATE:  04-JUL-1995
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Browdy, Roger L.
;       REGISTRATION NUMBER:  25,618
;       REFERENCE/DOCKET NUMBER:  MARUTA=3
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (202) 628-5197
;       TELEFAX:  (202) 737-3528
;   INFORMATION FOR SEQ ID NO:  1:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  720 amino acids
;       TYPE:  amino acid
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  protein
US-09-419-305-1

  Query Match             6.4%;  Score 81;  DB 10;  Length 720;
  Best Local Similarity   24.2%;  Pred. No. 14;
  Matches   38;  Conservative   22;  Mismatches   45;  Indels   52;  Gaps    9;

Qy          86 TQGKAFVKESLKCIANGVTSKVF-LAIRR-----------------CSTFQRMIA-EVQE 126
               |  |  : ||:| |    :  ::|   ::|                 |    |  | :: :
Db         299 TAEKISISESIKKIKAQIIDELFSYEVKRLASQLGISYDILRDYLSCIDVYRTYANQIVK 358

Qy         127 ECYSKLNVCSIAKRNPEAITEVVQ-LPNHFSNRY-------YNRLVRSLLECDEDTVSTI 178
               ||      :    ||||||  |:: | :|  ::  |       ||||: |: |   |
Db         359 ECDKTNEIEEATKRNPEAYTKLQQYMPAVYAKAYEDTFLFRYNRLI-SINEVGSDL---- 413

Qy         179 RDSLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRR 215
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Db         414 ---RYYKISPDQ---FHV-------------FNQKR 430


RESULT 13
US-09-736-968A-110
; Sequence 110, Application US/09736968A
; Patent No. US20020169283A1
; GENERAL INFORMATION:
;  APPLICANT: Lu, Peter
;  APPLICANT:  Garman, Jonathan David
;  APPLICANT:  Candia III, Albert Frederick
;  APPLICANT:  Arbor Vita Corporation
;  TITLE OF INVENTION: CLASP-7 Transmembrane Protein
;  FILE REFERENCE: 020054-000611US
;  CURRENT APPLICATION NUMBER: US/09/736,968A
;  CURRENT FILING DATE:  2000-12-13
;  PRIOR APPLICATION NUMBER: US 60/160,860
;  PRIOR FILING DATE: 1999-10-21
;  PRIOR APPLICATION NUMBER: US 60/162,498
;  PRIOR FILING DATE: 1999-10-29
;  PRIOR APPLICATION NUMBER: US 60/170,453
;  PRIOR FILING DATE: 1999-12-13
;  PRIOR APPLICATION NUMBER: US 60/176,195
;  PRIOR FILING DATE: 2000-01-14
;  PRIOR APPLICATION NUMBER: US 60/182,296
;  PRIOR FILING DATE: 2000-02-14
;  PRIOR APPLICATION NUMBER: US 09/547,276
;  PRIOR FILING DATE: 2000-04-11
;  PRIOR APPLICATION NUMBER: US 60/196,267
;  PRIOR FILING DATE: 2000-04-11
;  PRIOR APPLICATION NUMBER: US 60/196,460
;  PRIOR FILING DATE: 2000-04-11
;  PRIOR APPLICATION NUMBER: US 60/196,527
;  PRIOR FILING DATE: 2000-04-11
;  PRIOR APPLICATION NUMBER: US 60/196,528
;  PRIOR FILING DATE: 2000-04-11
;  PRIOR APPLICATION NUMBER: US 09/687,837
;  PRIOR FILING DATE: 2000-10-13
;  PRIOR APPLICATION NUMBER: US 60/240,503
;  PRIOR FILING DATE: 2000-10-13
;  PRIOR APPLICATION NUMBER: US 60/240,508
;  PRIOR FILING DATE: 2000-10-13
;  PRIOR APPLICATION NUMBER: US 60/240,539
;  PRIOR FILING DATE: 2000-10-13
;  PRIOR APPLICATION NUMBER: US 60/240,543
;  PRIOR FILING DATE: 2000-10-13
;  NUMBER OF SEQ ID NOS: 115
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 110
;   LENGTH: 2180
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: human CLASP-1
US-09-736-968A-110

  Query Match             6.3%;  Score 80;  DB 9;  Length 2180;
  Best Local Similarity   21.7%;  Pred. No. 84;
  Matches   40;  Conservative   30;  Mismatches   76;  Indels   38;  Gaps    6;

Qy          68 DGMYDICKSFLYSAAKFDTQG---KAFVKESLKCIANGVTSKVFLAIRRCSTFQRMIAEV 124
               ||    : |   :  :  :||     || :|  |                |     |   :
Db         831 DGGKPLFKVSTFVVSTVNTQDPHVNAFFQECQK-------------REKDMSQSPTSNF 876

Qy         125 QEECYSKLNVCSIAKRNPEAITEVVQLPNHFSNRYYNRLVRSLLECDEDTVSTIRDSLME 184
                  | : |||           | :     |     |:| : |:: :|| ::|     :
Db         877 IRSCKNLLNV-----------EKIHAIMSFLPIILNQLFKVLVQNEEDEITT----TVT 920

Qy         185 KIGPNMASLFHILQTDHCAQTHPRADFNRRRTNEPQKLKVLLRNLRG---EEDSPS--HI 239
               :: |:: :  |  | ||  |:: :  |  |   |    : | :|: |    |||:  |:
Db         921 RVLPDIVAKCHEEQLDHSVQSYIKFVFKTRACKERPVHEDLAKNVTGLLKSNDSPTVKHV 980

Qy         240 KRTS 243
                : |
Db         981 LKHS 984


RESULT 14
US-09-736-969A-96
; Sequence 96, Application US/09736969A
; Patent No. US20020068302A1
; GENERAL INFORMATION:
;  APPLICANT: Lu, Peter
;  APPLICANT:  Garman, Jonathan David
;  APPLICANT:  Candia III, Albert Frederick
;  APPLICANT:  Arbor Vita Corporation
;  TITLE OF INVENTION: CLASP-4 Transmembrane Protein
;  FILE REFERENCE: 020054-000411US
;  CURRENT APPLICATION NUMBER: US/09/736,969A
;  CURRENT FILING DATE:  2000-12-13
;  PRIOR APPLICATION NUMBER: US 60/160,860
;  PRIOR FILING DATE: 1999-10-21
;  PRIOR APPLICATION NUMBER: US 60/162,498
;  PRIOR FILING DATE: 1999-10-29
;  PRIOR APPLICATION NUMBER: US 60/170,453
;  PRIOR FILING DATE: 1999-12-13
;  PRIOR APPLICATION NUMBER: US 60/176,195
;  PRIOR FILING DATE: 2000-01-14
;  PRIOR APPLICATION NUMBER: US 60/182,296
;  PRIOR FILING DATE: 2000-02-14
;  PRIOR APPLICATION NUMBER: US 09/547,276
;  PRIOR FILING DATE: 2000-04-11
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;  PRIOR APPLICATION NUMBER: US 60/196,267
;  PRIOR FILING DATE: 2000-04-11
;  PRIOR APPLICATION NUMBER: US 60/196,460
;  PRIOR FILING DATE: 2000-04-11
;  PRIOR APPLICATION NUMBER: US 60/196,527
;  PRIOR FILING DATE: 2000-04-11
;  PRIOR APPLICATION NUMBER: US 60/196,528
;  PRIOR FILING DATE: 2000-04-11
;  PRIOR APPLICATION NUMBER: US 09/687,837
;  PRIOR FILING DATE: 2000-10-13
;  PRIOR APPLICATION NUMBER: US 60/240,503
;  PRIOR FILING DATE: 2000-10-13
;  PRIOR APPLICATION NUMBER: US 60/240,508
;  PRIOR FILING DATE: 2000-10-13
;  PRIOR APPLICATION NUMBER: US 60/240,539
;  PRIOR FILING DATE: 2000-10-13
;  PRIOR APPLICATION NUMBER: US 60/240,543
;  PRIOR FILING DATE: 2000-10-13
;  NUMBER OF SEQ ID NOS: 153
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 96
;   LENGTH: 2180
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: human CLASP-1
US-09-736-969A-96

  Query Match             6.3%;  Score 80;  DB 10;  Length 2180;
  Best Local Similarity   21.7%;  Pred. No. 84;
  Matches   40;  Conservative   30;  Mismatches   76;  Indels   38;  Gaps    6;

Qy         68 DGMYDICKSFLYSAAKFDTQG---KAFVKESLKCIANGVTSKVFLAIRRCSTFQRMIAEV 124
              ||   : |   :  :  :||     || :|  |             |     |   :
Db        831 DGGKPLFKVSTFVVSTVNTQDPHVNAFFQECQK-------------REKDMSQSPTSNF 876

Qy        125 QEECYSKLNVCSIAKRNPEAITEVVQLPNHFSNRYYNRLVRSLLECDEDTVSTIRDSLME 184
               | : |||          | :     |     |:| : |:: :|| ::|     :
Db        877 IRSCKNLLNV----------EKIHAIMSFLPIILNQLFKVLVQNEEDEITT----TVT 920

Qy        185 KIGPNMASLFHILQTDHCAQTHPRADFNRRRTNEPQKLKVLLRNLRG---EEDSPS--HI 239
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Db        921 RVLPDIVAKCHEEQLDHSVQSYIKFVFKTRACKERPVHEDLAKNVTGLLKSNDSPTVKHV 980

Qy        240 KRTS 243
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Db        981 LKHS 984


RESULT 15
US-09-736-960-93
; Sequence 93, Application US/09736960
; Patent No. US20020102267A1
; GENERAL INFORMATION:
;  APPLICANT: Lu, Peter
;  APPLICANT:  Garman, Jonathan David
;  APPLICANT:  Candia III, Albert Frederick
;  APPLICANT:  Arbor Vita Corporation
;  TITLE OF INVENTION: CLASP-5 Transmembrane Protein
;  FILE REFERENCE: 020054-000511US
;  CURRENT APPLICATION NUMBER: US/09/736,960
;  CURRENT FILING DATE:  2001-09-20
;  PRIOR APPLICATION NUMBER: US 60/160,860
;  PRIOR FILING DATE: 1999-10-21
;  PRIOR APPLICATION NUMBER: US 60/162,498
;  PRIOR FILING DATE: 1999-10-29
;  PRIOR APPLICATION NUMBER: US 60/170,453
;  PRIOR FILING DATE: 1999-12-13
;  PRIOR APPLICATION NUMBER: US 60/176,195
;  PRIOR FILING DATE: 2000-01-14
;  PRIOR APPLICATION NUMBER: US 60/182,296
;  PRIOR FILING DATE: 2000-02-14
;  PRIOR APPLICATION NUMBER: US 09/547,276
;  PRIOR FILING DATE: 2000-04-11
;  PRIOR APPLICATION NUMBER: US 60/196,267
;  PRIOR FILING DATE: 2000-04-11
;  PRIOR APPLICATION NUMBER: US 60/196,460
;  PRIOR FILING DATE: 2000-04-11
;  PRIOR APPLICATION NUMBER: US 60/196,527
;  PRIOR FILING DATE: 2000-04-11
;  PRIOR APPLICATION NUMBER: US 60/196,528
;  PRIOR FILING DATE: 2000-04-11
;  PRIOR APPLICATION NUMBER: US 09/687,837
;  PRIOR FILING DATE: 2000-10-13
;  PRIOR APPLICATION NUMBER: US 60/240,503
;  PRIOR FILING DATE: 2000-10-13
;  PRIOR APPLICATION NUMBER: US 60/240,508
;  PRIOR FILING DATE: 2000-10-13
;  PRIOR APPLICATION NUMBER: US 60/240,539
;  PRIOR FILING DATE: 2000-10-13
;  PRIOR APPLICATION NUMBER: US 60/240,543
;  PRIOR FILING DATE: 2000-10-13
;  NUMBER OF SEQ ID NOS: 134
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 93
;   LENGTH: 2180
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: human CLASP-1
US-09-736-960-93

  Query Match             6.3%;  Score 80;  DB 10;  Length 2180;
  Best Local Similarity   21.7%;  Pred. No. 84;
  Matches   40;  Conservative   30;  Mismatches   76;  Indels   38;  Gaps    6;

Qy         68 DGMYDICKSFLYSAAKFDTQG---KAFVKESLKCIANGVTSKVFLAIRRCSTFQRMIAEV 124
              ||   : |   :  :  :||     || :|  |             |     |   :
Db        831 DGGKPLFKVSTFVVSTVNTQDPHVNAFFQECQK-------------REKDMSQSPTSNF 876

Qy        125 QEECYSKLNVCSIAKRNPEAITEVVQLPNHFSNRYYNRLVRSLLECDEDTVSTIRDSLME 184
               | : |||          | :     |     |:| : |:: :|| ::|     :
Db        877 IRSCKNLLNV----------EKIHAIMSFLPIILNQLFKVLVQNEEDEITT----TVT 920

Qy        185 KIGPNMASLFHILQTDHCAQTHPRADFNRRRTNEPQKLKVLLRNLRG---EEDSPS--HI 239
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Db        921 RVLPDIVAKCHEEQLDHSVQSYIKFVFKTRACKERPVHEDLAKNVTGLLKSNDSPTVKHV 980

Qy        240 KRTS 243
               : |
Db        981 LKHS 984


Search completed: June 12, 2003, 20:05:27
Job time : 56 secs
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: June 12, 2003, 19:48:33 ; Search time 44 Seconds
(without alignments)
539.664 Million cell updates/sec

Title: US-09-705-500A-3
Perfect score: 1268
Sequence: 1 MLQNSAVLLVLVISASATHE.....NLRGEEDSPSHIKRTSHESA 247

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_73:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	680.5	53.7	263	2	A54648	stanniocalcin prec
2	662.5	52.2	256	2	I51197	stanniocalcin - co
3	354	27.9	302	2	JE0357	stanniocalcin homo
4	150	11.8	40	2	B60841	teleocalcin - coho
5	149	11.8	40	2	A60841	teleocalcin - sock
6	123	9.7	33	2	S06337	teleocalcin - rain
7	102	8.0	473	2	T04799	hypothetical prote
8	94	7.4	1105	2	T18295	Ap-3 adaptor compl
9	90.5	7.1	289	2	T50776	hypothetical prote
10	90.5	7.1	783	2	T38690	probable regulator
11	89.5	7.1	1126	2	T01491	ubiquitin-protein
12	89	7.0	305	2	T08121	peroxidase (EC 1.1
13	88	6.9	473	2	T45954	hypothetical prote
14	87.5	6.9	1465	2	S45628	DNA-directed DNA p
15	86	6.8	470	2	H72097	mg++ transporter (
16	86	6.8	470	2	F86526	Mg++ transporter [
17	86	6.8	510	2	T45952	hypothetical prote
18	86	6.8	556	2	S51858	probable membrane
19	86	6.8	581	2	S58201	probable membrane
20	83	6.5	250	2	S30584	hypothetical prote
21	83	6.5	250	2	D69215	conserved hypothet
22	83	6.5	365	2	T06693	hypothetical prote
23	83	6.5	1093	2	T50652	AP-3 complex beta3
24	83	6.5	1094	2	T50651	AP3-complex beta-3
25	82.5	6.5	869	2	A88710	protein C43G2.2 [i
26	82.5	6.5	1483	2	S30015	hypothetical prote
27	82.5	6.5	1757	2	T05204	hypothetical prote
28	82.5	6.5	2335	2	T40186	probable phosphati
29	82.5	6.5	2535	2	T04824	hypothetical prote
30	82	6.5	815	2	G72209	conserved hypothet
31	82	6.5	925	2	T01384	hypothetical prote
32	81.5	6.4	463	2	T15416	hypothetical prote
33	81.5	6.4	549	2	F64640	conserved hypothet
34	81.5	6.4	708	1	TFBOL	lactotransferrin p
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36	81	6.4	720	2	JC5131	glycosyltransferas
37	81	6.4	1375	2	T18961	FAB1 protein homol
38	81	6.4	4377	2	A55575	ankyrin 3, long sp
39	80	6.3	281	2	H84720	probable endonucle
40	80	6.3	509	1	VGNVPC	major envelope gly
41	80	6.3	509	2	T10395	protein gp64 - Org
42	80	6.3	985	2	T00633	Ca2+-transporting
43	80	6.3	998	2	T52581	Ca2+-transporting
44	80	6.3	1178	2	S54073	probable membrane
45	80	6.3	1188	2	T46608	zinc finger protei

ALIGNMENTS

RESULT 1
A54648
stanniocalcin precursor - Australian eel
N;Alternate names: Stannius corpuscle secretory protein
C;Species: Anguilla australis (Australian eel)
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 07-May-1999
C;Accession: A54648
R;Butkus, A.; Roche, P.J.; Fernley, R.T.; Haralambidis, J.; Penschow, J.D.; Ryan, G.B.;
Mol. Cell. Endocrinol. 54, 123-133, 1987
A;Title: Purification and cloning of a corpuscles of Stannius protein from Anguilla aust
A;Reference number: A54648; MUID:88083961; PMID:3319739
A;Accession: A54648
A;Status: preliminary
A;Molecule type: mRNA
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F;18-263/Product: stanniocalcin #status predicted <MAT>

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Best Local Similarity 61.4%; Pred. No. 2.4e-51;
Matches 124; Conservative 41; Mismatches 36; Indels 1; Gaps 1;

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Qy         61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM 120
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Db         60 DNSTCNTDGMHEICRSFLHGAAKFDTQGKTFVKESLKCIANGITSKVFLTIRRCSSFQKM 119

Qy        121 IAEVQEECYSKLNVCSIAKRNPEAITEVVQLPNHFSNRYYNRLVRSLLECDEDTVSTIRD 180
              |:|||||||||::||:|: |||||: || |:|: | ||||: |::||| |||||  :|
Db        120 ISEVQEECYSKLDLCSVAQSNPEAMGEVAQVPSQFPNRYYSTLLQSLLTCDEDTVEQVRA 179

Qy        181 SLMEKIGPNMASLFHILQTDHC 202
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Db        180 GLVSRLEPEMGVLFQLLQTKAC 201
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RESULT 2
I51197
stanniocalcin - coho salmon
C;Species: Oncorhynchus kisutch (coho salmon)
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jul-2000
C;Accession: I51197
R;Wagner, G.F.; Dimattia, G.E.; Davie, J.R.; Copp, D.H.; Friesen, H.G.
Mol. Cell. Endocrinol. 90, 7-15, 1992
A;Title: Molecular cloning and cDNA sequence analysis of coho salmon stanniocalcin.
A;Reference number: I51197; MUID:93246046; PMID:1363790
A;Accession: I51197
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA

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A;Residues: 1-256 <WAG>
A;Cross-references: GB:S59519; NID:g299926; PIDN:AAB26419.1; PID:g299927

  Query Match            52.2%;  Score 662.5;  DB 2;  Length 256;
  Best Local Similarity  53.4%;  Pred. No. 8.3e-50;
  Matches  125;  Conservative   46;  Mismatches   54;  Indels    9;  Gaps    4;

Qy         11 LVISASATHEAEQNDSVSPRKSRVAAQNSAEVVRCLNSALQVGCGAFACLENSTCDTDGM 70
              ||:  :|| : :  :: |||::| :: : ::| |||| || |||| ||||||||||||||
Db         12 LVLGTAATFDTDPEEA-SPRRARFSSNSPSDVARCLNGALAVGCGTFACLENSTCDTDGM 70

Qy         71 YDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRMIAEVQEECYS 130
              :|||: | ::|| |:|||| ||||||:|||||||||||  ||||  |||||:||||||||
Db         71 HDICQLFFHTAATFNTQGKTFVKESLRCIANGVTSKVFQTIRRCGVFQRMISEVQEECYS 130

Qy        131 KLNVCSIAKRNPEAITEVVQLPNHFSNRYYNRLVRSLLECDEDTVSTIRDSLMEKIGPNM 190
              :|::| :|: ||||| ||||:| || |||| |::||| |||:||: :|  |: ::||:|
Db        131 RLDICGVARSNPEAIGEVVQVPAHFPNRYYSTLLQSLLACDEETVAVVRAGLVARLGPDM 190

Qy        191 ASLFHILQTDHCAQTHPRADFN-----RRRTNEPQKLKVLLRNLRGEEDSPSHI 239
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RESULT 3
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N;Alternate names: STC2
C;Species: Homo sapiens (man)
C;Date: 05-Feb-1999 #sequence_revision 05-Feb-1999 #text_change 21-Jul-2000
C;Accession: JE0357
R;Ishibashi, K.; Miyamoto, K.; Taketani, Y.; Morita, K.; Takeda, E.; Sasaki, S.; Imai, M
Biochem. Biophys. Res. Commun. 250, 252-258, 1998
A;Title: Molecular cloning of a second human stanniocalcin homologue (STC2).
A;Reference number: JE0357; MUID:98440784; PMID:9753616
A;Accession: JE0357
A;Molecule type: mRNA
A;Residues: 1-302 <ISH>
A;Cross-references: DDBJ:AB012664; NID:g3702223; PIDN:BAA33489.1; PID:g3702224
C;Comment: This protein suppressed expression of renal sodium/phosphate cotransporter.
C;Genetics:
A;Introns: 51/1 98/3 169/2

  Query Match            27.9%;  Score 354;  DB 2;  Length 302;
  Best Local Similarity  32.4%;  Pred. No. 4.7e-23;
  Matches   83;  Conservative   45;  Mismatches  102;  Indels   26;  Gaps    4;

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Db         12 LALVLATFDPARGTDATNPPEGPQDRSSQQKGRLSLQNTAEIQHCLVNAGDVGCGVFECF 71

Qy         61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM 120
              ||::|:  |:: || :||::| ||| |||:|:|::||| |: :  :     |:|   : |
Db         72 ENNSCEIRGLHGICMTFLHNAGKFDAQGKSFIKDALKCKAHALRHRFGCISRKCPAIREM 131

Qy        121 IAEVQEECYSKLNVCSIAKRNPEAITEVVQLPNHFSNRYYNRLVRSLLECDEDTVSTIRD 180
              ::::| ||| | ::|: |: |   | |::   :   :  |  ||  || | |:    |
Db        132 VSQLQRECYLKHDLCAAAQENTRVIVEMIHFKDLLLHEPYVDLVNLLLTCGEEVKEAITH 191

Qy        181 SLMEKIGPNMASLFHILQ-TDHCAQTHPRADFNRRRTNEPQKL----------------- 222
              |:  :   |  ||  ||       |  | |   |:   :  ||
Db        192 SVQVQCEQNWGSLCSILSFCTSAIQKPPTAPPERQPQVDRTKLSRAHHGEAGHHLPEPSS 251

Qy        223 KVLLRNLRGEEDSPSH 238
              :   |  :||  | ||
Db        252 RETGRGAKGERGSKSH 267


RESULT 4
B60841
teleocalcin - coho salmon (fragment)
C;Species: Oncorhynchus kisutch (coho salmon)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 30-Sep-1993
C;Accession: B60841
R;Wagner, G.F.; Fenwick, J.C.; Park, C.M.; Milliken, C.; Copp, D.H.; Friesen, H.G.
Gen. Comp. Endocrinol. 72, 237-246, 1988
A;Title: Comparative biochemistry and physiology of teleocalcin from sockeye and coho sal
A;Reference number: A60841; MUID:89065334; PMID:3197944
A;Accession: B60841
A;Molecule type: protein
A;Residues: 1-40 <WAG>
C;Comment: This glycoprotein hormone from the corpuscles of Stannius regulates calcuim u
C;Keywords: disulfide bond; glycoprotein; hormone

  Query Match            11.8%;  Score 150;  DB 2;  Length 40;
  Best Local Similarity  66.7%;  Pred. No. 1.9e-06;
  Matches   26;  Conservative    6;  Mismatches    7;  Indels    0;  Gaps    0;

Qy         35 AAQNSAEVVRCLNSALQVGCGAFACLENSTCDTDGMYDI 73
              :: : ::| |||| || |||| ||||| |||||||||:||
Db          2 SSNSPSDVARCLNGALAVGCGTFACLEXSTCDTDGMHDI 40


RESULT 5
A60841
teleocalcin - sockeye salmon (fragment)
C;Species: Oncorhynchus nerka (sockeye salmon)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 30-Sep-1993
C;Accession: A60841
R;Wagner, G.F.; Fenwick, J.C.; Park, C.M.; Milliken, C.; Copp, D.H.; Friesen, H.G.
Gen. Comp. Endocrinol. 72, 237-246, 1988
A;Title: Comparative biochemistry and physiology of teleocalcin from sockeye and coho sal
A;Reference number: A60841; MUID:89065334; PMID:3197944
A;Accession: A60841
A;Molecule type: protein
A;Residues: 1-40 <WAG>
C;Comment: This glycoprotein hormone from the corpuscles of Stannius regulates calcuim u
C;Keywords: disulfide bond; glycoprotein; hormone

  Query Match            11.8%;  Score 149;  DB 2;  Length 40;
  Best Local Similarity  76.5%;  Pred. No. 2.3e-06;
  Matches   26;  Conservative    3;  Mismatches    5;  Indels    0;  Gaps    0;

Qy         40 AEVVRCLNSALQVGCGAFACLENSTCDTDGMYDI 73
              ::| |||| || |||| ||||| |||||||||:||
Db          7 SDVARCLNGALDVGCGTFACLEXSTCDTDGMHDI 40


RESULT 6
S06337
teleocalcin - rainbow trout (fragment)
N;Alternate names: hypocalcin
C;Species: Oncorhynchus mykiss (rainbow trout)
C;Date: 29-Jan-1993 #sequence_revision 29-Jan-1993 #text_change 18-Jun-1993
C;Accession: S06337
R;Lafeber, F.P.J.G.; Hanssen, R.G.J.M.; Choy, Y.M.; Flik, G.; Herrmann-Erlee, M.P.M.; Par
Gen. Comp. Endocrinol. 69, 19-30, 1988
A;Title: Identification of hypocalcin (teleocalcin) isolated from trout stannius corpusc
A;Reference number: S06337; MUID:88196801; PMID:3360288
A;Accession: S06337
A;Molecule type: protein
A;Residues: 1-33 <LAF>
A;Note: 7-Glu was also found
C;Keywords: dimer; glycoprotein; hormone
F;29/Binding site: carbohydrate (Asn) (covalent) #status experimental

  Query Match             9.7%;  Score 123;  DB 2;  Length 33;
  Best Local Similarity  65.6%;  Pred. No. 0.00032;
  Matches   21;  Conservative    5;  Mismatches    6;  Indels    0;  Gaps    0;

Qy         35 AAQNSAEVVRCLNSALQVGCGAFACLENSTCD 66
              :: : ::| |||| || |||| ||||||||||
Db          2 SSNSPSDVARCLNGALAVGCGTFACLENSTCD 33


RESULT 7
```

```
T04799
hypothetical protein F10M23.100 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 11-Jun-1999
C;Accession: T04799
R;Bevan, M.; Lecharny, A.; Chefdor, F.; Krivitzky, M.; Kreis, M.; Hoheisel, J.; Mewes, H
submitted to the Protein Sequence Database, February 1999
A;Reference number: Z15385
A;Accession: T04799
A;Molecule type: DNA
A;Residues: 1-473 <BEV>
A;Cross-references: EMBL:AL035440
A;Experimental source: cultivar Columbia; BAC clone F10M23
C;Genetics:
A;Map position: 4
A;Introns: 24/3; 92/3; 184/3; 256/3; 308/3; 412/3
A;Note: F10M23.100

  Query Match             8.0%;  Score 102;  DB 2;  Length 473;
  Best Local Similarity   21.0%;  Pred. No. 0.49;
  Matches   50;  Conservative   43;  Mismatches   67;  Indels   78;  Gaps   11;

Qy         26 SVSPRKSRVAAQNSAEVVRCLNSALQVGCGAFACLENSTCDT----DGMYDICKSF-LYS 80
Db         50 NVYKKKVELAAKSRAELLQTLSD---------ATVELSNLTTALGEKSYIDICDSMSLFP 100

Qy         81 AAKFDTQGKAFVKESLKCIA-----------------------------------NG-- 102
Db        101 LQPDKTSGT--IKEQLSAIAPALEQLWQQKEERVRAFSDVQSQIQKICEEIAGGLNNGPH 158

Qy        103 VTSKVFLAIRRCSTFQRMIAEVQEECYSKL-----------NVCSIAKRN-PEAITEV-- 148
Db        159 VVDETDLSLKRLDDFQRKLQELQKEKSDRLQKVLEFVSTVHDLCAVLRLDFLSTVTEVHP 218

Qy        149 -------VQLPNHFSNRYYNRLVRSLLECDEDTVSTIRDSLMEKIGPNMASLFHILQT 199
Db        219 SLDEANGVQTKS-ISNETLARLAKTVLTLKEDKMQRLKK--LQELATQLTDLWNLMDT 273


RESULT 8
T18295
Ap-3 adaptor complex beta3A chain - mouse
C;Species: Mus musculus (house mouse)
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T18295
R;Feng, L.; Seymour, A.B.; Jiang, S.Y.; To, A.; Peden, A.A.; Novak, E.K.; Zhen, L.; Rusi
Hum. Mol. Genet. 8, 323-330, 1999
A;Title: The beta3A subunit gene (Ap3b1) of the AP-3 adaptor complex is altered in the m
A;Reference number: Z18864; MUID:99135912; PMID:9931340
A;Accession: T18295
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-1105 <FEN>
A;Cross-references: EMBL:AF103809; NID:g3885987; PID:g3885988; PIDN:AAC78338.1
A;Experimental source: strain C3H/HeJ
C;Genetics:
A;Gene: Ap3b1
A;Map position: 13

  Query Match             7.4%;  Score 94;  DB 2;  Length 1105;
  Best Local Similarity   21.2%;  Pred. No. 6.5;
  Matches   55;  Conservative   40;  Mismatches  104;  Indels   60;  Gaps   11;

Qy          1 MLQNSAVLLVLVISASATHEAEQNDSVSPRKSRVAAQNSAEVVRCLNSALQVGCGAFACL 60
Db        308 LLQSRNAAVVMAVAQLYWH-------ISPKSE--AGVISKSLVRLLRSNREVQYIVLQNI 358

Qy         61 ENSTCDTDGMYD-ICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFL---------- 109
Db        359 ATMSIERKGMFEPYLKSF-YVRSTDPTMIKTLKLEILTNLANEANISTLLREFQTYVRSQ 417

Qy        110 ----------AIRRCSTFQRMIAEVQEECYSKLNVCSIAKRNPEAITE---VVQLPNHFS 156
Db        418 DKQFAAATIQTIGRCAT---SISEFTETCFNGL-VCLLSNRDEIVVAESVVVIKKLLQMQ 473

Qy        157 NRYYNRLVRSLLE-CDEDTVSTIRDSLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRR 215
Db        474 PAQHGEIIRHMAKFLDSITVPVARASILWLIGEN-----------CERVPKIA------ 515

Qy        216 TNEPQKLKVLLRNLRGEED 234
Db        516 ---PDVLRKMAKSFTSEDD 531


RESULT 9
T50776
hypothetical protein [imported] - Vitis vinifera
C;Species: Vitis vinifera
C;Date: 21-Jul-2000 #sequence_revision 21-Jul-2000 #text_change 21-Jul-2000
C;Accession: T50776
R;Matsumoto, S.; Dry, I.B.; Thomas, M.
DNA Seq. 8, 109-112, 1997
A;Title: Nucleotide sequence of grapevine (Vitis vinifera) cDNA similar to SNAP proteins.
A;Reference number: Z25233
A;Accession: T50776
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-289 <MAT>
A;Cross-references: EMBL:AB001375; PIDN:BAA19246.1
A;Experimental source: strain Shiraz

  Query Match             7.1%;  Score 90.5;  DB 2;  Length 289;
  Best Local Similarity   19.9%;  Pred. No. 2.7;
  Matches   41;  Conservative   33;  Mismatches   95;  Indels   37;  Gaps    5;

Qy          8 LLVLVISASATHEAEQNDSVSPRKSRVAAQNSAEVVRCLNSALQVGCGAFACLENSTCDT 67
Db         59 LSTVIQSSDSKHEAAQ--AYADAGHCYKKTSAKEAISCLEQA------AYLFLDNGRFNM 110

Qy         68 DG--------MYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQR 119
Db        111 AGKYYKEIAELYELEQNFEQAIIYFEKAADIYQSEEATTAANQCNAKVAQFAAQLEQYQK 170

Qy        120 MIAEVQEECYSKLN----------------VCSIAKRNPEAITEVVQL-----PNHFSNR 158
Db        171 AIQIYEDIGRPSLNNNLLKYGVKGHLLNAGICQLCKGDVVAITNALDRYQEMDPTFSGTR 230

Qy        159 YYNRLVRSLLECDEDTVSTIRDSLME 184
Db        231 EYKLLVDLAAAVDEEDVVKFTDAVKE 256


RESULT 10
T38690
probable regulatory protein - fission yeast (Schizosaccharomyces pombe)
C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jun-2000
C;Accession: T38690
R;Brown, D.; Churcher, C.M.; Wood, V.; Barrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, September 1997
A;Reference number: Z21805
A;Accession: T38690
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-783 <BRO>
A;Cross-references: EMBL:Z99568; PIDN:CAB16735.1; GSPDB:GN00066; SPDB:SPAC3C7.04
A;Experimental source: strain 972h-; cosmid c3C7
C;Genetics:
A;Gene: SPDB:SPAC3C7.04
A;Map position: 1
C;Superfamily: unassigned GAL4-type zinc cluster proteins; GAL4 zinc binuclear cluster ho
F;35-71/Domain: GAL4 zinc binuclear cluster homology <GL4>

  Query Match             7.1%;  Score 90.5;  DB 2;  Length 783;
  Best Local Similarity   23.3%;  Pred. No. 8.7;
  Matches   56;  Conservative   34;  Mismatches   87;  Indels   63;  Gaps   12;
```

```
Qy          10 VLVISASATHEAEQNDSVSPRKSRV------AAQNSAEVVRCLNSALQVGCGAF------ 57
               ::::|         :|   |||  |:       ||::   :|  | :  |: | :|
Db         535 IIIMSRPVLLHKMKNAKNSPRVDRINEDCILAARHLISLVHLLQNHSQLSCYSFFDYNYT 594

Qy          58 ---------ACLENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCI--------- 99
                        |:    |: |   ||   : |||  :  :|    |   : |
Db         595 FSSALVVLLHCV-TEPCEED---DIAMQYAYSALDYMAEGNEAAKNCARVIRLFDAHLKG 650

Qy         100 ----ANGVTSKV-FLAIRRCSTFQRMIAEVQ-----EECYSKLNVCSIAKRNPEAITEVV 149
                   || ||:  |:|      :|| ||||      |:  |  |      ||  ::|
Db         651 ARSDGNGNTSQSGFMA------WQRWIAEVSAKDEPEKLMSPYNKSIGGGRNSNSLTPNA 704

Qy         150 QLPNHFSNRYYNR------LVRSLLECDEDTVSTIRDSLMEKIGPNMA---SLFHILQTD 200
               |    |  ::        |  | |: | :  ::  | :  |  |::|   || :   ||
Db         705 NLGADVS--FFPTDDTSFLLDHSKLDDDLEKFASTLDPI--KTTPDLANDSSLLNWANTD 760


RESULT 11
T01491
ubiquitin-protein ligase homolog F17O7.15 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 04-Mar-2000
C;Accession: T01491
R;Vysotskaia, V.S.; Schwartz, J.R.; Toriumi, M.; Yu, G.; Kwan, A.; Oji, O.; Liu, S.; Li,
rtz, D.; Li, Y.; Palm, C.J.; Shinn, P.; Sun, H.; Davis, R.W.; Ecker, J.R.; Federspiel, M
submitted to the EMBL Data Library, June 1998
A;Description: Arabidopsis thaliana chromosome 1 BAC F17O7 sequence.
A;Reference number: Z14334
A;Accession: T01491
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-1126 <VYS>
A;Cross-references: EMBL:AC003671; NID:g2833627; PID:g3176690; GSPDB:GN00059; ATSP:F17O7
A;Experimental source: cultivar Columbia
C;Genetics:
A;Gene: ATSP:F17O7.15
A;Map position: 1
A;Introns: 118/3; 224/3; 292/1; 373/3; 457/2; 826/3; 875/3; 902/3; 1057/3; 1093/2
C;Superfamily: ubiquitin-protein ligase homology
F;756-1120/Domain: ubiquitin-protein ligase homology <UBI>

  Query Match             7.1%;  Score 89.5;  DB 2;  Length 1126;
  Best Local Similarity   22.1%;  Pred. No. 16;
  Matches   46;  Conservative   39;  Mismatches   76;  Indels   47;  Gaps    8;

Qy          14 SASATHEAEQNDSVSPRKSRVAAQNSAEVVRCLNSALQVGCGAFACLENSTCD------- 66
               |:    :||   ||: ||       | ||:    |  ||:         ::  |:
Db         412 SSETQKDAESELSVARRK------NCAEL---YNIFLQLP-------QSDLCNLCMLLGY 455

Qy          67 ---TDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRMIAE 123
                 :| :| :    |   |  |   : |  : |  :|:|::|      :   || |:|
Db         456 EGLSDKIYSLAGEVLKKLAAVDVTHRKFFTKELSELASGLSSSTVRVLATLSTTQKM--- 512

Qy         124 VQEECYSKLNVCSIAKRNPEAITEVVQLPNHFSNRYYNRLVRSLLECDEDTVSTIR---- 179
                     | ||:|     :|  |:|: :  ::   :  | :  | |::  : ::
Db         513 -------SQNTCSMA---GASILRVLQVLSSLTSTIDDSNVGTDKETDQEEQNIMQGLKV 562

Qy         180 --DSLMEKIGPNMASLFHILQTDHCAQT 205
                 : | :::|  ::     || || | |
Db         563 ALEPLWQELGQCIS--MTELQLDHTAAT 588


RESULT 12
T08121
peroxidase (EC 1.11.1.7) - flax (fragment)
C;Species: Linum usitatissimum (flax)
C;Date: 21-May-1999 #sequence_revision 21-May-1999 #text_change 04-Mar-2000
C;Accession: T08121
R;Omann, F.; Tyson, H.
submitted to the EMBL Data Library, February 1998
A;Description: cDNA sequence of a basic peroxidase (FLXPER4) in flax.
A;Reference number: Z16366
A;Accession: T08121
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-305 <OMA>
A;Cross-references: EMBL:AF049881; NID:g2944416; PIDN:AAC05277.1; PID:g2944417
A;Experimental source: cv. Stormont Cirrus
C;Genetics:
A;Gene: PER4
C;Superfamily: peroxidase
C;Keywords: chromoprotein; heme; iron; metalloprotein; oxidoreductase
F;23-103/Disulfide bonds: #status predicted
F;50/Active site: Arg #status predicted
F;54,181/Binding site: heme iron (His) (axial ligands) #status predicted
F;56-61/Disulfide bonds: #status predicted
F;109-301/Disulfide bonds: #status predicted
F;188-213/Disulfide bonds: #status predicted

  Query Match             7.0%;  Score 89;  DB 2;  Length 305;
  Best Local Similarity   21.9%;  Pred. No. 3.8;
  Matches   57;  Conservative   39;  Mismatches   92;  Indels   72;  Gaps   15;

Qy          11 LVISASATHEAEQNDSVSPRKSRVAAQNSAEVVRCLNSALQVGCGA-FACLE-NSTCDTD 68
               |::  :||   |:|    | :: |      :::  : : ::  | |  :| :  :    |
Db          65 LLLDDTATFTGEKN--AGPNQNSV---RGFDIIDTIKTRVEAACNATVSCADILALAARD 119

Qy          69 GMYDI-------------CKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLA----- 110
               |:  :              ::   |||           ||  | |  |:|   |
Db         120 GVVLVGGPTWTVPLGRRDARTASQSAANAQIPAPG---SSLGTITNLFTNKGLTARDVTI 176

Qy         111 --------IRRCSTFQRMIAEVQEECYSKLNV----CSIAKRN-PEA-----ITEVVQLP 152
                      ||:||:: |       |:  |:     :  : | |:|     :  :   |
Db         177 LSGAHTIGQARCTTFRQRI-------YNDTNIDPAFATTRRGNCPQAGAGANLAPLDGTP 229

Qy         153 NHFSNRYYNRLV--RSLLECDEDTVST-IRDSLMEKIGPNMASLFHILQTDHCAQ----- 204
               | ||||  ||  | ||  |::  :   :|:|:     | |:      ||  |
Db         230 TQFDNRYYQDLVARRGLLHSDQELFNNGTQDALVRTYSNNAAT----FATDFAAAMVRMG 285

Qy         205 -------THPRADFNRRRTN 217
                     |:    || || | |
Db         286 NISPLTGTNGEIRFNCRRPN 305


RESULT 13
T45954
hypothetical protein F7J8.120 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 20-Jun-2000
C;Accession: T45954
R;Bevan, M.; Zimmermann, W.; Grueneisen, A.; Wambutt, R.; Bancroft, I.; Mewes, H.W.; Lemc
submitted to the Protein Sequence Database, January 2000
A;Reference number: Z23018
A;Accession: T45954
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-473 <BEV>
A;Cross-references: EMBL:AL137189
A;Experimental source: cultivar Columbia; BAC clone F7J8
C;Genetics:
A;Map position: 5
A;Introns: 29/1; 428/3
A;Note: F7J8.120
C;Superfamily: Arabidopsis thaliana hypothetical protein F7J8.130

  Query Match             6.9%;  Score 88;  DB 2;  Length 473;
  Best Local Similarity   22.6%;  Pred. No. 7.9;
  Matches   54;  Conservative   42;  Mismatches  103;  Indels   40;  Gaps   13;

Qy          27 VSPRKSRVAAQNSAEVVRCLNSALQVGCGAFACLEN---STCD---TDGMYDICKS-FLY 79
               :   |::|    :  :|| |    :        || |   |  |     |   | ||   ||
Db          16 IDEEKNKVVLAEAGTIVRLLAKHRKSDPVTIGCLRNLYTSVVDMELDDFETDACKQMLLY 75

Qy          80 SAAKFDTQGKAF-----VKESLKCIANGVTSKVFLAIRRCSTFQRMIAE----VQEEC-- 128
                     : | : |       |||||       : |   | || |   : :    : ||
```

```
Db          76 PKNIREAQYRNFKLNIDTNESLKCFG----CRFFSICRMCSNFNTSLCKCGKLMNEEISF 131

Qy         129 --YSKLNVCSIAKRNPEA--ITEVVQLPNHFSNRYYNRLVRSLLECDEDTVSTIRDSLME 184
               | : :|  :  |:  :  ||: ::| :  :    : |:::| :     || :|: :::
Db         132 LEYEENDVEGVFMRDKSSFIITDDLRLTDDST----SSLLQTLKDLGCADVSKLREQVLD 187

Qy         185 KIGPNMASLFHILQTDHCAQTH--PRAD--FNRRRTNEPQKLKVLLRNLRGEEDSPSHI 239
                ||    |  ::   |  |   |  |    : :|  :|:   | : :|:|  |  :
Db         188 -IG-----LKEVMTLMQCVFTSNTPLTDAFLKNQSSNTVRKIYRKLSDDKGDEAEPDKV 240


RESULT 14
S45628
DNA-directed DNA polymerase (EC 2.7.7.7) alpha 180K chain - mouse
N;Alternate names: DNA polymerase alpha/DNA primase complex 180K chain
C;Species: Mus musculus (house mouse)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Jun-2000
C;Accession: S45628; A46642
R;Stadlbauer, F.; Brueckner, A.; Rehfuess, C.; Eckerskorn, C.; Lottspeich, F.; Foerster,
Eur. J. Biochem. 222, 781-793, 1994
A;Title: DNA replication in vitro by recombinant DNA-polymerase-alpha-primase.
A;Reference number: S45628; MUID:94298818; PMID:8026492
A;Accession: S45628
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-1465 <STA>
A;Cross-references: EMBL:D17384; NID:g397829; PIDN:BAA04202.1; PID:g442471
R;Miyazawa, H.; Izumi, M.; Tada, S.; Takada, R.; Masutani, M.; Ui, M.; Hanaoka, F.
J. Biol. Chem. 268, 8111-8122, 1993
A;Title: Molecular cloning of the cDNAs for the four subunits of mouse DNA polymerase al
A;Reference number: A46642; MUID:93216788; PMID:8463324
A;Accession: A46642
A;Status: preliminary
A;Molecule type: mRNA; protein
A;Residues: 4-1465 <MIY>
A;Experimental source: FM3A cells
A;Note: sequence extracted from NCBI backbone (NCBIN:129146, NCBIP:129147)
C;Superfamily: herpesvirus DNA-directed DNA polymerase
C;Keywords: DNA binding; nucleotidyltransferase; nucleus

  Query Match             6.9%;  Score 87.5;  DB 2;  Length 1465;
  Best Local Similarity   20.7%;  Pred. No. 33;
  Matches   34;  Conservative   32;  Mismatches   55;  Indels   43;  Gaps    7;

Qy           6 AVLLVLVISASAT-------HEAEQNDSVSPRKSRVAAQNSAEVVRCLNSALQVGCGAFA 58
               |||: | :   :|       |: |:||::    :::  :   :           |  |
Db        1236 AVLIALWLGLDSTQFRVHQYHKDEENDALLGGPAQLTDEEKYK-----------DCEKFK 1284

Qy          59 CLENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVT------SKVFLAIR 112
               ||  | | |: :||     ::  :  | :   :   :: |  : :|      :|: : ||
Db        1285 CLCPS-CGTENIYD----NVFEGSGLDMEPSLYRCSNVDCKVSPLTFMVQLSNKLIMDIR 1339

Qy         113 RCSTFQRMIAEVQEECYSKLNVCSIAKRNPEAITEVVQLPNHFS 156
               ||           :: |    :|      |   : : :|| |||
Db        1340 RCI----------KKYYDGWLIC----EEPTCCSRLRRLPLHFS 1369


RESULT 15
H72097
mg++ transporter (cbs domain) - Chlamydophila pneumoniae (strain CWL029)
C;Species: Chlamydophila pneumoniae, Chlamydia pneumoniae
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 05-May-2000
C;Accession: H72097
R;Kalman, S.; Mitchell, W.; Marathe, R.; Lammel, C.; Fan, J.; Olinger, L.; Grimwood, J.;
Nature Genet. 21, 385-389, 1999
A;Title: Comparative genomes of Clamydia pneumoniae and C. trachomatis.
A;Reference number: A72000; MUID:99206606; PMID:10192388
A;Accession: H72097
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-470 <ARN>
A;Cross-references: GB:AE001613; GB:AE001363; NID:g4376550; PIDN:AAD18435.1; PID:g437656
A;Experimental source: strain CWL029
C;Genetics:
A;Gene: mgtE
C;Superfamily: magnesium transport protein mgtE

  Query Match             6.8%;  Score 86;  DB 2;  Length 470;
  Best Local Similarity   22.9%;  Pred. No. 12;
  Matches   47;  Conservative   33;  Mismatches   61;  Indels   64;  Gaps   13;

Qy          56 AFACLENSTCDTD-GMYDICK--------SFLYSAAKFDTQGKAFVKESLKCIANGVTSK 106
               || ||       ||   :|: |           |: :   :: :| : ::| ||    |:|
Db          19 AFTCL-----STDIHSHDLSKIVIEYNPIDLAYAVSCLPSESRAILYKNLSCI----TAK 69

Qy         107 VFLAIR-----RCSTFQRMIAEVQEECYSKLNVCSIAKRNP--EAITEVVQLPNHFSNRY 159
               |  |       | : |:|:          |   ||:: :: |  ||:  :  :|    :|
Db          70 VAFIINTDSASRWAIFRRL---------SDSEVCALIEQMPPDEAVWVLDDIP----DRR 116

Qy         160 YNRLVRSLLECDEDTVSTIRDSLMEKIGPNMA------SLFHIL------QTDHCAQTHP 207
               | |::  :   |       |||  ::| | | |         |  |           | :::|
Db         117 YRRILELI---DSKKALKIRD--LQKHGRNTAGRLMTNEFFAFLMETTVKDVSACIRSNP 171

Qy         208 RADFNRRRTNEPQKLKVLLRNLRGE 232
                 |  |           | : : :||
Db         172 GIDLTR---------LVFVLDFKGE 187


Search completed: June 12, 2003, 19:57:52
Job time : 47 secs
```

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: June 12, 2003, 18:20:03 ; Search time 36 Seconds
(without alignments)
284.574 Million cell updates/sec

Title: US-09-705-500A-3
Perfect score: 1268
Sequence: 1 MLQNSAVLLVLVISASATHE.....NLRGEEDSPSHIKRTSHESA 247

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1268	100.0	247	1	STC1_HUMAN	P52823 homo sapien
2	1234	97.3	247	1	STC1_MOUSE	O55183 mus musculu
3	1231	97.1	247	1	STC1_RAT	P97574 rattus norv
4	682	53.8	250	1	STC_ANGAU	P18301 anguilla au
5	662.5	52.2	256	1	STC_ONCKI	Q08264 oncorhynchu
6	662.5	52.2	256	1	STC_ONCMY	P43648 oncorhynchu
7	617	48.7	179	1	STC_ONCKE	P43647 oncorhynchu
8	354.5	28.0	296	1	STC2_MOUSE	O88452 mus musculu
9	354	27.9	302	1	STC2_HUMAN	O76061 homo sapien
10	352	27.8	302	1	STC2_MACNE	O97561 macaca neme
11	349	27.5	296	1	STC2_RAT	Q9r0k8 rattus norv
12	181.5	14.3	197	1	STC2_CAVPO	P57675 cavia porce
13	156	12.3	40	1	STC_ONCNE	P43649 oncorhynchu
14	94	7.4	1105	1	A3B1_MOUSE	Q9z1t1 mus musculu
15	90.5	7.1	289	1	SNAA_VITVI	P93798 vitis vinif
16	87.5	6.9	1465	1	DPOA_MOUSE	P33609 mus musculu
17	86.5	6.8	509	1	VP67_NPVCF	P41717 choristoneu
18	86	6.8	581	1	YMM7_YEAST	Q03124 saccharomyc
19	86	6.8	695	1	TRFL_HORSE	O77811 equus cabal
20	84.5	6.7	1451	1	DPOA_RAT	O89042 rattus norv
21	83	6.5	1094	1	A3B1_HUMAN	O00203 homo sapien
22	82.5	6.5	1483	1	UFD4_YEAST	P33202 saccharomyc
23	81.5	6.4	708	1	TRFL_BOVIN	P24627 bos taurus
24	81	6.4	4377	1	ANK3_HUMAN	Q12955 homo sapien
25	80	6.3	509	1	VP64_NPVOP	P13625 orgyia pseu
26	80	6.3	998	1	ECA3_ARATH	Q9sy55 arabidopsis
27	79.5	6.3	708	1	TRFL_BUBBU	O77698 bubalus bub
28	79	6.2	440	1	V117_FOWPV	Q9j5a5 fowlpox vir
29	78.5	6.2	132	1	IL4_HORSE	P42202 equus cabal
30	78.5	6.2	708	1	TRFL_CAPHI	Q29477 capra hircu
31	78.5	6.2	1127	1	MDM1_YEAST	Q01846 saccharomyc
32	78	6.2	458	1	IF3T_TORCA	P23729 torpedo cal
33	78	6.2	688	1	DNAK_ANAVA	O05714 anabaena va
34	78	6.2	803	1	GYRB_BUCAI	P57126 buchnera ap
35	78	6.2	1816	1	KF1B_MOUSE	Q60575 mus musculu
36	77.5	6.1	228	1	Z313_MOUSE	Q9et26 mus musculu
37	77.5	6.1	640	1	CLAT_MOUSE	Q03059 mus musculu
38	77	6.1	249	1	TPIS_TREPA	O83548 treponema p
39	76.5	6.0	455	1	TBA1_SCHPO	P04688 schizosacch
40	76	6.0	324	1	NAA2_RHILO	Q982f2 rhizobium l
41	76	6.0	385	1	LEF3_NPVAC	P41453 autographa
42	76	6.0	820	1	CTNB_TRIGR	P35223 tripneustes
43	75.5	6.0	366	1	APN1_YEAST	P22936 saccharomyc
44	75.5	6.0	688	1	DNAK_ANASP	Q9zej6 anabaena sp
45	75.5	6.0	849	1	AKA4_MOUSE	Q60662 mus musculu

ALIGNMENTS

RESULT 1
STC1_HUMAN
ID STC1_HUMAN STANDARD; PRT; 247 AA.
AC P52823;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Stanniocalcin 1 precursor (STC-1).
GN STC1 OR STC.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung carcinoma, and Fibrosarcoma;
RX MEDLINE=96077825; PubMed=7489828;
RA Chang A.C.-M., Janosi J., Hulsbeek M., de Jong D., Jeffrey K.J.,
RA Noble J.R., Reddel R.R.;
RT "A novel human cDNA highly homologous to the fish hormone
RT stanniocalcin.";
RL Mol. Cell. Endocrinol. 112:241-247(1995).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Fetal lung;
RX MEDLINE=96312491; PubMed=8700837;
RA Olsen H.S., Cepeda M.A., Zhang Q.-Q., Rosen C.A., Vozzolo B.L.,
RA Wagner G.F.;
RT "Human stanniocalcin: a possible hormonal regulator of mineral
RT metabolism.";
RL Proc. Natl. Acad. Sci. U.S.A. 93:1792-1796(1996).
RN [3]
RP SEQUENCE FROM N.A.
RA Jeffrey K.J., Reddel R.R.;
RT "Characterization of the human stanniocalcin 1 gene.";
RL Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
CC -!- FUNCTION: STIMULATES RENAL PHOSPHATE REABSORPTION, AND COULD
CC THEREFORE PREVENT HYPERCALCEMIA.
CC -!- SUBUNIT: HOMODIMER; DISULFIDE-LINKED (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: EXPRESSED IN MOST TISSUES, WITH THE HIGHEST
CC LEVELS IN OVARY, PROSTATE, HEART, KIDNEY AND THYROID. IN THE
CC KIDNEY, EXPRESSION IS CONFINED TO THE NEPHRON, SPECIFICALLY IN THE
CC DISTAL CONVOLUTED TUBULE AND IN THE COLLECTING TUBULE. NOT
CC DETECTED IN THE BRAIN, LIVER, SPLEEN, PERIPHERAL BLOOD LEUKOCYTES
CC AND ADRENAL MEDULLA.
CC -!- SIMILARITY: BELONGS TO THE STANNIOCALCIN FAMILY.
CC ---

CC ---

```
DR   EMBL; U25997; AAC09472.1; -.
DR   EMBL; U46768; AAA88903.1; -.
DR   EMBL; AF242179; AAL79522.1; -.
DR   Genew; HGNC:11373; STC1.
DR   MIM; 601185; -.
DR   InterPro; IPR004978; Stanniocalcin.
DR   Pfam; PF03298; Stanniocalcin; 1.
KW   Hormone; Signal; Glycoprotein.
FT   SIGNAL       1     17       POTENTIAL.
FT   PROPEP      18     33       POTENTIAL.
FT   CHAIN       34    247       STANNIOCALCIN 1.
FT   DISULFID    45     59       BY SIMILARITY.
FT   DISULFID    54     74       BY SIMILARITY.
FT   DISULFID    65    114       BY SIMILARITY.
FT   DISULFID    98    128       BY SIMILARITY.
FT   DISULFID   135    170       BY SIMILARITY.
FT   DISULFID   202    202       INTERCHAIN (BY SIMILARITY).
FT   CARBOHYD    62     62       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   247 AA;  27621 MW;  1E4A8BD861B49AED CRC64;

  Query Match             100.0%;  Score 1268;  DB 1;  Length 247;
  Best Local Similarity   100.0%;  Pred. No. 2.8e-102;
  Matches  247;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MLQNSAVLLVLVISASATHEAEQNDSVSPRKSRVAAQNSAEVVRCLNSALQVGCGAFACL 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MLQNSAVLLVLVISASATHEAEQNDSVSPRKSRVAAQNSAEVVRCLNSALQVGCGAFACL 60

Qy         61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM 120

Qy        121 IAEVQEECYSKLNVCSIAKRNPEAITEVVQLPNHFSNRYYNRLVRSLLECDEDTVSTIRD 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 IAEVQEECYSKLNVCSIAKRNPEAITEVVQLPNHFSNRYYNRLVRSLLECDEDTVSTIRD 180

Qy        181 SLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRRTNEPQKLKVLLRNLRGEEDSPSHIK 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 SLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRRTNEPQKLKVLLRNLRGEEDSPSHIK 240

Qy        241 RTSHESA 247
              |||||||
Db        241 RTSHESA 247


RESULT 2
STC1_MOUSE
ID   STC1_MOUSE     STANDARD;      PRT;   247 AA.
AC   O55183;
DT   15-JUL-1998 (Rel. 36, Created)
DT   15-JUL-1998 (Rel. 36, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Stanniocalcin 1 precursor (STC-1).
GN   STC1 OR STC.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BALB/c;
RX   MEDLINE=97179050; PubMed=9027337;
RA   Chang A.C.-M., Dunham M.A., Jeffrey K.J., Reddel R.R.;
RT   "Molecular cloning and characterization of mouse stanniocalcin cDNA.";
RL   Mol. Cell. Endocrinol. 124:185-187(1996).
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Strausberg R.;
RL   Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: STIMULATES RENAL PHOSPHATE REABSORPTION, AND COULD
CC       THEREFORE PREVENT HYPERCALCEMIA (BY SIMILARITY).
CC   -!- SUBUNIT: HOMODIMER; DISULFIDE-LINKED (BY SIMILARITY).
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- TISSUE SPECIFICITY: EXPRESSED IN MANY TISSUES.
CC   -!- SIMILARITY: BELONGS TO THE STANNIOCALCIN FAMILY.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; U47815; AAC00050.1; -.
DR   EMBL; BC021425; AAH21425.1; -.
DR   MGD; MGI:109131; Stc.
DR   InterPro; IPR004978; Stanniocalcin.
DR   Pfam; PF03298; Stanniocalcin; 1.
KW   Hormone; Signal; Glycoprotein.
FT   SIGNAL       1     17       POTENTIAL.
FT   PROPEP      18     33       POTENTIAL.
FT   CHAIN       34    247       STANNIOCALCIN 1.
FT   DISULFID    45     59       BY SIMILARITY.
FT   DISULFID    54     74       BY SIMILARITY.
FT   DISULFID    65    114       BY SIMILARITY.
FT   DISULFID    98    128       BY SIMILARITY.
FT   DISULFID   135    170       BY SIMILARITY.
FT   DISULFID   202    202       INTERCHAIN (BY SIMILARITY).
FT   CARBOHYD    62     62       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   247 AA;  27480 MW;  DAD30D08575A513B CRC64;

  Query Match             97.3%;  Score 1234;  DB 1;  Length 247;
  Best Local Similarity   96.4%;  Pred. No. 2.4e-99;
  Matches  238;  Conservative    5;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 MLQNSAVLLVLVISASATHEAEQNDSVSPRKSRVAAQNSAEVVRCLNSALQVGCGAFACL 60
              |||||||:| |||||:| ||||||||||||||||||||||||||||||||||||||||||||
Db          1 MLQNSAVILALVISAAAAHEAEQNDSVSPRKSRVAAQNSAEVVRCLNSALQVGCGAFACL 60

Qy         61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM 120
              ||||||||||||||||||||||||||||||||||||||||||||:||||||||||||||||
Db         61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGITSKVFLAIRRCSTFQRM 120

Qy        121 IAEVQEECYSKLNVCSIAKRNPEAITEVVQLPNHFSNRYYNRLVRSLLECDEDTVSTIRD 180
              ||||||:||||||||||||||||||:||||||||||||||||||||||||||||||||||||
Db        121 IAEVQEDCYSKLNVCSIAKRNPEAITEVIQLPNHFSNRYYNRLVRSLLECDEDTVSTIRD 180

Qy        181 SLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRRTNEPQKLKVLLRNLRGEEDSPSHIK 240
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 SLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRRTNEPQKLKVLLRNLRGEGDSPSHIK 240

Qy        241 RTSHESA 247
              ||| |||
Db        241 RTSQESA 247


RESULT 3
STC1_RAT
ID   STC1_RAT       STANDARD;      PRT;   247 AA.
AC   P97574;
DT   15-JUL-1998 (Rel. 36, Created)
DT   15-JUL-1998 (Rel. 36, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Stanniocalcin 1 precursor (STC-1).
GN   STC1 OR STC.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Sprague-Dawley; TISSUE=Kidney;
RA   Abe T., Tanemoto M., Hall A.E., Brown E.M., Hebert S.C.;
RL   Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: STIMULATES RENAL PHOSPHATE REABSORPTION, AND COULD
```

```
CC       THEREFORE PREVENT HYPERCALCEMIA (BY SIMILARITY).
CC   -!- SUBUNIT: HOMODIMER; DISULFIDE-LINKED (BY SIMILARITY).
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- SIMILARITY: BELONGS TO THE STANNIOCALCIN FAMILY.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; U62667; AAB39541.1; -.
DR   InterPro; IPR004978; Stanniocalcin.
DR   Pfam; PF03298; Stanniocalcin; 1.
KW   Hormone; Signal; Glycoprotein.
FT   SIGNAL        1     17       POTENTIAL.
FT   PROPEP       18     33       POTENTIAL.
FT   CHAIN        34    247       STANNIOCALCIN 1.
FT   DISULFID     45     59       BY SIMILARITY.
FT   DISULFID     54     74       BY SIMILARITY.
FT   DISULFID     65    114       BY SIMILARITY.
FT   DISULFID     98    128       BY SIMILARITY.
FT   DISULFID    135    170       BY SIMILARITY.
FT   DISULFID    202    202       INTERCHAIN (BY SIMILARITY).
FT   CARBOHYD     62     62       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   247 AA;  27507 MW;  DAC2FD08575A513B CRC64;

  Query Match             97.1%;  Score 1231;  DB 1;  Length 247;
  Best Local Similarity   96.0%;  Pred. No. 4.3e-99;
  Matches  237;  Conservative    6;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 MLQNSAVLLVLVISASATHEAEQNDSVSPRKSRVAAQNSAEVVRCLNSALQVGCGAFACL 60
              |||||||:| |||||:| ||||||||||||||||||||||||||||||||||||||||||
Db          1 MLQNSAVILALVISAAAAHEAEQNDSVSPRKSRVAAQNSAEVVRCLNSALQVGCGAFACL 60

Qy         61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM 120
              ||||||||||||||||||||||||||||||||||||||||:||||||||||||||||||
Db         61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGITSKVFLAIRRCSTFQRM 120

Qy        121 IAEVQEECYSKLNVCSIAKRNPEAITEVVQLPNHFSNRYYNRLVRSLLECDEDTVSTIRD 180
              ||||||:|||||||||||||||||||:||||||||||||||||||||||||||||||||
Db        121 IAEVQEDCYSKLNVCSIAKRNPEAITEVIQLPNHFSNRYYNRLVRSLLECDEDTVSTIRD 180

Qy        181 SLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRRTNEPQKLKVLLRNLRGEEDSPSHIK 240
              |||||||||||||||||||||||||||||||||||||||||||||||||||| |||||||
Db        181 SLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRRTNEPQKLKVLLRNLRGEGDSPSHIK 240

Qy        241 RTSHESA 247
              ||| |:|
Db        241 RTSQENA 247


RESULT 4
STC_ANGAU
ID   STC_ANGAU      STANDARD;      PRT;   250 AA.
AC   P18301;
DT   01-NOV-1990 (Rel. 16, Created)
DT   15-JUL-1998 (Rel. 36, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Stanniocalcin precursor (STC) (Corpuscles of stannius protein) (CS)
DE   (Hypocalcin) (Teleocalcin).
GN   STC.
OS   Anguilla australis (Australian eel).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Anguilliformes; Anguillidae;
OC   Anguilla.
OX   NCBI_TaxID=7940;
RN   [1]
RP   SEQUENCE FROM N.A., AND SEQUENCE OF 33-57.
RX   MEDLINE=88083961; PubMed=3319739;
RA   Butkus A., Roche P.J., Fernley R.T., Haralambidis J.,
RA   Penschow J.D., Ryan G.B., Trahair J.F., Tregear G.W., Coghlan J.P.;
RT   "Purification and cloning of a corpuscles of Stannius protein from
RT   Anguilla australis.";
RL   Mol. Cell. Endocrinol. 54:123-133(1987).
RN   [2]
RP   REVISIONS.
RA   Roche P.J.;
RL   Submitted (DEC-1997) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: ITS PRIMARY FUNCTION IS THE PREVENTION OF HYPERCALCEMIA.
CC       UPON RELEASE INTO THE CIRCULATION, IT LOWERS CALCIUM TRANSPORT BY
CC       THE GILLS, THEREBY REDUCING ITS RATE OF INFLUX FROM THE
CC       ENVIRONMENT INTO THE EXTRACELLULAR COMPARTMENT. STC ALSO
CC       STIMULATES PHOSPHATE REABSORPTION BY RENAL PROXIMAL TUBULES. THE
CC       CONSEQUENCE OF THIS ACTION IS INCREASED LEVELS OF PLASMA
CC       PHOSPHATE, WHICH COMBINES WITH EXCESS CALCIUM AND PROMOTES ITS
CC       DISPOSAL INTO BONE AND SCALES.
CC   -!- SUBUNIT: HOMODIMER; DISULFIDE-LINKED.
CC   -!- TISSUE SPECIFICITY: CORPUSCLES OF STANNIUS.
CC   -!- SIMILARITY: BELONGS TO THE STANNIOCALCIN FAMILY.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; M36967; AAB91483.1; -.
DR   PIR; A54648; A54648.
DR   InterPro; IPR004978; Stanniocalcin.
DR   Pfam; PF03298; Stanniocalcin; 1.
KW   Hormone; Signal; Glycoprotein.
FT   SIGNAL        1     17       POTENTIAL.
FT   PROPEP       18     32       POTENTIAL.
FT   CHAIN        33    250       STANNIOCALCIN.
FT   DISULFID     44     58       BY SIMILARITY.
FT   DISULFID     53     73       BY SIMILARITY.
FT   DISULFID     64    113       BY SIMILARITY.
FT   DISULFID     97    127       BY SIMILARITY.
FT   DISULFID    134    169       BY SIMILARITY.
FT   DISULFID    201    201       INTERCHAIN (BY SIMILARITY).
FT   CARBOHYD     61     61       N-LINKED (GLCNAC. . .) (PROBABLE).
SQ   SEQUENCE   250 AA;  27174 MW;  BB972BD951F75B3E CRC64;

  Query Match             53.8%;  Score 682;  DB 1;  Length 250;
  Best Local Similarity   54.3%;  Pred. No. 8.8e-52;
  Matches  138;  Conservative   47;  Mismatches   57;  Indels   12;  Gaps    6;

Qy          1 MLQNSAVLLVLVISASATHEAEQNDSVSPRKSRVAAQNSAEVVRCLNSALQVGCGAFACL 60
              ||: | ::| ||:  :| :| :::: :||| :| :| : ::| |||| |||||| |||||
Db          1 MLRMSGLILTLVL-VTAAYEQDESEPLSPRTARFSASSPSDVARCLNGALQVGCSAFACL 59

Qy         61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM 120
              :||||:||||::||:|||: |||||||| ||||||||||:|||||| |||||:||:|
Db         60 DNSTCNTDGMHEICRSFLHGAAKFDTQGKTFVKESLKCIANGITSKVFLTIRRCSSFQKM 119

Qy        121 IAEVQEECYSKLNVCSIAKRNPEAITEVVQLPNHFSNRYYNRLVRSLLECDEDTVSTIRD 180
              |:||||||||||::||:|: |||| || |:|: | |||| |::||| ||||||  :|
Db        120 ISEVQEECYSKLDLCSVAQSNPEAMGEVAQVPSQFPNRYYSTLLQSLLTCDEDTVEQVRA 179

Qy        181 SLMEKIGPNMASLFHILQTDHC-----AQTHP-RADFNRRRTNEPQKLKVLLRNLRGEED 234
              |: :: | |  || :|||  |       | |  |  : |    |   |:   |||  :
Db        180 GLVSRLEPEMGVLFQLLQTKACPPSAAGGTGPVGAGGSWRWPMGPPMFKI-QPNLRSRD- 237

Qy        235 SPSHI--KRTSHES 246
              |:|:  |: |  |
Db        238 -PTHLFAKKRSTSS 250


RESULT 5
STC_ONCKI
ID   STC_ONCKI      STANDARD;      PRT;   256 AA.
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AC   Q08264;
DT   01-FEB-1995 (Rel. 31, Created)
DT   01-FEB-1995 (Rel. 31, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Stanniocalcin precursor (STC) (Corpuscles of stannius protein) (CS)
DE   (Hypocalcin) (Teleocalcin).
GN   STC.
OS   Oncorhynchus kisutch (Coho salmon).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC   Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX   NCBI_TaxID=8019;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=93246046; PubMed=1363790;
RA   Wagner G.F., Dimattia G.E., Davie J.R., Copp D.H., Friesen H.G.;
RT   "Molecular cloning and cDNA sequence analysis of coho salmon
RT   stanniocalcin.";
RL   Mol. Cell. Endocrinol. 90:7-15(1992).
RN   [2]
RP   SEQUENCE OF 34-73.
RX   MEDLINE=89065334; PubMed=3197944;
RA   Wagner G.F., Fenwick J.C., Park C.M., Milliken C., Copp D.H.,
RA   Friesen H.G.;
RT   "Comparative biochemistry and physiology of teleocalcin from sockeye
RT   and coho salmon.";
RL   Gen. Comp. Endocrinol. 72:237-246(1988).
CC   -!- FUNCTION: ITS PRIMARY FUNCTION IS THE PREVENTION OF HYPERCALCEMIA.
CC       UPON RELEASE INTO THE CIRCULATION, IT LOWERS CALCIUM TRANSPORT BY
CC       THE GILLS, THEREBY REDUCING ITS RATE OF INFLUX FROM THE
CC       ENVIRONMENT INTO THE EXTRACELLULAR COMPARTMENT. STC ALSO
CC       STIMULATES PHOSPHATE REABSORPTION BY RENAL PROXIMAL TUBULES. THE
CC       CONSEQUENCE OF THIS ACTION IS INCREASED LEVELS OF PLASMA
CC       PHOSPHATE, WHICH COMBINES WITH EXCESS CALCIUM AND PROMOTES ITS
CC       DISPOSAL INTO BONE AND SCALES.
CC   -!- SUBUNIT: HOMODIMER; DISULFIDE-LINKED.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- TISSUE SPECIFICITY: PRODUCED AND SECRETED BY THE CORPUSCLES OF
CC       STANNIUS.
CC   -!- SIMILARITY: BELONGS TO THE STANNIOCALCIN FAMILY.
CC   ---------------------------------------------------------------------
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; S59519; AAB26419.1; -.
DR   PIR; B60841; B60841.
DR   InterPro; IPR004978; Stanniocalcin.
DR   Pfam; PF03298; Stanniocalcin; 1.
KW   Hormone; Signal; Glycoprotein; Calcium transport.
FT   SIGNAL        1     18       POTENTIAL.
FT   PROPEP       19     33       BY SIMILARITY.
FT   CHAIN        34    256       STANNIOCALCIN.
FT   CARBOHYD     62     62       N-LINKED (GLCNAC. . .).
SQ   SEQUENCE   256 AA;  28074 MW;  E688B930B394A8D3 CRC64;

  Query Match           52.2%;  Score 662.5;  DB 1;  Length 256;
  Best Local Similarity 53.4%;  Pred. No. 4.3e-50;
  Matches  125;  Conservative   46;  Mismatches   54;  Indels    9;  Gaps    4;

Qy         11 LVISASATHEAEQNDSVSPRKSRVAAQNSAEVVRCLNSALQVGCGAFACLENSTCDTDGM 70
              ||:  :|| : :  :: |||::| :: : ::| |||| || |||| ||||||||||||||
Db         12 LVLGTAATFDTDPEEA-SPRRARFSSNSPSDVARCLNGALAVGCGTFACLENSTCDTDGM 70

Qy         71 YDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRMIAEVQEECYS 130
              :|||: | ::|| |:|||| ||||||:|||||||||||  ||||  |||||:||||||||
Db         71 HDICQLFFHTAATFNTQGKTFVKESLRCIANGVTSKVFQTIRRCGVFQRMISEVQEECYS 130

Qy        131 KLNVCSIAKRNPEAITEVVQLPNHFSNRYYNRLVRSLLECDEDTVSTIRDSLMEKIGPNM 190
              :|::| :|: ||||| ||||:| || |||| |::||| |||:||: :|  |: ::||:|
Db        131 RLDICGVARSNPEAIGEVVQVPAHFPNRYYSTLLQSLLACDEETVAVVRAGLVARLGPDM 190

Qy        191 ASLFHILQTDHCAQTHPRADFN-----RRRTNEPQKLKVLLRNLRGEEDSPSHI 239
              :|| :||  || |   :   :      |     |   |:   ::|| :  |:|:
Db        191 ETLFQLLQNKHCPQGSNQGPNSAPAGWRWPMGSPPSFKI-QPSMRGRD--PTHL 241


RESULT 6
STC_ONCMY
ID   STC_ONCMY      STANDARD;      PRT;   256 AA.
AC   P43648; Q98SE1;
DT   01-NOV-1995 (Rel. 32, Created)
DT   15-JUN-2002 (Rel. 41, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Stanniocalcin precursor (STC) (Corpuscles of stannius protein) (CS)
DE   (Hypocalcin) (Teleocalcin).
GN   STC.
OS   Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC   Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX   NCBI_TaxID=8022;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Ovary;
RA   McCudden C.R., Wagner G.F.;
RT   "Rainbow trout ovarian stanniocalcin.";
RL   Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE OF 34-66.
RC   TISSUE=Stannius corpuscules;
RX   MEDLINE=88196801; PubMed=3360288;
RA   Lafeber F.P.J.G., Hanssen R.G.J.M., Choy Y.M., Flik G.,
RA   Herrmann-Erlee M.P.M., Pang P.K.T., Wendelaar Bonga S.E.;
RT   "Identification of hypocalcin (teleocalcin) isolated from trout
RT   Stannius corpuscles.";
RL   Gen. Comp. Endocrinol. 69:19-30(1988).
CC   -!- FUNCTION: ITS PRIMARY FUNCTION IS THE PREVENTION OF HYPERCALCEMIA.
CC       UPON RELEASE INTO THE CIRCULATION, IT LOWERS CALCIUM TRANSPORT BY
CC       THE GILLS, THEREBY REDUCING ITS RATE OF INFLUX FROM THE
CC       ENVIRONMENT INTO THE EXTRACELLULAR COMPARTMENT. STC ALSO
CC       STIMULATES PHOSPHATE REABSORPTION BY RENAL PROXIMAL TUBULES. THE
CC       CONSEQUENCE OF THIS ACTION IS INCREASED LEVELS OF PLASMA
CC       PHOSPHATE, WHICH COMBINES WITH EXCESS CALCIUM AND PROMOTES ITS
CC       DISPOSAL INTO BONE AND SCALES.
CC   -!- SUBUNIT: HOMODIMER; DISULFIDE-LINKED.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- TISSUE SPECIFICITY: PRODUCED AND SECRETED BY THE CORPUSCLES OF
CC       STANNIUS.
CC   -!- SIMILARITY: BELONGS TO THE STANNIOCALCIN FAMILY.
CC   ---------------------------------------------------------------------
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AF326317; AAK01423.1; -.
DR   EMBL; AF326318; AAK01424.1; -.
DR   PIR; S06337; S06337.
DR   InterPro; IPR004978; Stanniocalcin.
DR   Pfam; PF03298; Stanniocalcin; 1.
KW   Hormone; Signal; Glycoprotein; Calcium transport.
FT   SIGNAL        1     18       POTENTIAL.
FT   PROPEP       19     33
FT   CHAIN        34    256       STANNIOCALCIN.
FT   CARBOHYD     62     62       N-LINKED (GLCNAC. . .).
FT   VARIANT      41     41       D -> E.
SQ   SEQUENCE   256 AA;  28104 MW;  E688A0E0B394A8D3 CRC64;
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  Query Match           52.2%;  Score 662.5;  DB 1;  Length 256;
  Best Local Similarity  53.4%;  Pred. No. 4.3e-50;
  Matches  125;  Conservative   46;  Mismatches   54;  Indels    9;  Gaps    4;

Qy         11 LVISASATHEAEQNDSVSPRKSRVAAQNSAEVVRCLNSALQVGCGAFACLENSTCDTDGM 70
              ||:  :|| : :  :: |||::| :: : ::| |||| || |||| ||||||||||||||
Db         12 LVLGTAATFDTDPEEA-SPRRARFSSNSPSDVARCLNGALAVGCGTFACLENSTCDTDGM 70

Qy         71 YDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRMIAEVQEECYS 130
              :|||: | ::|| |:|||| ||||||:||||||||||  ||||  |||||:||||||||
Db         71 HDICQLFFHTAATFNTQGKTFVKESLRCIANGVTSKVFQTIRRCGVFQRMISEVQEECYS 130

Qy        131 KLNVCSIAKRNPEAITEVVQLPNHFSNRYYNRLVRSLLECDEDTVSTIRDSLMEKIGPNM 190
              :|::| :|: ||||| ||||:| || |||| |::||| |||:|| :|  |: ::||:|
Db        131 RLDICGVARSNPEAIGEVVQVPAHFPNRYYSTLLQSLLACDEETVAVVRAGLVARLGPDM 190

Qy        191 ASLFHILQTDHCAQTHPRADFN-----RRRTNEPQKLKVLLRNLRGEEDSPSHI 239
              :|| :||  || |   :   :     |     |   |:   ::|| :  |:|:
Db        191 ETLFQLLQNKHCPQGSNQGPNSAPAGWRWPMGSPPSFKI-QPSMRGRD--PTHL 241


RESULT 7
STC_ONCKE
ID   STC_ONCKE      STANDARD;      PRT;   179 AA.
AC   P43647; Q91427;
DT   01-NOV-1995 (Rel. 32, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Stanniocalcin (STC) (Corpuscles of stannius protein) (CS) (Hypocalcin)
DE   (Teleocalcin).
GN   STC.
OS   Oncorhynchus keta (Chum salmon).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC   Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX   NCBI_TaxID=8018;
RN   [1]
RP   SEQUENCE FROM N.A., AND SEQUENCE.
RC   TISSUE=Stannius corpuscules;
RX   MEDLINE=96077816; PubMed=7489819;
RA   Yamashita K., Koide Y., Itoh H., Kawada N., Kawauchi H.;
RT   "The complete amino acid sequence of chum salmon stanniocalcin, a
RT   calcium-regulating hormone in teleosts.";
RL   Mol. Cell. Endocrinol. 112:159-167(1995).
RN   [2]
RP   SEQUENCE OF 1-33.
RC   TISSUE=Stannius corpuscules;
RX   MEDLINE=93055697; PubMed=1430418;
RA   Sundell K., Bjoernsson B.T., Itoh H., Kawauchi H.;
RT   "Chum salmon (Oncorhynchus keta) stanniocalcin inhibits in vitro
RT   intestinal calcium uptake in Atlantic cod (Gadus morhua).";
RL   J. Comp. Physiol. B 162:489-495(1992).
RN   [3]
RP   DISULFIDE BONDS.
RX   MEDLINE=99216273; PubMed=10198206;
RA   Hulova I., Kawauchi H.;
RT   "Assignment of disulfide linkages in chum salmon stanniocalcin.";
RL   Biochem. Biophys. Res. Commun. 257:295-299(1999).
CC   -!- FUNCTION: ITS PRIMARY FUNCTION IS THE PREVENTION OF HYPERCALCEMIA.
CC       UPON RELEASE INTO THE CIRCULATION, IT LOWERS CALCIUM TRANSPORT BY
CC       THE GILLS, THEREBY REDUCING ITS RATE OF INFLUX FROM THE
CC       ENVIRONMENT INTO THE EXTRACELLULAR COMPARTMENT. STC ALSO
CC       STIMULATES PHOSPHATE REABSORPTION BY RENAL PROXIMAL TUBULES. THE
CC       CONSEQUENCE OF THIS ACTION IS INCREASED LEVELS OF PLASMA
CC       PHOSPHATE, WHICH COMBINES WITH EXCESS CALCIUM AND PROMOTES ITS
CC       DISPOSAL INTO BONE AND SCALES.
CC   -!- SUBUNIT: HOMODIMER; DISULFIDE-LINKED.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- TISSUE SPECIFICITY: PRODUCED AND SECRETED BY THE CORPUSCLES OF
CC       STANNIUS.
CC   -!- SIMILARITY: BELONGS TO THE STANNIOCALCIN FAMILY.
CC   ---------------------------------------------------------------------
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CC   use by non-profit institutions as long as its content is in no way
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; S80134; AAB35648.2; -.
DR   InterPro; IPR004978; Stanniocalcin.
DR   Pfam; PF03298; Stanniocalcin; 1.
KW   Hormone; Glycoprotein; Calcium transport.
FT   DISULFID     12     26
FT   DISULFID     21     41
FT   DISULFID     32     81
FT   DISULFID     65     95
FT   DISULFID    102    137
FT   DISULFID    169    169       INTERCHAIN.
FT   CARBOHYD     29     29       N-LINKED (GLCNAC. . .).
FT   CONFLICT    160    160       P -> L (IN REF. 1; AA SEQUENCE).
FT   CONFLICT    170    170       S -> P (IN REF. 1; AA SEQUENCE).
SQ   SEQUENCE   179 AA;  19518 MW;  0298CAC33E2BE445 CRC64;

  Query Match           48.7%;  Score 617;  DB 1;  Length 179;
  Best Local Similarity  66.1%;  Pred. No. 2.4e-46;
  Matches  109;  Conservative   28;  Mismatches   28;  Indels    0;  Gaps    0;

Qy         40 AEVVRCLNSALQVGCGAFACLENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCI 99
              ::| |||| || |||| |||||||||||||:|||: | ::|| |:|||| ||||||:||
Db          7 SDVARCLNGALDVGCGTFACLENSTCDTDGMHDICQLFFHTAATFNTQGKTFVKESLRCI 66

Qy        100 ANGVTSKVFLAIRRCSTFQRMIAEVQEECYSKLNVCSIAKRNPEAITEVVQLPNHFSNRY 159
              |||||||||  ||||  |||||:||||||||:|::| :|: ||||| ||||:| || |||
Db         67 ANGVTSKVFQTIRRCGVFQRMISEVQEECYSRLDICGVARSNPEAIGEVVQVPAHFPNRY 126

Qy        160 YNRLVRSLLECDEDTVSTIRDSLMEKIGPNMASLFHILQTDHCAQ 204
              |: |::||| |||:||: :|  |: ::||:| : | :||  ||:|
Db        127 YSTLLQSLLACDEETVAVVRAGLVARLGPDMETPFQLLQNKHCSQ 171


RESULT 8
STC2_MOUSE
ID   STC2_MOUSE     STANDARD;      PRT;   296 AA.
AC   O88452;
DT   30-MAY-2000 (Rel. 39, Created)
DT   30-MAY-2000 (Rel. 39, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Stanniocalcin 2 precursor (STC-2).
GN   STC2.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98389283; PubMed=9723890;
RA   Chang A.C.-M., Reddel R.R.;
RT   "Identification of a second stanniocalcin cDNA in mouse and human:
RT   stanniocalcin 2.";
RL   Mol. Cell. Endocrinol. 141:95-99(1998).
RN   [2]
RP   SEQUENCE FROM N.A., AND CHARACTERIZATION.
RC   TISSUE=Breast carcinoma;
RX   MEDLINE=99378040; PubMed=10450831;
RA   Moore E.E., Kuestner R.E., Conklin D.C., Whitmore T.E., Downey W.,
RA   Buddle M.M., Adams R.L., Bell L.A., Thompson D.L., Wolf A., Chen L.,
RA   Stamm M.R., Grant F.J., Lok S., Ren H., de Jongh K.S.;
RT   "Stanniocalcin 2: characterization of the protein and its localization
RT   to human pancreatic alpha cells.";
RL   Horm. Metab. Res. 31:406-414(1999).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Breast tumor;
RA   Strausberg R.;
```

```
RL   Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: HAS AN ANTI-HYPOCALCEMIC ACTION ON CALCIUM AND PHOSPHATE
CC       HOMEOSTASIS.
CC   -!- SUBUNIT: HOMODIMER; DISULFIDE-LINKED (BY SIMILARITY).
CC   -!- SUBCELLULAR LOCATION: Secreted (Potential).
CC   -!- TISSUE SPECIFICITY: FOUND IN A VARIETY OF TISSUES INCLUDING
CC       SKELETAL MUSCLE, SMALL INTESTINE, KIDNEY, LIVER AND BRAIN.
CC   -!- SIMILARITY: BELONGS TO THE STANNIOCALCIN FAMILY.
CC   ---------------------------------------------------------------------
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CC   the European Bioinformatics Institute. There are no restrictions on its
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AF056244; AAC27507.1; -.
DR   EMBL; AF031035; AAD01921.1; -.
DR   EMBL; BC012206; AAH12206.1; -.
DR   MGD; MGI:1316731; Stc2.
DR   InterPro; IPR004978; Stanniocalcin.
DR   Pfam; PF03298; Stanniocalcin; 1.
KW   Hormone; Signal; Glycoprotein.
FT   SIGNAL        1     24       POTENTIAL.
FT   CHAIN        25    296       STANNIOCALCIN 2.
FT   CARBOHYD     73     73       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   296 AA;  32601 MW;  0C1EF4008912DE68 CRC64;

  Query Match             28.0%;  Score 354.5;  DB 1;  Length 296;
  Best Local Similarity   31.7%;  Pred. No. 1.8e-23;
  Matches   85;  Conservative   45;  Mismatches  109;  Indels   29;  Gaps    5;

Qy          7 VLLVLVISASATHEAEQNDSVSP----------RKSRVAAQNSAEVVRCLNSALQVGCGA 56
              | | ||   :    |:  || :|          :| |:: ||:||:  || :|  ||||
Db         10 VTLALVF--ATLDPAQGTDSTNPPEGPQDRSSQQKGRLSLQNTAEIQHCLVNAGDVGCGV 67

Qy         57 FACLENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCST 116
              | | ||::|:  |:: || :||::| ||| |||:|:|::|:| |: :  |      |:|
Db         68 FECFENNSCEIQGLHGICMTFLHNAGKFDAQGKSFIKDALRCKAHALRHKFGCISRKCPA 127

Qy        117 FQRMIAEVQEECYSKLNVCSIAKRNPEAITEVVQLPNHFSNRYYNRLVRSLLECDEDTVS 176
              : |: ::| |||. | ::|| |: |   | |::   :   :  |  ||  || | ||
Db        128 IREMVFQLQRECYLKHDLCSAAQENVGVIVEMIHFKDLLLHEPYVDLVNLLLTCGEDVKE 187

Qy        177 TIRDSLMEKIGPNMASLFHIL--------QTDHCAQTH----PRADFNRRRTNEPQKLKV 224
              :  |:  :   :   | ||          :   |  |     ||  :|    :
Db        188 AVTRSVQAQCEQSWGGLCSILSFCTSNIQRPPTAAPEHQPLADRAQLSRPHHRDTDHHLT 247

Qy        225 LLRNLRGEEDSPSHIK-----RTSHESA 247
                |  :||  | ||       ||  :||
Db        248 ANRGAKGERGSKSHPNAHARGRTGGQSA 275


RESULT 9
STC2_HUMAN
ID   STC2_HUMAN     STANDARD;      PRT;   302 AA.
AC   O76061;
DT   30-MAY-2000 (Rel. 39, Created)
DT   30-MAY-2000 (Rel. 39, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Stanniocalcin 2 precursor (STC-2) (Stanniocalcin-related protein)
DE   (STCRP) (STC-related protein).
GN   STC2.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98389283; PubMed=9723890;
RA   Chang A.C.-M., Reddel R.R.;
RT   "Identification of a second stanniocalcin cDNA in mouse and human:
RT   stanniocalcin 2.";
RL   Mol. Cell. Endocrinol. 141:95-99(1998).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Osteosarcoma;
RX   MEDLINE=98440784; PubMed=9753616;
RA   Ishiabshi K., Miyamoto K., Taketani Y., Morita K., Takeda E.,
RA   Sasaki S., Imai M.;
RT   "Molecular cloning of a second human stanniocalcin homologue (STC2).";
RL   Biochem. Biophys. Res. Commun. 250:252-258(1998).
RN   [3]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=99145369; PubMed=10022771;
RA   DiMattia G.E., Varghese R., Wagner G.F.;
RT   "Molecular cloning and characterization of stanniocalcin-related
RT   protein.";
RL   Mol. Cell. Endocrinol. 146:137-140(1998).
RN   [4]
RP   SEQUENCE FROM N.A., AND CHARACTERIZATION.
RC   TISSUE=Breast carcinoma;
RX   MEDLINE=99378040; PubMed=10450831;
RA   Moore E.E., Kuestner R.E., Conklin D.C., Whitmore T.E., Downey W.,
RA   Buddle M.M., Adams R.L., Bell L.A., Thompson D.L., Wolf A., Chen L.,
RA   Stamm M.R., Grant F.J., Lok S., Ren H., de Jongh K.S.;
RT   "Stanniocalcin 2: characterization of the protein and its localization
RT   to human pancreatic alpha cells.";
RL   Horm. Metab. Res. 31:406-414(1999).
RN   [5]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Kidney, and Muscle;
RA   Strausberg R.;
RL   Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: HAS AN ANTI-HYPOCALCEMIC ACTION ON CALCIUM AND PHOSPHATE
CC       HOMEOSTASIS.
CC   -!- SUBUNIT: HOMODIMER; DISULFIDE-LINKED.
CC   -!- SUBCELLULAR LOCATION: Secreted (Potential).
CC   -!- TISSUE SPECIFICITY: EXPRESSED IN A VARIETY OF TISSUES INCLUDING
CC       MUSCLE, HEART, PANCREAS, KIDNEY, SPLEEN, PROSTATE, SMALL
CC       INTESTINE, COLON AND PERIPHERAL BLOOD LEUCOCYTES.
CC   -!- SIMILARITY: BELONGS TO THE STANNIOCALCIN FAMILY.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AF055460; AAC27036.1; -.
DR   EMBL; AB012664; BAA33489.1; -.
DR   EMBL; AF098462; AAC97948.1; -.
DR   EMBL; AF031036; AAD01922.1; -.
DR   EMBL; BC000658; AAH00658.1; -.
DR   EMBL; BC006352; AAH06352.1; -.
DR   EMBL; BC013958; AAH13958.1; -.
DR   Genew; HGNC:11374; STC2.
DR   MIM; 603665; -.
DR   InterPro; IPR004978; Stanniocalcin.
DR   Pfam; PF03298; Stanniocalcin; 1.
KW   Hormone; Signal; Glycoprotein.
FT   SIGNAL        1     24       POTENTIAL.
FT   CHAIN        25    302       STANNIOCALCIN 2.
FT   CARBOHYD     73     73       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   302 AA;  33248 MW;  9B90D8911524FA22 CRC64;

  Query Match             27.9%;  Score 354;  DB 1;  Length 302;
  Best Local Similarity   32.4%;  Pred. No. 2e-23;
  Matches   83;  Conservative   45;  Mismatches  102;  Indels   26;  Gaps    4;

Qy          9 LVLVIS-------ASATHEAE-QNDSVSPRKSRVAAQNSAEVVRCLNSALQVGCGAFACL 60
              | ||::         ||:  |   |  | :| |:: ||:||:  || :|  |||| | |
Db         12 LALVLATFDPARGTDATNPPEGPQDRSSQQKGRLSLQNTAEIQHCLVNAGDVGCGVFECF 71
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Qy          61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM 120
               ||::|:  |:: || :||::| ||| |||:|:|::||| |: :  :     |:|   : |
Db          72 ENNSCEIRGLHGICMTFLHNAGKFDAQGKSFIKDALKCKAHALRHRFGCISRKCPAIREM 131

Qy         121 IAEVQEECYSKLNVCSIAKRNPEAITEVVQLPNHFSNRYYNRLVRSLLECDEDTVSTIRD 180
               ::::| ||| | ::|: |: |   | |::   :   :  |  ||  || | |:    |
Db         132 VSQLQRECYLKHDLCAAAQENTRVIVEMIHFKDLLLHEPYVDLVNLLLTCGEEVKEAITH 191

Qy         181 SLMEKIGPNMASLFHILQ-TDHCAQTHPRADFNRRRTNEPQKL---------------- 222
               |:  :   |  ||  ||      | | |   |:   :  ||
Db         192 SVQVQCEQNWGSLCSILSFCTSAIQKPPTAPPERQPQVDRTKLSRAHHGEAGHHLPEPSS 251

Qy         223 KVLLRNLRGEEDSPSH 238
               :   |  :||  | ||
Db         252 RETGRGAKGERGSKSH 267


RESULT 10
STC2_MACNE
ID   STC2_MACNE     STANDARD;      PRT;   302 AA.
AC   O97561;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Stanniocalcin 2 precursor (STC-2).
GN   STC2.
OS   Macaca nemestrina (Pig-tailed macaque).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC   Cercopithecinae; Macaca.
OX   NCBI_TaxID=9545;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Pancreatic islets;
RX   MEDLINE=99378040; PubMed=10450831;
RA   Moore E.E., Kuestner R.E., Conklin D.C., Whitmore T.E., Downey W.,
RA   Buddle M.M., Adams R.L., Bell L.A., Thompson D.L., Wolf A., Chen L.,
RA   Stamm M.R., Grant F.J., Lok S., Ren H., de Jongh K.S.;
RT   "Stanniocalcin 2: characterization of the protein and its localization
RT   to human pancreatic alpha cells.";
RL   Horm. Metab. Res. 31:406-414(1999).
CC   -!- FUNCTION: HAS AN ANTI-HYPOCALCEMIC ACTION ON CALCIUM AND PHOSPHATE
CC       HOMEOSTASIS.
CC   -!- SUBUNIT: HOMODIMER; DISULFIDE-LINKED (BY SIMILARITY).
CC   -!- SUBCELLULAR LOCATION: Secreted (Potential).
CC   -!- SIMILARITY: BELONGS TO THE STANNIOCALCIN FAMILY.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AF035377; AAD02027.1; -.
DR   InterPro; IPR004978; Stanniocalcin.
DR   Pfam; PF03298; Stanniocalcin; 1.
KW   Hormone; Signal; Glycoprotein.
FT   SIGNAL        1     24       POTENTIAL.
FT   CHAIN        25    302       STANNIOCALCIN 2.
FT   CARBOHYD     73     73       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   302 AA;  33281 MW;  62953CE958AF64C1 CRC64;

  Query Match             27.8%;  Score 352;  DB 1;  Length 302;
  Best Local Similarity   32.8%;  Pred. No. 3e-23;
  Matches   84;  Conservative   44;  Mismatches  102;  Indels   26;  Gaps    5;

Qy           9 LVLVIS-------ASATHEAE-QNDSVSPRKSRVAAQNSAEVVRCLNSALQVGCGAFACL 60
               | ||::          ||:  |   |  | :| |:: ||:||:  || :|  ||||  | |
Db          12 LALVLATIDPARGTDATNPPEGPQDRSSQQKGRLSLQNTAEIQHCLVNAGDVGCGVFECF 71

Qy          61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM 120
               ||::|:  |:: || :||::| ||| |||:|:|::||| |: :  :     |:|   : |
Db          72 ENNSCEIRGLHGICMTFLHNAGKFDAQGKSFIKDALKCKAHALRHRFGCISRKCPAIREM 131

Qy         121 IAEVQEECYSKLNVCSIAKRNPEAITEVVQLPNHFSNRYYNRLVRSLLECDEDTVSTIRD 180
               : ::| ||| | ::|: |: |   | |::   :   :  |  ||  || | |:    |
Db         132 VFQLQRECYLKHDLCAAAQENTRVIVEMIHFKDLLLHEPYVDLVNLLLTCGEEVKEAITH 191

Qy         181 SLMEKIGPNMASLFHILQTDHCAQTHP------------RADFNRRRTNE-----PQ-KL 222
               |:  :   |  ||  ||      |   |             ||  :|    |     |:
Db         192 SVQVQCEQNWGSLCSILSFCTSAIQRPPTAPPERQPQVDRAKLSRAHHGEAGHHLPEPSS 251

Qy         223 KVLLRNLRGEEDSPSH 238
               :   |  :||  | ||
Db         252 RETGRGAKGERGSKSH 267


RESULT 11
STC2_RAT
ID   STC2_RAT       STANDARD;      PRT;   296 AA.
AC   Q9R0K8;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Stanniocalcin 2 precursor (STC-2).
GN   STC2.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Sprague-Dawley;
RX   MEDLINE=99439722; PubMed=10508929;
RA   Honda S., Kashiwagi M., Ookata K., Tojo A., Hirose S.;
RT   "Regulation by 1alpha,25-dihydroxyvitamin D(3) of expression of
RT   stanniocalcin messages in the rat kidney and ovary.";
RL   FEBS Lett. 459:119-122(1999).
CC   -!- FUNCTION: HAS AN ANTI-HYPOCALCEMIC ACTION ON CALCIUM AND PHOSPHATE
CC       HOMEOSTASIS.
CC   -!- SUBUNIT: HOMODIMER; DISULFIDE-LINKED (BY SIMILARITY).
CC   -!- SUBCELLULAR LOCATION: Secreted (Potential).
CC   -!- TISSUE SPECIFICITY: EXPRESSED IN A VARIETY OF TISSUES. STRONGLY
CC       EXPRESSED IN OVARY AND TO A LESSER EXTENT IN KIDNEY.
CC   -!- SIMILARITY: BELONGS TO THE STANNIOCALCIN FAMILY.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AB030707; BAA85251.1; -.
DR   InterPro; IPR004978; Stanniocalcin.
DR   Pfam; PF03298; Stanniocalcin; 1.
KW   Hormone; Signal; Glycoprotein.
FT   SIGNAL        1     24       POTENTIAL.
FT   CHAIN        25    296       STANNIOCALCIN 2.
FT   CARBOHYD     73     73       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   296 AA;  32621 MW;  0903639858D9B2DC CRC64;

  Query Match             27.5%;  Score 349;  DB 1;  Length 296;
  Best Local Similarity   31.8%;  Pred. No. 5.3e-23;
  Matches   81;  Conservative   44;  Mismatches  106;  Indels   24;  Gaps    4;

Qy           7 VLLVLVISASATHEAEQNDSVSP----------RKSRVAAQNSAEVVRCLNSALQVGCGA 56
               | | ||   :     |   || :|          :| |:: ||:||:  || :|  ||||
Db          10 VTLALVF--ATLDPARGTDSTNPPEGPQDRGSQQKGRLSLQNTAEIQHCLVNAGDVGCGV 67

Qy          57 FACLENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCST 116
               | | ||::|:  |:: || :||::| ||| |||:|:|::|:| |: :  |     |:|
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Db          68 FECFENNSCEIQGLHGICMTFLHNAGKFDAQGKSFIKDALRCKAHALRHKFGCISRKCPA 127

Qy         117 FQRMIAEVQEECYSKLNVCSIAKRNPEAITEVVQLPNHFSNRYYNRLVRSLLECDEDTVS 176

Db         128 IREMVYQLQRECYLKHDLCSAAQENVVVIVEMIHFKDLLLHEPYVDLVNLLLTCGEDVRE 187

Qy         177 TIRDSLMEKIGPNMASLFHIL--------QTDHCAQTH----PRADFNRRRTNEPQKLKV 224

Db         188 AVTRSVQAQCEQSWGGLCSILSFCTSNIQRPPTAAPEHQPLADRAQLSRPYHRDTDHHLT 247

Qy         225 LLRNLRGEEDSPSHI 239

Db         248 ANRGAKGERGSKSHL 262


RESULT 12
STC2_CAVPO
ID   STC2_CAVPO     STANDARD;      PRT;   197 AA.
AC   P57675;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Stanniocalcin 2 (STC-2) (Fragments).
GN   STC2.
OS   Cavia porcellus (Guinea pig).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
OX   NCBI_TaxID=10141;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=99378040; PubMed=10450831;
RA   Moore E.E., Kuestner R.E., Conklin D.C., Whitmore T.E., Downey W.,
RA   Buddle M.M., Adams R.L., Bell L.A., Thompson D.L., Wolf A., Chen L.,
RA   Stamm M.R., Grant F.J., Lok S., Ren H., de Jongh K.S.;
RT   "Stanniocalcin 2: characterization of the protein and its localization
RT   to human pancreatic alpha cells.";
RL   Horm. Metab. Res. 31:406-414(1999).
CC   -!- FUNCTION: HAS AN ANTI-HYPOCALCEMIC ACTION ON CALCIUM AND PHOSPHATE
CC       HOMEOSTASIS.
CC   -!- SUBUNIT: HOMODIMER; DISULFIDE-LINKED (BY SIMILARITY).
CC   -!- SUBCELLULAR LOCATION: Secreted (Potential).
CC   -!- SIMILARITY: BELONGS TO THE STANNIOCALCIN FAMILY.
KW   Hormone.
FT   NON_CONS      60     61
FT   NON_CONS      64     65
FT   NON_CONS      69     70
FT   NON_CONS      75     76
FT   NON_CONS      92     93
FT   NON_CONS     154    155
SQ   SEQUENCE   197 AA;  21899 MW;  1512DA859C8A8E67 CRC64;

  Query Match             14.3%;  Score 181.5;  DB 1;  Length 197;
  Best Local Similarity   25.8%;  Pred. No. 8.8e-09;
  Matches   58;  Conservative   27;  Mismatches   85;  Indels   55;  Gaps    6;

Qy          25 DSVSPRKSRVAAQNSAEVVRCLNSALQVGCGAFACLENSTCDTDGMYDICKSFLYSAAKF 84

Db          12 DRGSQQKGRLSLQNTAEIQHCLVNAGDVGCGVFECFENNXCXIXXLHXI---------- 60

Qy          85 DTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRMIAEVQEECYSKLNVCSIAKRNPEA 144

Db          61 -----SFIKAH--------------ALRFGCISREMVFQLQRECYLKHDLCMINFR---- 97

Qy         145 ITEVVQLPNHFSNRYYNRLVRSLLECDEDTVSTIRDSLMEKIGPNMASLFHIL-----QT 199

Db          98 --------DLLLHEPYVDLVNLLLTCGEDVKEAVTRSIQAQCEQNWGGLCSILSFCTSNV 149

Qy         200 DHCAQTHPRADFNRRRTNEP------QKLKVLLRNLRGEEDSPSH 238

Db         150 QRPXAXQPXAD--RAQVSRPHHHDTGHHLLEAIXGAKGERGSKSH 192


RESULT 13
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STC_ONCNE
ID   STC_ONCNE      STANDARD;      PRT;    40 AA.
AC   P43649;
DT   01-NOV-1995 (Rel. 32, Created)
DT   01-NOV-1995 (Rel. 32, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Stanniocalcin (STC) (Corpuscles of stannius protein) (CS) (Hypocalcin)
DE   (Teleocalcin) (Fragment).
GN   STC.
OS   Oncorhynchus nerka (Sockeye salmon).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC   Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX   NCBI_TaxID=8023;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=89065334; PubMed=3197944;
RA   Wagner G.F., Fenwick J.C., Park C.M., Milliken C., Copp D.H.,
RA   Friesen H.G.;
RT   "Comparative biochemistry and physiology of teleocalcin from sockeye
RT   and coho salmon.";
RL   Gen. Comp. Endocrinol. 72:237-246(1988).
CC   -!- FUNCTION: ITS PRIMARY FUNCTION IS THE PREVENTION OF HYPERCALCEMIA.
CC       UPON RELEASE INTO THE CIRCULATION, IT LOWERS CALCIUM TRANSPORT BY
CC       THE GILLS, THEREBY REDUCING ITS RATE OF INFLUX FROM THE
CC       ENVIRONMENT INTO THE EXTRACELLULAR COMPARTMENT. STC ALSO
CC       STIMULATES PHOSPHATE REABSORPTION BY RENAL PROXIMAL TUBULES. THE
CC       CONSEQUENCE OF THIS ACTION IS INCREASED LEVELS OF PLASMA
CC       PHOSPHATE, WHICH COMBINES WITH EXCESS CALCIUM AND PROMOTES ITS
CC       DISPOSAL INTO BONE AND SCALES.
CC   -!- SUBUNIT: HOMODIMER; DISULFIDE-LINKED.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- TISSUE SPECIFICITY: PRODUCED AND SECRETED BY THE CORPUSCLES OF
CC       STANNIUS.
CC   -!- SIMILARITY: BELONGS TO THE STANNIOCALCIN FAMILY.
DR   PIR; A60841; A60841.
DR   InterPro; IPR004978; Stanniocalcin.
DR   Pfam; PF03298; Stanniocalcin; 1.
KW   Hormone; Glycoprotein; Calcium transport.
FT   CARBOHYD      29     29       N-LINKED (GLCNAC. . .).
FT   UNSURE        29     29
FT   NON_TER       40     40
SQ   SEQUENCE   40 AA;  4134 MW;  0C517B7BBBC5EE6C CRC64;

  Query Match             12.3%;  Score 156;  DB 1;  Length 40;
  Best Local Similarity   79.4%;  Pred. No. 2.1e-07;
  Matches   27;  Conservative    3;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          40 AEVVRCLNSALQVGCGAFACLENSTCDTDGMYDI 73

Db           7 SDVARCLNGALDVGCGTFACLENSTCDTDGMHDI 40


RESULT 14
A3B1_MOUSE
ID   A3B1_MOUSE     STANDARD;      PRT;  1105 AA.
AC   Q9Z1T1;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Adapter-related protein complex 3 beta 1 subunit (Beta-adaptin 3A)
DE   (AP-3 complex beta-3A subunit) (Beta-3A-adaptin).
GN   AP3B1.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C3H/HeJ;
RX   MEDLINE=99135912; PubMed=9931340;
RA   Feng L., Seymour A.B., Jiang S.Y., To A., Peden A.A., Novak E.K.,
RA   Zhen L., Rusiniak M.E., Eicher E.M., Robinson M.S., Gorin M.B.,
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```
RA   Swank R.T.;
RT   "The beta-3A subunit gene (Ap3b1) of the AP-3 adaptor complex is
RT   altered in the mouse hypopigmentation mutant pearl, a model for
RT   Hermansky-Pudlak syndrome and night blindness.";
RL   Hum. Mol. Genet. 8:323-330(1999).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=129/Sv;
RX   MEDLINE=20512043; PubMed=11056055;
RA   Feng L., Rigatti B.W., Novak E.K., Gorin M.B., Swank R.T.;
RT   "Genomic structure of the mouse ap3b1 gene in normal and pearl mice.";
RL   Genomics 69:370-379(2000).
CC   -!- FUNCTION: PART OF THE AP-3 COMPLEX, AN ADAPTOR-RELATED COMPLEX
CC       WHICH IS NOT CLATHRIN-ASSOCIATED. THE COMPLEX IS ASSOCIATED WITH
CC       THE GOLGI REGION AS WELL AS MORE PERIPHERAL STRUCTURES. IT
CC       FACILITATES THE BUDDING OF VESICLES FROM THE GOLGI MEMBRANE AND
CC       MAY BE DIRECTLY INVOLVED IN TRAFFICKING TO LYSOSOMES.
CC   -!- SUBUNIT: ASSEMBLY PROTEIN COMPLEX 3 (AP-3) IS A HETEROTETRAMER
CC       COMPOSED OF TWO LARGE CHAINS (DELTA AND BETA3), A MEDIUM CHAIN
CC       (MU3) AND A SMALL CHAIN (SIGMA3).
CC   -!- PTM: PHOSPHORYLATED ON SERINE (By similarity).
CC   -!- DISEASE: Defects in AP3B1 are the cause of the autosomal recessive
CC       phenotype 'pearl' (pe). Pearl mice exhibit hypopigmentation,
CC       lysosomal secretion abnormalities, and platelet-dense granules
CC       with reduced levels of adenine nucleotides and serotonin. The
CC       changes in platelets lead to prolonged bleeding. Additionally,
CC       pearl mice exhibit reduced sensitivity in the dark-adapted state.
CC   -!- SIMILARITY: BELONGS TO THE ADAPTOR COMPLEXES LARGE SUBUNITS
CC       FAMILY.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AF103809; AAC78338.1; -.
DR   EMBL; AF255589; AAG23622.1; -.
DR   EMBL; AF255566; AAG23622.1; JOINED.
DR   EMBL; AF255567; AAG23622.1; JOINED.
DR   EMBL; AF255568; AAG23622.1; JOINED.
DR   EMBL; AF255569; AAG23622.1; JOINED.
DR   EMBL; AF255570; AAG23622.1; JOINED.
DR   EMBL; AF255571; AAG23622.1; JOINED.
DR   EMBL; AF255572; AAG23622.1; JOINED.
DR   EMBL; AF255573; AAG23622.1; JOINED.
DR   EMBL; AF255574; AAG23622.1; JOINED.
DR   EMBL; AF255575; AAG23622.1; JOINED.
DR   EMBL; AF255576; AAG23622.1; JOINED.
DR   EMBL; AF255577; AAG23622.1; JOINED.
DR   EMBL; AF255578; AAG23622.1; JOINED.
DR   EMBL; AF255579; AAG23622.1; JOINED.
DR   EMBL; AF255580; AAG23622.1; JOINED.
DR   EMBL; AF255581; AAG23622.1; JOINED.
DR   EMBL; AF255582; AAG23622.1; JOINED.
DR   EMBL; AF255583; AAG23622.1; JOINED.
DR   EMBL; AF255584; AAG23622.1; JOINED.
DR   EMBL; AF255585; AAG23622.1; JOINED.
DR   EMBL; AF255586; AAG23622.1; JOINED.
DR   EMBL; AF255587; AAG23622.1; JOINED.
DR   EMBL; AF255588; AAG23622.1; JOINED.
DR   MGD; MGI:1333879; Ap3b1.
DR   InterPro; IPR002553; Adaptin_N.
DR   Pfam; PF01602; Adaptin_N; 1.
KW   Golgi stack; Protein transport; Transport; Phosphorylation.
FT   DOMAIN      678    802       GLU/SER-RICH.
SQ   SEQUENCE   1105 AA;  122869 MW;  586B818CE4FB5AEE CRC64;

  Query Match             7.4%;  Score 94;  DB 1;  Length 1105;.
  Best Local Similarity   21.2%;  Pred. No. 2.3;
  Matches   55;  Conservative   40;  Mismatches  104;  Indels   60;  Gaps   11;

Qy          1 MLQNSAVLLVLVISASATHEAEQNDSVSPRKSRVAAQNSAEVVRCLNSALQVGCGAFACL 60
              :||:    :|: ::    |       :||:    |   |  :|| | |  :|       :
Db        308 LLQSRNAAVVMAVAQLYWH-------ISPKSE--AGVISKSLVRLLRSNREVQYIVLQNI 358

Qy         61 ENSTCDTDGMYD-ICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFL---------- 109
               : :  ||::   ||| |  :   |  |    | |  :||       |
Db        359 ATMSIERKGMFEPYLKSF-YVRSTDPTMIKTLKLEILTNLANEANISTLLREFQTYVRSQ 417

Qy        110 ----------AIRRCSTFQRMIAEVQEECYSKLNVCSIAKRNPEAITE---VVQLPNHFS 156
                       | ||:|    |:|  | |:: | || :: |:   : |   |::
Db        418 DKQFAAATIQTIGRCAT---SISEFTETCFNGL-VCLLSNRDEIVVAESVVVIKKLLQMQ 473

Qy        157 NRYYNRLVRSLLE-CDEDTVSTIRDSLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRR 215
               :  ::| : :  |  ||   | |::  || |            | :    |
Db        474 PAQHGEIIRHMAKFLDSITVPVARASILWLIGEN-----------CERVPKIA------ 515

Qy        216 TNEPQKLKVLLRNLRGEED 234
              |  |: : ::   |:|
Db        516 ---PDVLRKMAKSFTSEDD 531


RESULT 15
SNAA_VITVI
ID   SNAA_VITVI     STANDARD;      PRT;   289 AA.
AC   P93798;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Alpha-soluble NSF attachment protein (Alpha-SNAP) (N-ethylmaleimide-
DE   sensitive factor attachment protein, alpha).
OS   Vitis vinifera (Grape).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Vitaceae;
OC   Vitis.
OX   NCBI_TaxID=29760;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=cv. Shiraz; TISSUE=Fruit;
RX   MEDLINE=98182598; PubMed=9522131;
RA   Matsumoto S., Dry I.B., Thomas M.;
RT   "Nucleotide sequence of grapevine (Vitis vinifera) cDNA similar to
RT   SNAP proteins.";
RL   DNA Seq. 8:109-112(1997).
CC   -!- FUNCTION: REQUIRED FOR VESICULAR TRANSPORT BETWEEN THE ENDOPLASMIC
CC       RETICULUM AND THE GOLGI APPARATUS (By similarity).
CC   -!- SUBCELLULAR LOCATION: CYTOPLASMIC PERIPHERAL MEMBRANE PROTEIN (By
CC       similarity).
CC   -!- SIMILARITY: BELONGS TO THE SNAP FAMILY.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AB001375; BAA19246.1; -.
DR   InterPro; IPR000744; NSF_attach.
DR   InterPro; IPR001440; TPR.
DR   Pfam; PF02071; NSF; 6.
KW   Transport; Protein transport; Endoplasmic reticulum; Golgi stack.
SQ   SEQUENCE   289 AA;  32485 MW;  939E49A56C1388D4 CRC64;

  Query Match             7.1%;  Score 90.5;  DB 1;  Length 289;
  Best Local Similarity   19.9%;  Pred. No. 0.96;
  Matches   41;  Conservative   33;  Mismatches   95;  Indels   37;  Gaps    5;

Qy          8 LLVLVISASATHEAEQNDSVSPRKSRVAAQNSAEVVRCLNSALQVGCGAFACLENSTCDT 67
              |  :: |: : ||| |  : :          :: | : ||  |      |:  |:|   :
Db         59 LSTVIQSSDSKHEAAQ--AYADAGHCYKKTSAKEAISCLEQA------AYLFLDNGRFNM 110
```

```
Qy          68 DG--------MYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQR 119
               |         :|:: ::|  :   |:     :  |     ||   :||     :   :|:
Db         111 AGKYYKEIAELYELEQNFEQAIIYFEKAADIYQSEEATTAANQCNAKVAQFAAQLEQYQK 170

Qy         120 MIAEVQEECYSKLN----------------VCSIAKRNPEAITEVVQL-----PNHFSNR 158
               |   ::     ||                 :| : | :  |||  :        |     |
Db         171 AIQIYEDIGRPSLNNNLLKYGVKGHLLNAGICQLCKGDVVAITNALDRYQEMDPTFSGTR 230

Qy         159 YYNRLVRSLLECDEDTVSTIRDSLME 184
               |  ||      ||: |    |:: |
Db         231 EYKLLVDLAAAVDEEDVVKFTDAVKE 256
```

Search completed: June 12, 2003, 19:55:42
Job time : 38 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: June 12, 2003, 19:05:48 ; Search time 59 Seconds
(without alignments)
862.604 Million cell updates/sec

Title: US-09-705-500A-3
Perfect score: 1268
Sequence: 1 MLQNSAVLLVLVISASATHE.....NLRGEEDSPSHIKRTSHESA 247

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_21:*
1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1199	94.6	247	6	Q9N0T1	Q9n0t1 bos taurus
2	654	51.6	249	13	Q98TB7	Q98tb7 osteoglossu
3	354.5	28.0	296	11	Q9DCS6	Q9dcs6 mus musculu
4	102	8.0	473	10	Q9SZ16	Q9sz16 arabidopsis
5	92	7.3	1108	11	Q91YR4	Q91yr4 mus musculu
6	90.5	7.1	454	5	Q9GV74	Q9gv74 dictyosteli
7	90.5	7.1	783	3	O14130	O14130 schizosacch
8	89.5	7.1	1126	10	O64605	O64605 arabidopsis
9	89.5	7.1	3658	10	Q9M7K6	Q9m7k6 arabidopsis
10	89	7.0	305	10	O65029	O65029 linum usita
11	89	7.0	1728	10	Q9LUI2	Q9lui2 arabidopsis
12	88	6.9	473	10	Q9LFC2	Q9lfc2 arabidopsis
13	87	6.9	284	10	Q8VY30	Q8vy30 arabidopsis
14	86	6.8	470	16	Q9Z8Q2	Q9z8q2 chlamydia p
15	86	6.8	510	10	Q9LFC4	Q9lfc4 arabidopsis
16	86	6.8	556	3	Q03899	Q03899 saccharomyc
17	85.5	6.7	290	10	Q948Q0	Q948q0 hevea brasi
18	85.5	6.7	634	5	Q95PL8	Q95pl8 trypanosoma
19	85	6.7	806	10	Q9FFZ5	Q9ffz5 arabidopsis
20	83.5	6.6	427	5	Q9N3E2	Q9n3e2 caenorhabdi
21	83.5	6.6	1026	3	O74669	O74669 pneumocysti
22	83.5	6.6	1028	3	O74668	O74668 pneumocysti
23	83.5	6.6	1273	5	Q9BL02	Q9bl02 caenorhabdi
24	83	6.5	250	17	Q04927	Q04927 methanobact
25	83	6.5	297	12	Q91BJ2	Q91bj2 spodoptera
26	83	6.5	365	10	Q9SU53	Q9su53 arabidopsis
27	83	6.5	848	6	Q9XS94	Q9xs94 bos taurus
28	82.5	6.5	869	5	Q94174	Q94174 caenorhabdi
29	82.5	6.5	1757	10	Q9SMY5	Q9smy5 arabidopsis
30	82.5	6.5	2335	3	O14356	O14356 schizosacch
31	82.5	6.5	2535	10	Q9SZ40	Q9sz40 arabidopsis
32	82	6.5	329	12	Q9PYT2	Q9pyt2 xestia c-ni
33	82	6.5	453	2	Q8RQV5	Q8rqv5 lactobacill
34	82	6.5	815	16	Q9X2B4	Q9x2b4 thermotoga
35	82	6.5	925	10	Q9ZTA5	Q9zta5 arabidopsis
36	81.5	6.4	189	10	Q8VWW1	Q8vww1 gossypium h
37	81.5	6.4	463	5	Q17665	Q17665 caenorhabdi
38	81.5	6.4	549	16	O25619	O25619 helicobacte
39	81.5	6.4	757	4	Q8TAG9	Q8tag9 homo sapien
40	81.5	6.4	826	12	Q9PZ22	Q9pz22 xestia c-ni
41	81.5	6.4	974	10	Q9FIT7	Q9fit7 arabidopsis
42	81.5	6.4	974	10	Q94BP1	Q94bp1 arabidopsis
43	81.5	6.4	2931	5	Q9W2C6	Q9w2c6 drosophila
44	81	6.4	332	2	Q59904	Q59904 serratia en
45	81	6.4	358	16	Q55875	Q55875 synechocyst

ALIGNMENTS

RESULT 1
Q9N0T1
ID Q9N0T1 PRELIMINARY; PRT; 247 AA.
AC Q9N0T1;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Stanniocalcin.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=OVARY;
RA DiMattia G.E.;
RT "bovine stanniocalcin cDNA sequence.";
RL Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AF257506; AAF68996.1; -.
DR InterPro; IPR000719; Euk_pkinase.
DR InterPro; IPR004978; Stanniocalcin.
DR Pfam; PF03298; Stanniocalcin; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; UNKNOWN_1.
SQ SEQUENCE 247 AA; 27555 MW; F9942A715E2A3DE0 CRC64;

Query Match 94.6%; Score 1199; DB 6; Length 247;
Best Local Similarity 94.7%; Pred. No. 2.2e-106;
Matches 234; Conservative 5; Mismatches 8; Indels 0; Gaps 0;

```
Qy          1 MLQNSAVLLVLVISASATHEAEQNDSVSPRKSRVAAQNSAEVVRCLNSALQVGCGAFACL 60
              |||||||:|||||||||||||||||||| ||||||||||||:||||||||||||||||||
Db          1 MLQNSAVILVLVISASATHEAEQNDSVSLRKSRVAAQNSAEVIRCLNSALQVGCGAFACL 60

Qy         61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM 120

Qy        121 IAEVQEECYSKLNVCSIAKRNPEAITEVVQLPNHFSNRYYNRLVRSLLECDEDTVSTIRD 180
```

```
                 |||||||||:||||||:||||||||||||||||||||||||||||||:||||||||||
Db        121 IAEVQEECYTKLNVCSVAKRNPEAITEVVQLPNHFSNRYYNRLVRSLLDCDEDTVSTIRD 180

Qy        181 SLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRRTNEPQKLKVLLRNLRGEEDSPSHIK 240
              ||||||||||||||||||||| |  |||||||| ||||||||||||||| ||||||
Db        181 SLMEKIGPNMASLFHILQTDHCAHTQQRADFNRRRANEPQKLKVLLRNLRGEVASPSHIK 240

Qy        241 RTSHESA 247
              ||| |||
Db        241 RTSQESA 247


RESULT 2
Q98TB7
ID   Q98TB7      PRELIMINARY;      PRT;   249 AA.
AC   Q98TB7;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Stanniocalcin precursor.
GN   STC.
OS   Osteoglossum bicirrhosum (silver arawana).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Osteoglossomorpha;
OC   Osteoglossiformes; Osteoglossidae; Osteoglossum.
OX   NCBI_TaxID=109271;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=CORPUSCLE OF STANNIUS;
RA   Amemiya Y., Marra L.E., Reyhani N., Youson J.H.;
RT   "Stanniocalcin from an ancient teleost. Evidence for a monomeric form
RT   of the hormone and an extracorpuscular distribution.";
RL   Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AB060558; BAB43868.1; -.
DR   InterPro; IPR004978; Stanniocalcin.
DR   Pfam; PF03298; Stanniocalcin; 1.
KW   Signal.
FT   SIGNAL        1     31       POTENTIAL.
FT   CHAIN        32    249       POTENTIAL.
SQ   SEQUENCE   249 AA;  27389 MW;  10297D054A2BEB3A CRC64;

  Query Match             51.6%;  Score 654;  DB 13;  Length 249;
  Best Local Similarity   57.5%;  Pred. No. 2.2e-54;
  Matches  122;  Conservative   43;  Mismatches   45;  Indels    2;  Gaps    1;

Qy          1 MLQNSAVLLVLVISASATHEAEQNDSVSPRKSRVAAQNSAEVVRCLNSALQVGCGAFACL 60
              |:|   :||:  ::|||       :  | | :| || : ::| |||: |||||| |||||
Db          1 MIQKCMLLLLFFLTASAF--VIDQEEPSTRTARFAANSLSDVARCLSGALQVGCSAFACL 58

Qy         61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM 120
              ||||||||||::|||:|||:|||||||| ||||||:|:|||:||| || :|||||| |
Db         59 ENSTCDTDGMHEICKTFLYTAAKFDTQGKTFVKESLRCMANGITSKGFLMVRRCSTFQSM 118

Qy        121 IAEVQEECYSKLNVCSIAKRNPEAITEVVQLPNHFSNRYYNRLVRSLLECDEDTVSTIRD 180
              :|:|||:||:||::| :|: ||||| || |||| | ||:|: |::||||||::||| :||
Db        119 LADVQEDCYNKLDLCGVARANPEAIGEVAQLPNSFPNRHYSTLLQSLLECDQETVSLVRD 178

Qy        181 SLMEKIGPNMASLFHILQTDHCAQTHPRADFN 212
              |:  ::|| :| || :||:   : :  :|  |
Db        179 SMSARLGPEVAMLFKLLQSSSRSGSAAQASNN 210


RESULT 3
Q9DCS6
ID   Q9DCS6      PRELIMINARY;      PRT;   296 AA.
AC   Q9DCS6;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Stanniocalcin 2.
GN   STC2.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=KIDNEY;
RX   MEDLINE=21085660; PubMed=11217851;
RA   Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA   Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA   Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA   Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA   Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA   Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA   Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA   Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA   Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA   Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA   Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA   Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA   Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA   Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA   Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA   Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA   Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA   Hayashizaki Y.;
RT   "Functional annotation of a full-length mouse cDNA collection.";
RL   Nature 409:685-690(2001).
DR   EMBL; AK002527; BAB22164.1; -.
DR   MGD; MGI:1316731; Stc2.
DR   InterPro; IPR004978; Stanniocalcin.
DR   Pfam; PF03298; Stanniocalcin; 1.
SQ   SEQUENCE   296 AA;  32488 MW;  BD8961CEFFA47508 CRC64;

  Query Match             28.0%;  Score 354.5;  DB 11;  Length 296;
  Best Local Similarity   31.7%;  Pred. No. 1e-25;
  Matches   85;  Conservative   45;  Mismatches  109;  Indels   29;  Gaps    5;

Qy          7 VLLVLVISASATHEAEQNDSVSP----------RKSRVAAQNSAEVVRCLNSALQVGCGA 56
              | | ||   :    |:  || :|          :| |:: ||:||:  || :|  ||||
Db         10 VTLALVF--ATLDPAQGTDSTNPPEGPQDRSSQQKGRLSLQNTAEIQHCLVNAGDVGCGV 67

Qy         57 FACLENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCST 116
              | | ||::|:  |:: || :||::| ||| |||:|:|::|:|  |: :  |      :|
Db         68 FECFENNSCEIQGLHGICMTFLHNAGKFDAQGKSFIKDALRCKAHALRHKFGCISRKCPA 127

Qy        117 FQRMIAEVQEECYSKLNVCSIAKRNPEAITEVVQLPNHFSNRYYNRLVRSLLECDEDTVS 176
              : |: ::| ||| | ::|| |: |   | |::   :   :  |  ||  || | ||
Db        128 IREMVFQLQRECYLKHDLCSAAQENVGVIVEMIHFKDLLLHEPYVDLVNLLLTCGEDVKE 187

Qy        177 TIRDSLMEKIGPNMASLFHIL--------QTDHCAQTH----PRADFNRRRTNEPQKLKV 224
              :  |:  :   :   |  ||         :   |  |     ||  :|    :
Db        188 AVTRSVQAQCEQSWGGLCSILSFCTSNIQRPPTAAPEHQPLADRAQLSRPHHRDTDHHLT 247

Qy        225 LLRNLRGEEDSPSHIK-----RTSHESA 247
              |  :||  | ||        ||  :||
Db        248 ANRGAKGERGSKSHPNAHARGRTGGQSA 275


RESULT 4
Q9SZ16
ID   Q9SZ16      PRELIMINARY;      PRT;   473 AA.
AC   Q9SZ16;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE   Hypothetical 53.7 kDa protein.
GN   F10M23.100 OR AT4G26760.
OS   Arabidopsis thaliana (Mouse-ear cress).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC   eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX   NCBI_TaxID=3702;
RN   [1]
RP   SEQUENCE FROM N.A:
```

```
RA   Bevan M., Lecharny A., Chefdor F., Krivitzky M., Kreis M.,
RA   Hoheisel J., Mewes H.W., Mayer K.F.X., Schueller C.;
RL   Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RA   EU Arabidopsis sequencing project;
RL   Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE FROM N.A.
RA   Lecharny A., Chefdor F., Krivitzky M., Kreis M., Mewes H.W.,
RA   Lemcke K., Mayer K.F.X.;
RL   Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
RN   [4]
RP   SEQUENCE FROM N.A.
RA   EU Arabidopsis sequencing project;
RL   Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AL035440; CAB36522.1; -.
DR   EMBL; AL161565; CAB79531.1; -.
KW   Hypothetical protein.
SQ   SEQUENCE   473 AA;  53737 MW;  8CB8B883CF5CCCD1 CRC64;

  Query Match             8.0%;  Score 102;  DB 10;  Length 473;
  Best Local Similarity   21.0%;  Pred. No. 0.23;
  Matches   50;  Conservative   43;  Mismatches   67;  Indels   78;  Gaps   11;

Qy         26 SVSPRKSRVAAQNSAEVVRCLNSALQVGCGAFACLENSTCDT----DGMYDICKSF-LYS 80
              :|  :|  :||:: ||::: |:          | :| |   |        ||| |  |: 
Db         50 NVYKKKVELAAKSRAELLQTLSD---------ATVELSNLTTALGEKSYIDICDSMSLFP 100

Qy         81 AAKFDTQGKAFVKESLKCIA-----------------------------------NG-- 102
                 | |   :|| |  ||                                     ||   
Db        101 LQPDKTSGT--IKEQLSAIAPALEQLWQQKEERVRAFSDVQSQIQKICEEIAGGLNNGPH 158

Qy        103 VTSKVFLAIRRCSTFQRMIAEVQEECYSKL-----------NVCSIAKRN-PEAITEV-- 148
              |  :  |:::|   ||| : |:|:|   :|          ::|:: : :    :|||  
Db        159 VVDETDLSLKRLDDFQRKLQELQKEKSDRLQKVLEFVSTVHDLCAVLRLDFLSTVTEVHP 218

Qy        149 -------VQLPNHFSNRYYNRLVRSLLECDEDTVSTIRDSLMEKIGPNMASLFHILQT 199
                    ||  :  ||    || :::|   || :  ::   ::::   :  |:::: | 
Db        219 SLDEANGVQTKS-ISNETLARLAKTVLTLKEDKMQRLKK--LQELATQLTDLWNLMDT 273


RESULT 5
Q91YR4
ID   Q91YR4      PRELIMINARY;      PRT;  1108 AA.
AC   Q91YR4;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE   Similar to adaptor-related protein complex AP-3, beta 1 subunit.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Strausberg R.;
RL   Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC015068; AAH15068.1; -.
DR   InterPro; IPR002553; Adaptin_N.
DR   InterPro; IPR000130; Zn_MTpeptdse.
DR   Pfam; PF01602; Adaptin_N; 1.
DR   PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN_1.
SQ   SEQUENCE   1108 AA;  123155 MW;  7B436C3E32C3E2E3 CRC64;

  Query Match             7.3%;  Score 92;  DB 11;  Length 1108;
  Best Local Similarity   21.2%;  Pred. No. 5.9;
  Matches   55;  Conservative   40;  Mismatches  104;  Indels   60;  Gaps   11;

Qy          1 MLQNSAVLLVLVISASATHEAEQNDSVSPRKSRVAAQNSAEVVRCLNSALQVGCGAFACL 60
              :||:    :|: ::    |       :||:    |   |  :|| | |  :|       :
Db        307 LLQSRNAAVVMAVAQLYWH-------ISPKSE--AGVISKSLVRLLRSNREVQYIVLQNI 357

Qy         61 ENSTCDTDGMYD-ICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFL---------- 109
              : :  ||::   ||| |  :   |  |    | |  :||      |
Db        358 ATMSIERKGMFEPYLKSF-YVRSTDPTMIKTLKLEILTNLANEANISTLLREFQTYVRSQ 416

Qy        110 ----------AIRRCSTFQRMIAEVQEECYSKLNVCSIAKRNPEAITE---VVQLPNHFS 156
                       | ||:|    |:|| : | : | || :: |:   : |   |::
Db        417 DKQFAAATIQTIGRCAT---SISEVTDTCLNGL-VCLLSNRDEIVVAESVVVIKKLLQMQ 472

Qy        157 NRYYNRLVRSLLE-CDEDTVSTIRDSLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRR 215
                 ::| : :  |  ||   | |::  || |              | :    |
Db        473 PAQHGEIIRHMAKLLDSITVPVARASILWLIGEN-----------CERVPKIA------ 514

Qy        216 TNEPQKLKVLLRNLRGEED 234
                |  |: : ::   |:|
Db        515 ---PDVLRKMAKSFTSEDD 530


RESULT 6
Q9GV74
ID   Q9GV74      PRELIMINARY;      PRT;  454 AA.
AC   Q9GV74;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE   Differentiation associate-1.
GN   DIA-1.
OS   Dictyostelium discoideum (Slime mold).
OC   Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
OX   NCBI_TaxID=44689;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=20347020; PubMed=10887082;
RA   Hirose S., Inazu Y., Chae S., Maeda Y.;
RT   "Suppression of the growth/differentiation transition in Dictyostelium
RT   development by transient expression of a novel gene, dia1.";
RL   Development 127:3263-3270(2000).
DR   EMBL; AB007026; BAB13513.1; -.
SQ   SEQUENCE   454 AA;  48601 MW;  529D28B2D1908B85 CRC64;

  Query Match             7.1%;  Score 90.5;  DB 5;  Length 454;
  Best Local Similarity   21.1%;  Pred. No. 2.7;
  Matches   46;  Conservative   42;  Mismatches   93;  Indels   37;  Gaps   11;

Qy         45 CLNSALQVGCGAFACLENSTCDTDGMYDICKSFLYSAAKFDTQGK----AFVKESLKCIA 100
              ||| |    | ::  :|| :||    | :| |  | : | :::||    :: | : :|
Db        227 CLNGANGYSCKSY--VENQSCDPSDEYPVCNSD-YQSCKCNSKGKGSCQSYYKLTQEC-- 281

Qy        101 NGVTSKVFLAIRRCSTFQRMIAE-----VQEECYSKLNVCSIAKRNPEAITEVVQLPNHF 155
                 ::|: |    |:  :  |         |  | |:|  |: ::   : |    ::  |
Db        282 KDSSNKLVL----CAKSKNSIPSYKDYVTQINCQSQL--CNYSR---DCIDPKAKVSTCF 332

Qy        156 SN------RYYNRLVRSLLECDEDTVSTIRDSLMEKIGPNMASLFHILQTDHCAQTHPRA 209
                 ::      |||           : |:   |     |  |: :: :|:::   :     :
Db        333 NDLFLMCPRYYQEPEIGSSSSSSSSSSSSGSSSNSNIFINIINIINIIRSSE-SSNGSNS 391

Qy        210 DFNRRRTNEPQKLKVLLRNLRGEEDSPSHIKRTSHESA 247
                 :    :: |    |       | | |    || ||:
Db        392 NSVSSESSSPSSSSV-------ESSSNSKSNHTSSESS 422


RESULT 7
O14130
ID   O14130      PRELIMINARY;      PRT;  783 AA.
AC   O14130;
DT   01-JAN-1999 (TrEMBLrel. 09, Created)
DT   01-JAN-1999 (TrEMBLrel. 09, Last sequence update)
DT   01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE   Putative 88.0 kDa transcriptional regulatory protein C3C7.04 in
DE   chromosome I.
GN   SPAC3C7.04.
OS   Schizosaccharomyces pombe (Fission yeast).
OC   Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC   Schizosaccharomycetales; Schizosaccharomycetaceae;
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OC   Schizosaccharomyces.
OX   NCBI_TaxID=4896;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=972;
RA   Brown D., Churcher C.M., Wood V., Barrell B.G., Rajandream M.A.;
RL   Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases.
CC   -!- SUBCELLULAR LOCATION: NUCLEAR (POTENTIAL).
CC   -!- SIMILARITY: CONTAINS A ZN(2)-CYS(6), FUNGAL-TYPE BINUCLEAR CLUSTER
CC       DOMAIN.
DR   EMBL; Z99568; CAB16735.1; -.
DR   HSSP; P12351; 1HWT.
DR   InterPro; IPR002106; AAtRNA_ligaseII.
DR   InterPro; IPR001138; Fungi_TrN.
DR   Pfam; PF00172; Zn_clus; 1.
DR   SMART; SM00066; GAL4; 1.
DR   PROSITE; PS00339; AA_TRNA_LIGASE_II_2; UNKNOWN_1.
DR   PROSITE; PS00463; ZN2_CY6_FUNGAL_1; 1.
DR   PROSITE; PS50048; ZN2_CY6_FUNGAL_2; 1.
KW   Hypothetical protein; Transcription regulation; DNA-binding;
KW   Nuclear protein; Zinc; Metal-binding; Transmembrane.
FT   DNA_BIND      40     66       ZN(2)-CYS(6), FUNGAL-TYPE.
FT   DOMAIN        24     27       POLY-ARG.
FT   DOMAIN        32     35       POLY-ARG.
FT   DOMAIN       276    279       POLY-PHE.
FT   TRANSMEM     302    322       POTENTIAL.
FT   TRANSMEM     583    603       POTENTIAL.
SQ   SEQUENCE   783 AA;  87957 MW;  4DD04F3865C448D2 CRC64;

  Query Match             7.1%;  Score 90.5;  DB 3;  Length 783;
  Best Local Similarity   23.3%;  Pred. No. 5.3;
  Matches   56;  Conservative   34;  Mismatches   87;  Indels   63;  Gaps   12;

Qy         10 VLVISASATHEAEQNDSVSPRKSRV------AAQNSAEVVRCLNSALQVGCGAF------ 57
              ::::|         :|   |||  |:      ||::   :|  | :  |: | :|
Db        535 IIIMSRPVLLHKMKNAKNSPRVDRINEDCILAARHLISLVHLLQNHSQLSCYSFFDYNYT 594

Qy         58 ---------ACLENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCI--------- 99
                      |:    |: |   ||   : |||  :  :|    |   : |
Db        595 FSSALVVLLHCV-TEPCEED---DIAMQYAYSALDYMAEGNEAAKNCARVIRLFDAHLKG 650

Qy        100 -----ANGVTSKV-FLAIRRCSTFQRMIAEVQ-----EECYSKLNVCSIAKRNPEAITEVV 149
                  || ||:  |:|      :|| ||||      |:  |  |      ||  ::|
Db        651 ARSDGNGNTSQSGFMA------WQRWIAEVSAKDEPEKLMSPYNKSIGGGRNSNSLTPNA 704

Qy        150 QLPNHFSNRYYNR------LVRSLLECDEDTVSTIRDSLMEKIGPNMA---SLFHILQTD 200
              |    |  ::        |  | |: | :  ::  | :  |  |::|   || :  ||
Db        705 NLGADVS--FFPTDDTSFLLDHSKLDDDLEKFASTLDPI--KTTPDLANDSSLLNWANTD 760


RESULT 8
O64605
ID   O64605      PRELIMINARY;      PRT;  1126 AA.
AC   O64605;
DT   01-AUG-1998 (TrEMBLrel. 07, Created)
DT   01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   F17O7.15 protein.
GN   F17O7.15.
OS   Arabidopsis thaliana (Mouse-ear cress).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC   eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX   NCBI_TaxID=3702;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=CV. COLUMBIA;
RA   Vysotskaia V.S., Schwartz J.R., Toriumi M., Yu G., Kwan A., Oji O.,
RA   Liu S., Li J., Araujo R., Au M., Brendel V., Buehler E., Conway A.B.,
RA   Conway A.R., Dewar K., Feng J., Kim C., Kurtz D., Li Y., Palm C.J.,
RA   Shinn P., Sun H., Davis R.W., Ecker J.R., Federspiel N.A.,
RA   Theologis A.;
RT   "Arabidopsis thaliana chromosome 1 BAC F17O7 sequence.";
RL   Submitted (DEC-1997) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=CV. COLUMBIA;
RA   Theologis A.;
RL   Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AC003671; AAC18813.1; -.
DR   InterPro; IPR000569; HECT_domain.
DR   Pfam; PF00632; HECT; 1.
DR   SMART; SM00119; HECTc; 1.
DR   PROSITE; PS50237; HECT; 1.
SQ   SEQUENCE   1126 AA;  126148 MW;  0DA1A3ACF6A8F64E CRC64;

  Query Match             7.1%;  Score 89.5;  DB 10;  Length 1126;
  Best Local Similarity   22.1%;  Pred. No. 10;
  Matches   46;  Conservative   39;  Mismatches   76;  Indels   47;  Gaps    8;

Qy         14 SASATHEAEQNDSVSPRKSRVAAQNSAEVVRCLNSALQVGCGAFACLENSTCD------- 66
              |:    :||   ||: ||      | ||:    |  ||:        ::  |:
Db        412 SSETQKDAESELSVARRK------NCAEL---YNIFLQLP-------QSDLCNLCMLLGY 455

Qy         67 ---TDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRMIAE 123
                 :| :|  :     |   |  |   : |  : |  :|:|::|      :   || |:|
Db        456 EGLSDKIYSLAGEVLKKLAAVDVTHRKFFTKELSELASGLSSSTVRVLATLSTTQKM--- 512

Qy        124 VQEECYSKLNVCSIAKRNPEAITEVVQLPNHFSNRYYNRLVRSLLECDEDTVSTIR---- 179
                    | ||:|      :|  |:|: :  ::   :  | :  | |::  : ::
Db        513 -------SQNTCSMA---GASILRVLQVLSSLTSTIDDSNVGTDKETDQEEQNIMQGLKV 562

Qy        180 --DSLMEKIGPNMASLFHILQTDHCAQT 205
                : | :::|  ::      || || | |
Db        563 ALEPLWQELGQCIS--MTELQLDHTAAT 588


RESULT 9
Q9M7K6
ID   Q9M7K6      PRELIMINARY;      PRT;  3658 AA.
AC   Q9M7K6;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Ubiquitin-protein ligase 2.
GN   UPL2.
OS   Arabidopsis thaliana (Mouse-ear cress).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC   eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX   NCBI_TaxID=3702;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=CV. COLUMBIA;
RX   MEDLINE=20040063; PubMed=10571878;
RA   Bates P.W., Vierstra R.D.;
RT   "UPL1 and 2, two 405 kDa ubiquitin-protein ligases from Arabidopsis
RT   thaliana related to the HECT-domain protein family.";
RL   Plant J. 20:183-195(1999).
DR   EMBL; AF127565; AAF36455.1; -.
DR   InterPro; IPR000569; HECT_domain.
DR   InterPro; IPR002950; Josephin.
DR   InterPro; IPR000449; UBA_domain.
DR   InterPro; IPR003903; UIM.
DR   Pfam; PF00632; HECT; 1.
DR   Pfam; PF00627; UBA; 1.
DR   Pfam; PF02809; UIM; 1.
DR   SMART; SM00119; HECTc; 1.
DR   SMART; SM00165; UBA; 1.
DR   PROSITE; PS50237; HECT; 1.
KW   Ligase.
SQ   SEQUENCE   3658 AA;  403582 MW;  1FB4F8EB8C1F73D1 CRC64;

  Query Match             7.1%;  Score 89.5;  DB 10;  Length 3658;
  Best Local Similarity   22.1%;  Pred. No. 45;
  Matches   46;  Conservative   39;  Mismatches   76;  Indels   47;  Gaps    8;
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Qy          14 SASATHEAEQNDSVSPRKSRVAAQNSAEVVRCLNSALQVGCGAFACLENSTCD------- 66
               |:    :||   ||: ||      | ||:    |  ||:        ::  |:
Db        2977 SSETQKDAESELSVARRK------NCAEL---YNIFLQLP-------QSDLCNLCMLLGY 3020

Qy          67 ---TDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRMIAE 123
                  :| :| :    |   | |   : | : |  :|:|::|     :   || |:|
Db        3021 EGLSDKIYSLAGEVLKKLAAVDVTHRKFFTKELSELASGLSSSTVRVLATLSTTQKM--- 3077

Qy         124 VQEECYSKLNVCSIAKRNPEAITEVVQLPNHFSNRYYNRLVRSLLECDEDTVSTIR---- 179
                   | ||:|     :|  |:|: :  ::   :  | :  | |::  : ::
Db        3078 -------SQNTCSMA---GASILRVLQVLSSLTSTIDDSNVGTDKETDQEEQNIMQGLKV 3127

Qy         180 --DSLMEKIGPNMASLFHILQTDHCAQT 205
                 : | :::|  ::     || || | |
Db        3128 ALEPLWQELGQCIS--MTELQLDHTAAT 3153


RESULT 10
O65029
ID   O65029      PRELIMINARY;      PRT;   305 AA.
AC   O65029;
DT   01-AUG-1998 (TrEMBLrel. 07, Created)
DT   01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   Peroxidase FLXPER4 (EC 1.11.1.7) (Fragment).
GN   PER4.
OS   Linum usitatissimum (Flax) (Linseed).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC   eurosids I; Malpighiales; Linaceae; Linum.
OX   NCBI_TaxID=4006;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=CV. STORMONT CIRRUS; TISSUE=LEAF;
RA   Omann F., Tyson H.;
RT   "cDNA sequence of a basic peroxidase (FLXPER4) in flax.";
RL   Submitted (FEB-1998) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF049881; AAC05277.1; -.
DR   HSSP; P22195; 1SCH.
DR   InterPro; IPR002016; Peroxidase.
DR   Pfam; PF00141; peroxidase; 1.
DR   PRINTS; PR00458; PEROXIDASE.
DR   PROSITE; PS00435; PEROXIDASE_1; UNKNOWN_1.
DR   PROSITE; PS00436; PEROXIDASE_2; 1.
KW   Oxidoreductase; Peroxidase.
FT   NON_TER       1       1
SQ   SEQUENCE   305 AA;  32431 MW;  F79BB1FADF697253 CRC64;

  Query Match             7.0%;  Score 89;  DB 10;  Length 305;
  Best Local Similarity   21.9%;  Pred. No. 2.3;
  Matches   57;  Conservative   39;  Mismatches   92;  Indels   72;  Gaps   15;

Qy          11 LVISASATHEAEQNDSVSPRKSRVAAQNSAEVVRCLNSALQVGCGA-FACLE-NSTCDTD 68
               |::  :||   |:|    | :: |      :::  : : ::  | |  :| :  :    |
Db          65 LLLDDTATFTGEKN--AGPNQNSV---RGFDIIDTIKTRVEAACNATVSCADILALAARD 119

Qy          69 GMYDI-------------CKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLA----- 110
               |:  :             ::   |||             ||  | |  |:|   |
Db         120 GVVLVGGPTWTVPLGRRDARTASQSAANAQIPAPG---SSLGTITNLFTNKGLTARDVTI 176

Qy         111 --------IRRCSTFQRMIAEVQEECYSKLNV----CSIAKRN-PEA-----ITEVVQLP 152
                      ||:||:: |       |:  |:     :  : | |:|     :  :   |
Db         177 LSGAHTIGQARCTTFRQRI-------YNDTNIDPAFATTRRGNCPQAGAGANLAPLDGTP 229

Qy         153 NHFSNRYYNRLV--RSLLECDEDTVST-IRDSLMEKIGPNMASLFHILQTDHCAQ----- 204
                 | ||||  ||  | ||  |::  :   :|:|:     | |:      ||  |
Db         230 TQFDNRYYQDLVARRGLLHSDQELFNNGTQDALVRTYSNNAAT----FATDFAAAMVRMG 285

Qy         205 -------THPRADFNRRRTN 217
                     |:    || || |
Db         286 NISPLTGTNGEIRFNCRRPN 305


RESULT 11
Q9LUI2
ID   Q9LUI2      PRELIMINARY;      PRT;  1728 AA.
AC   Q9LUI2;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE   Centromere protein.
OS   Arabidopsis thaliana (Mouse-ear cress).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC   eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX   NCBI_TaxID=3702;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=COLUMBIA;
RA   Sato S., Nakamura Y., Kaneko T., Kato T., Asamizu E., Tabata S.;
RL   Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=COLUMBIA;
RX   MEDLINE=20277480; PubMed=10819329;
RA   Nakamura Y.;
RT   "Structural analysis of Arabidopsis thaliana chromosome 3. I. Sequence
RT   features of the regions of 4,504,864 bp covered by sixty P1 and TAC
RT   clones.";
RL   DNA Res. 7:131-135(2000).
DR   EMBL; AB022223; BAB01254.1; -.
SQ   SEQUENCE   1728 AA;  198850 MW;  0F393BC8C839B6D0 CRC64;

  Query Match             7.0%;  Score 89;  DB 10;  Length 1728;
  Best Local Similarity   21.3%;  Pred. No. 20;
  Matches   48;  Conservative   37;  Mismatches   82;  Indels   58;  Gaps    7;

Qy          39 SAEVVRCLNSALQVGCGAFACLENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVK----- 93
               | |  : : | ||    |    ||      :|      |    : :: :     |::
Db         459 SQEEQKVITSELQSRIGMLRDLETRNLKLEGDISSVKEENQNLSELNDSSMIFLETQKCE 518

Qy          94 -ESLKCIANGVTSKVFLAIRRCSTFQRMIAEVQEECYS------------------KLN 133
                |||  |   :  :|    | : | ||  |  :::|  |                  |
Db         519 ISSLKEIKEKLEEEVARHINQSSAFQEEIRRLKDEIDSLNKRYQAIMEQVNLAGLDPKSL 578

Qy         134 VCSIAKRNPEAITEVVQLPNHFSNRYYNRLVRSLLECDEDTVSTIRDSLMEKIGPNMASL 193
               ||: |   |  ::: :| || |:                      :|:| ||    : |
Db         579 ACSVRKLQDEN-SKLTELCNHQSDD-------------------KDALTEK----LREL 613

Qy         194 FHILQTDHC-----AQTHPRADFNRRRTNEPQKLKVLLRNLRGEE 233
               :||: : |      ::: : | :| :|  :    |:    :||||:
Db         614 DNILRKNVCLEKLLLESNTKLDGSREKTKD---LQERCESLRGEK 655


RESULT 12
Q9LFC2
ID   Q9LFC2      PRELIMINARY;      PRT;   473 AA.
AC   Q9LFC2;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE   Hypothetical 53.5 kDa protein.
GN   F7J8_120.
OS   Arabidopsis thaliana (Mouse-ear cress).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC   eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX   NCBI_TaxID=3702;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Bevan M., Zimmermann W., Grueneisen A., Wambutt R., Kalicki J.,
RA   Wohldmann P., Smith A., Bancroft I., Mewes H.W., Rudd S., Lemcke K.,
RA   Mayer K.F.X.;
RL   Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
RN   [2]
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RP   SEQUENCE FROM N.A.
RA   EU Arabidopsis sequencing project;
RL   Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AL137189; CAB69842.1; -.
KW   Hypothetical protein.
SQ   SEQUENCE   473 AA;  53510 MW;  6029A5DC35B876D9 CRC64;

  Query Match             6.9%;  Score 88;  DB 10;  Length 473;
  Best Local Similarity   22.6%;  Pred. No. 4.9;
  Matches   54;  Conservative   42;  Mismatches  103;  Indels   40;  Gaps   13;

Qy         27 VSPRKSRVAAQNSAEVVRCLNSALQVGCGAFACLEN---STCD---TDGMYDICKS-FLY 79
              :   |::|    :  :|| |    :       || |   |  |    |   | ||   ||
Db         16 IDEEKNKVVLAEAGTIVRLLAKHRKSDPVTIGCLRNLYTSVVDMELDDFETDACKQMLLY 75

Qy         80 SAAKFDTQGKAF-----VKESLKCIANGVTSKVFLAIRRCSTFQRMIAE----VQEEC-- 128
                : | : |       |||||       : |   | || |   : :    : ||
Db         76 PKNIREAQYRNFKLNIDTNESLKCFG----CRFFSICRMCSNFNTSLCKCGKLMNEEISF 131

Qy        129 --YSKLNVCSIAKRNPEA--ITEVVQLPNHFSNRYYNRLVRSLLECDEDTVSTIRDSLME 184
                | : :|  :  |:  :  ||: ::| :  :    : |:::| :     || :|: :::
Db        132 LEYEENDVEGVFMRDKSSFIITDDLRLTDDST----SSLLQTLKDLGCADVSKLREQVLD 187

Qy        185 KIGPNMASLFHILQTDHCAQTH--PRAD--FNRRRTNEPQKLKVLLRNLRGEEDSPSHI 239
               ||    |  ::    |  |   |  |     : :|  :|:   | : :|:|  |  :
Db        188 -IG-----LKEVMTLMQCVFTSNTPLTDAFLKNQSSNTVRKIYRKLSDDKGDEAEPDKV 240


RESULT 13
Q8VY30
ID   Q8VY30      PRELIMINARY;      PRT;   284 AA.
AC   Q8VY30;
DT   01-MAR-2002 (TrEMBLrel. 20, Created)
DT   01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT   01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE   Hypothetical 32.1 kDa protein.
GN   AT4G26760.
OS   Arabidopsis thaliana (Mouse-ear cress).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC   eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX   NCBI_TaxID=3702;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Yamada K., Banh J., Chan M.M., Chang C.H., Chang E., Dale J.M.,
RA   Deng J.M., Goldsmith A.D., Lee J.M., Onodera C.S., Quach H.L.,
RA   Tang C., Toriumi M., Wu H.C., Yamamura Y., Yu G., Bowser L.,
RA   Carninci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jones T.,
RA   Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Lam B., Lin J.,
RA   Meyers M.C., Miranda M., Narusaka M., Nguyen M., Palm C.J.,
RA   Sakurai T., Satou M., Seki M., Shinn P., Southwick A., Shinozaki K.,
RA   Davis R.W., Ecker J.R., Theologis A.;
RT   "Full Length cDNA of gene At4g26760 (GI:15236873).";
RL   Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY074259; AAL66956.1; -.
KW   Hypothetical protein.
SQ   SEQUENCE   284 AA;  32133 MW;  C2363214A405E77E CRC64;

  Query Match             6.9%;  Score 87;  DB 10;  Length 284;
  Best Local Similarity   18.4%;  Pred. No. 3.2;
  Matches   40;  Conservative   56;  Mismatches   75;  Indels   46;  Gaps    8;

Qy         26 SVSPRKSRVAAQNSAEVVRCLNSA--------LQVGCGAFACLENSTCDT---------- 67
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Db         50 NVYKKKVELAAKSRAELLQTLSDATVELSNLTTALGEKSYIDIPDKTSGTIKEQLSAIAP 109

Qy         68 --DGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANG--VTSKVFLAIRRCSTFQRMIAE 123
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Qy        124 VQEECYSKL----------NVCSIAKRN-PEAITEV---------VQLPNHFSNRYYNR 162
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Db        170 LQKEKSDRLQKVLEFVSTVHDLCAVLRLDFLSTVTEVHPSLDEANGVQTKS-ISNETLAR 228

Qy        163 LVRSLLECDEDTVSTIRDSLMEKIGPNMASLFHILQT 199
              | :::|   || : ::   ::::   :  |:::: |
Db        229 LAKTVLTLKEDKMQRLKK--LQELATQLTDLWNLMDT 263


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Q9Z8Q2
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AC   Q9Z8Q2;
DT   01-MAY-1999 (TrEMBLrel. 10, Created)
DT   01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   MG++ transporter (CBS domain).
GN   MGTE OR CPN0286 OR CP0472.
OS   Chlamydia pneumoniae (Chlamydophila pneumoniae).
OC   Bacteria; Chlamydiales; Chlamydiaceae; Chlamydophila.
OX   NCBI_TaxID=83558;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=CWL029;
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RA   Kalman S., Mitchell W., Marathe R., Lammel C., Fan J., Hyman R.W.,
RA   Olinger L., Grimwood J., Davis R.W., Stephens R.S.;
RT   "Comparative genomes of Chlamydia pneumoniae and C. trachomatis.";
RL   Nat. Genet. 21:385-389(1999).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=AR39;
RX   MEDLINE=20150255; PubMed=10684935;
RA   Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F.,
RA   White O., Hickey E.K., Peterson J., Utterback T., Berry K., Bass S.,
RA   Linher K., Weidman J., Khouri H., Craven B., Bowman C., Dodson R.,
RA   Gwinn M., Nelson W., DeBoy R., Kolonay J., McClarty G., Salzberg S.L.,
RA   Eisen J., Fraser C.M.;
RT   "Genome sequences of Chlamydia trachomatis MoPn and Chlamydia
RT   pneumoniae AR39.";
RL   Nucleic Acids Res. 28:1397-1406(2000).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   STRAIN=J138;
RX   MEDLINE=20330349; PubMed=10871362;
RA   Shirai M., Hirakawa H., Kimoto M., Tabuchi M., Kishi F., Ouchi K.,
RA   Shiba T., Ishii K., Hattori M., Kuhara S., Nakazawa T.;
RT   "Comparison of whole genome sequences of Chlamydia pneumoniae J138
RT   from Japan and CWL029 from USA.";
RL   Nucleic Acids Res. 28:2311-2314(2000).
DR   EMBL; AE001613; AAD18435.1; -.
DR   EMBL; AE002208; AAF73674.1; -.
DR   EMBL; AP002546; BAA98496.1; -.
DR   TIGR; CP0472; -.
DR   InterPro; IPR000644; CBS_domain.
DR   InterPro; IPR002665; MgtE.
DR   Pfam; PF00571; CBS; 2.
DR   Pfam; PF01769; MgtE; 1.
DR   Pfam; PF03448; MgtE_N; 1.
DR   SMART; SM00116; CBS; 2.
DR   TIGRFAMs; TIGR00400; mgtE; 1.
KW   Complete proteome.
SQ   SEQUENCE   470 AA;  51739 MW;  5B178FB939494DBF CRC64;

  Query Match             6.8%;  Score 86;  DB 16;  Length 470;
  Best Local Similarity   22.9%;  Pred. No. 7.5;
  Matches   47;  Conservative   33;  Mismatches   61;  Indels   64;  Gaps   13;

Qy         56 AFACLENSTCDTD-GMYDICK--------SFLYSAAKFDTQGKAFVKESLKCIANGVTSK 106
              || ||      ||   :|: |          |: :   :: :| : ::| ||    |:|
Db         19 AFTCL-----STDIHSHDLSKIVIEYNPIDLAYAVSCLPSESRAILYKNLSCI----TAK 69

Qy        107 VFLAIR-----RCSTFQRMIAEVQEECYSKLNVCSIAKRNP--EAITEVVQLPNHFSNRY 159
              |   |       | :|:|:          |   ||:: :: |  ||:  :  :|    :|
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DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE   Hypothetical 56.9 kDa protein.
GN   F7J8_100.
OS   Arabidopsis thaliana (Mouse-ear cress).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC   eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX   NCBI_TaxID=3702;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Bevan M., Zimmermann W., Grueneisen A., Wambutt R., Kalicki J.,
RA   Wohldmann P., Smith A., Bancroft I., Mewes H.W., Rudd S., Lemcke K.,
RA   Mayer K.F.X.;
RL   Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RA   EU Arabidopsis sequencing project;
RL   Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AL137189; CAB69840.1; -.
DR   InterPro; IPR000923; BlueCu_1.
DR   PROSITE; PS00196; COPPER_BLUE; UNKNOWN_1.
KW   Hypothetical protein.
SQ   SEQUENCE   510 AA;  56940 MW;  9D1D0684F79CFA80 CRC64;

  Query Match             6.8%;  Score 86;  DB 10;  Length 510;
  Best Local Similarity   23.5%;  Pred. No. 8.3;
  Matches   38;  Conservative   22;  Mismatches   70;  Indels   32;  Gaps    5;

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Db        108 DDSEATKCFMCPMFVRSGQCSKGYSNFKTSRCS-------CGNFMDEVIQFQGEGGRGNG 160

Qy         86 TQGKAFVK---------ESLKCIANGVTSKV----FLAIRRCSTFQRMIAEVQEECYSKL 132
              :| : ||:         : ||   | | | :     ||    |     || ||  :  : |
Db        161 SQAEVFVRGAHTSFIITDDLKVQVNSVGSTLNVLKDLAYADCDKLVEMILEVNLQEVATL 220

Qy        133 NVCSIAKRNPEAITEVVQLPNHFSNRYYNRLVRSLLECDEDT 174
               ||      |   | : :  :|  || : |   || |  |:|
Db        221 LVCLFTSDTPLTDTFLKKKSSHGMNRIHKRPSPSLSEDREET 262


Search completed: June 12, 2003, 19:56:55
Job time : 62 secs
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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: June 9, 2003, 09:55:48 ; Search time 203 Seconds
(without alignments)
5683.340 Million cell updates/sec

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Perfect score: 3762
Sequence: 1 ggtggcagcagcagcatcac.....tgttacgttttattggtttc 3762

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
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	2	769.4	20.5	771	2	US-09-038-597A-1	Sequence 1, Appli
	3	769.4	20.5	771	2	US-08-431-117A-1	Sequence 1, Appli
	4	122.8	3.3	906	3	US-08-831-132-1	Sequence 1, Appli
	5	122.8	3.3	906	4	US-09-416-150-1	Sequence 1, Appli
	6	121.2	3.2	892	2	US-08-460-529B-1	Sequence 1, Appli
	7	110	2.9	888	3	US-08-831-132-13	Sequence 13, Appl
	8	110	2.9	888	4	US-09-416-150-13	Sequence 13, Appl
	9	82	2.2	7218	1	US-08-232-463-14	Sequence 14, Appl
c	10	44	1.2	4383	6	5175095-4	Patent No.5175095
c	11	43.4	1.2	1988	4	US-09-402-002-3	Sequence 3, Appli
c	12	43.2	1.1	2447	2	US-09-014-969-14	Sequence 14, Appl
c	13	42.8	1.1	7218	1	US-08-232-463-14	Sequence 14, Appl
c	14	41.4	1.1	19124	2	US-08-487-826B-13	Sequence 13, Appl
c	15	40.4	1.1	618	4	US-08-953-326-22	Sequence 22, Appl
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	18	40	1.1	660	1	US-08-107-755A-32	Sequence 32, Appl
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	25	40	1.1	3321	1	US-08-484-438-5	Sequence 5, Appli
	26	40	1.1	4810	3	US-08-852-629-11	Sequence 11, Appl
	27	40	1.1	4838	3	US-08-852-629-15	Sequence 15, Appl
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	30	39.8	1.1	837	4	US-08-998-416-288	Sequence 288, App
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	34	39.4	1.0	260	4	US-08-897-126-29	Sequence 29, Appl
c	35	39.4	1.0	2058	2	US-08-749-391-1	Sequence 1, Appli
c	36	39.4	1.0	2058	3	US-09-390-200-1	Sequence 1, Appli
c	37	39.4	1.0	2239	4	US-09-196-390-1	Sequence 1, Appli
	38	39.4	1.0	19124	2	US-08-487-826B-13	Sequence 13, Appl
c	39	39.2	1.0	3528	4	US-08-984-320-2	Sequence 2, Appli
c	40	39.2	1.0	3528	4	US-08-487-087A-2	Sequence 2, Appli
c	41	39.2	1.0	4383	4	US-08-397-653B-2	Sequence 2, Appli
	42	39	1.0	2244	4	US-09-272-414-1	Sequence 1, Appli
	43	39	1.0	9636	1	US-08-323-170B-1	Sequence 1, Appli
	44	39	1.0	9636	4	US-08-954-441-1	Sequence 1, Appli
c	45	38.6	1.0	2010	1	US-07-864-475A-4	Sequence 4, Appli

ALIGNMENTS

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RESULT 1
US-08-208-005C-1
; Sequence 1, Application US/08208005C
; Patent No. 5837498
;  GENERAL INFORMATION:
;    APPLICANT:  OLSEN, ET AL.
;    TITLE OF INVENTION:  Corpuscles of Stannius Protein, Stanniocalcin
;    NUMBER OF SEQUENCES:  5
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  CARELLA, BYRNE, BAIN, GILFILLAN,
;      ADDRESSEE:  CECCHI, STEWART & OLSTEIN
;      STREET:  6 BECKER FARM ROAD
;      CITY:  ROSELAND
;      STATE:  NEW JERSEY
;      COUNTRY:  USA
;      ZIP:  07068
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5 INCH DISKETTE
;      COMPUTER:  IBM PS/2
;      OPERATING SYSTEM:  MS-DOS
;      SOFTWARE:  WORD PERFECT 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/208,005C
;      FILING DATE:  8 MARCH 1994
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  FERRARO, GREGORY D.
;      REGISTRATION NUMBER:  36,134
;      REFERENCE/DOCKET NUMBER:  325800-78
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  201-994-1700
;      TELEFAX:  201-994-1744
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  771 BASE PAIRS
;      TYPE:  NUCLEIC ACID
;      STRANDEDNESS:  SINGLE
;      TOPOLOGY:  LINEAR
;    MOLECULE TYPE:  cDNA
US-08-208-005C-1

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  Best Local Similarity  99.9%;  Pred. No. 5.9e-206;
  Matches  770;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

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Qy        279 GCTCAAAACTCAGCTGAAGTGGTTCGTTGCCTCAACAGTGCTCTACAGGTCGGCTGCGGG 338
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Qy        339 GCTTTTGCATGCCTGGAAAACTCCACCTGTGACACAGATGGGATGTATGACATCTGTAAA 398
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Qy        579 AGCATCGCCAAGCGGAACCCTGAAGCCATCACTGAGGTCGTCCAGCTGCCCAATCACTTC 638
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Db        721 CCCTCCCACATCAAACGCACATCCCATGAGAGTGCATAACCAGGGAGAGGT 771


RESULT 2
US-09-038-597A-1
; Sequence 1, Application US/09038597A
; Patent No. 5877290
;  GENERAL INFORMATION:
;    APPLICANT:  OLSEN, ET AL.
;    TITLE OF INVENTION:  Corpuscles of Stannius Protein,
;    TITLE OF INVENTION:  Stanniocalcin
;    NUMBER OF SEQUENCES:  5
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  CARELLA, BYRNE, BAIN, GILFILLAN,
;      ADDRESSEE:  CECCHI, STEWART & OLSTEIN
;      STREET:  6 BECKER FARM ROAD
;      CITY:  ROSELAND
;      STATE:  NEW JERSEY
;      COUNTRY:  USA
;      ZIP:  07068
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5 INCH DISKETTE
;      COMPUTER:  IBM PS/2
;      OPERATING SYSTEM:  MS-DOS
;      SOFTWARE:  WORD PERFECT 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/038,597A
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/208,005
;      FILING DATE:  8-MARCH-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  FERRARO, GREGORY D.
;      REGISTRATION NUMBER:  36,134
;      REFERENCE/DOCKET NUMBER:  325800-78
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  201-994-1700
;      TELEFAX:  201-994-1744
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  771 BASE PAIRS
;      TYPE:  NUCLEIC ACID
;      STRANDEDNESS:  SINGLE
;      TOPOLOGY:  LINEAR
;    MOLECULE TYPE:  cDNA
US-09-038-597A-1

  Query Match             20.5%;  Score 769.4;  DB 2;  Length 771;
  Best Local Similarity   99.9%;  Pred. No. 5.9e-206;
  Matches  770;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        159 GAAACTTCTCAGAGAATGCTCCAAAACTCAGCAGTGCTTCTGGTGCTGGTGATCAGTGCT 218
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Qy        279 GCTCAAAACTCAGCTGAAGTGGTTCGTTGCCTCAACAGTGCTCTACAGGTCGGCTGCGGG 338
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Qy        339 GCTTTTGCATGCCTGGAAAACTCCACCTGTGACACAGATGGGATGTATGACATCTGTAAA 398
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Db        181 GCTTTTGCATGCCTGGAAAACTCCACCTGTGACACAGATGGGATGTATGACATCTGTAAA 240

Qy        399 TCCTTCTTGTACAGCGCTGCTAAATTTGACACTCAGGGAAAAGCATTCGTCAAAGAGAGC 458
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TCCTTCTTGTACAGCGCTGCTAAATTTGACACTCAGGGAAAAGCATTCGTCAAAGAGAGC 300

Qy        459 TTAAAATGCATCGCCAACGGGGTCACCTCCAAGGTCTTCCTCGCCATTCGGAGGTGCTCC 518
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TTAAAATGCATCGCCAACGGGGTCACCTCCAAGGTCTTCCTCGCCATTCGGAGGTGCTCC 360

Qy        519 ACTTTCCAAAGGATGATTGCTGAGGTGCAGGAAGAGTGCTACAGCAAGCTGAATGTGTGC 578
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 ACTTTCCAAAGGATGATTGCTGAGGTGCAGGAAGAGTGCTACAGCAAGCTGAATGTGTGC 420

Qy        579 AGCATCGCCAAGCGGAACCCTGAAGCCATCACTGAGGTCGTCCAGCTGCCCAATCACTTC 638
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 AGCATCGCCAAGCGGAACCCTGAAGCCATCACTGAGGTCGTCCAGCTGCCCAATCACTTC 480

Qy        639 TCCAACAGATACTATAACAGACTTGTCCGAAGCCTGCTGGAATGTGATGAAGACACAGTC 698
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 TCCAACAGATACTATAACAGACTTGTCCGAAGCCTGCTGGAATGTGATGAAGACACAGTC 540

Qy        699 AGCACAATCAGAGACAGCCTGATGGAGAAAATTGGGCCTAACATGGCCAGCCTCTTCCAC 758
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 AGCACAATCAGAGACAGCCTGATGGAGAAAATTGGGCCTAACATGGCCAGCCTCTTCCAC 600

Qy        759 ATCCTGCAGACAGACCACTGTGCCCAAACACACCCACGAGCTGACTTCAACAGGAGACGC 818
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 ATCCTGCAGACAGACCACTGTGCCCAAACACACCCACGAGCTGACTTCAACAGGAGACGC 660

Qy        819 ACCAATGAGCCGCAGAAGCTGAAAGTCCTCCTCAGGAACCTCCGAGGTGAGGAGGACTCT 878
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        661 ACCAATGAGCCGCAGAAGCTGAAAGTCCTCCTCAGGAACCTCCGAGGTGAGGAGGACTCT 720

Qy        879 CCCTCCCACATCAAACGCACATCCCATGAGAGTGCATAACCAGGGAGAGGT 929
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 CCCTCCCACATCAAACGCACATCCCATGAGAGTGCATAACCAGGGAGAGGT 771


RESULT 3
US-08-431-117A-1
; Sequence 1, Application US/08431117A
; Patent No. 5994301
;  GENERAL INFORMATION:
;    APPLICANT:  OLSEN, ET AL.
;    TITLE OF INVENTION:  Corpuscles of Stannius Protein, Stanniocalcin
;    NUMBER OF SEQUENCES:  8
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  CARELLA, BYRNE, BAIN, GILFILLAN,
;      ADDRESSEE:  CECCHI, STEWART & OLSTEIN
;      STREET:  6 BECKER FARM ROAD
;      CITY:  ROSELAND
;      STATE:  NEW JERSEY
;      COUNTRY:  USA
;      ZIP:  07068
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5 INCH DISKETTE
;      COMPUTER:  IBM PS/2
;      OPERATING SYSTEM:  MS-DOS
;      SOFTWARE:  WORD PERFECT 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/431,117A
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/208,005
;      FILING DATE:  8 MARCH 1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  FERRARO, GREGORY D.
;      REGISTRATION NUMBER:  36,134
;      REFERENCE/DOCKET NUMBER:  325800-296
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  201-994-1700
;      TELEFAX:  201-994-1744
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  771 BASE PAIRS
;      TYPE:  NUCLEIC ACID
;      STRANDEDNESS:  SINGLE
;      TOPOLOGY:  LINEAR
;    MOLECULE TYPE:  cDNA
US-08-431-117A-1

  Query Match             20.5%;  Score 769.4;  DB 2;  Length 771;
  Best Local Similarity   99.9%;  Pred. No. 5.9e-206;
  Matches  770;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        159 GAAACTTCTCAGAGAATGCTCCAAAACTCAGCAGTGCTTCTGGTGCTGGTGATCAGTGCT 218
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GAAACTTCTCAGAGAATGCTCCAAAACTCAGCAGTGCTTCTGGTGCTGGTGATCAGTGCT 60

Qy        219 TCTGCAACCCATGAGGCGGAGCAGAATGACTCTGTGAGCCCCAGGAAATCCCGAGTGGCG 278
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TCTGCAACCCATGAGGCGGAGCAGAATGACTCTGTGAGCCCCAGGAAATCCCGAGTGGCG 120

Qy        279 GCTCAAAACTCAGCTGAAGTGGTTCGTTGCCTCAACAGTGCTCTACAGGTCGGCTGCGGG 338
              || ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GCCCAAAACTCAGCTGAAGTGGTTCGTTGCCTCAACAGTGCTCTACAGGTCGGCTGCGGG 180

Qy        339 GCTTTTGCATGCCTGGAAAACTCCACCTGTGACACAGATGGGATGTATGACATCTGTAAA 398
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GCTTTTGCATGCCTGGAAAACTCCACCTGTGACACAGATGGGATGTATGACATCTGTAAA 240

Qy        399 TCCTTCTTGTACAGCGCTGCTAAATTTGACACTCAGGGAAAAGCATTCGTCAAAGAGAGC 458
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TCCTTCTTGTACAGCGCTGCTAAATTTGACACTCAGGGAAAAGCATTCGTCAAAGAGAGC 300

Qy        459 TTAAAATGCATCGCCAACGGGGTCACCTCCAAGGTCTTCCTCGCCATTCGGAGGTGCTCC 518
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TTAAAATGCATCGCCAACGGGGTCACCTCCAAGGTCTTCCTCGCCATTCGGAGGTGCTCC 360

Qy        519 ACTTTCCAAAGGATGATTGCTGAGGTGCAGGAAGAGTGCTACAGCAAGCTGAATGTGTGC 578
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 ACTTTCCAAAGGATGATTGCTGAGGTGCAGGAAGAGTGCTACAGCAAGCTGAATGTGTGC 420

Qy        579 AGCATCGCCAAGCGGAACCCTGAAGCCATCACTGAGGTCGTCCAGCTGCCCAATCACTTC 638
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 AGCATCGCCAAGCGGAACCCTGAAGCCATCACTGAGGTCGTCCAGCTGCCCAATCACTTC 480

Qy        639 TCCAACAGATACTATAACAGACTTGTCCGAAGCCTGCTGGAATGTGATGAAGACACAGTC 698
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 TCCAACAGATACTATAACAGACTTGTCCGAAGCCTGCTGGAATGTGATGAAGACACAGTC 540

Qy        699 AGCACAATCAGAGACAGCCTGATGGAGAAAATTGGGCCTAACATGGCCAGCCTCTTCCAC 758
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 AGCACAATCAGAGACAGCCTGATGGAGAAAATTGGGCCTAACATGGCCAGCCTCTTCCAC 600

Qy        759 ATCCTGCAGACAGACCACTGTGCCCAAACACACCCACGAGCTGACTTCAACAGGAGACGC 818
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 ATCCTGCAGACAGACCACTGTGCCCAAACACACCCACGAGCTGACTTCAACAGGAGACGC 660

Qy        819 ACCAATGAGCCGCAGAAGCTGAAAGTCCTCCTCAGGAACCTCCGAGGTGAGGAGGACTCT 878
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 ACCAATGAGCCGCAGAAGCTGAAAGTCCTCCTCAGGAACCTCCGAGGTGAGGAGGACTCT 720

Qy        879 CCCTCCCACATCAAACGCACATCCCATGAGAGTGCATAACCAGGGAGAGGT 929
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 CCCTCCCACATCAAACGCACATCCCATGAGAGTGCATAACCAGGGAGAGGT 771


RESULT 4
US-08-831-132-1
; Sequence 1, Application US/08831132
; Patent No. 6008322
;  GENERAL INFORMATION:
;    APPLICANT:  Kuestner, Rolf E.
;    APPLICANT:  Conklin, Darrell C.
;    APPLICANT:  Lok, Si
;    APPLICANT:  Buddle, Michele
;    APPLICANT:  Downey, William
;    TITLE OF INVENTION:  STANNIOCALCIN-2
;    NUMBER OF SEQUENCES:  22
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  ZymoGenetics, Inc.
;      STREET:  1201 Eastlake Avenue East
;      CITY:  Seattle
;      STATE:  WA
;      COUNTRY:  USA
;      ZIP:  98102
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/831,132
;      FILING DATE:
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Sawislak, Deborah A.
;      REGISTRATION NUMBER:  37,438
;      REFERENCE/DOCKET NUMBER:  96-01
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  206-442-6672
;      TELEFAX:  206-442-6678
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  906 base pairs
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;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  cDNA
;     FEATURE:
;       NAME/KEY:  sig_peptide
;       LOCATION:  1..72
;     FEATURE:
;       NAME/KEY:  mat_peptide
;       LOCATION:  73..906
;     FEATURE:
;       NAME/KEY:  CDS
;       LOCATION:  1..906
US-08-831-132-1

  Query Match             3.3%;  Score 122.8;  DB 3;  Length 906;
  Best Local Similarity   52.8%;  Pred. No. 1.8e-24;
  Matches  265;  Conservative    0;  Mismatches  237;  Indels    0;  Gaps    0;

Qy        263 GAAATCCCGAGTGGCGGCTCAAAACTCAGCTGAAGTGGTTCGTTGCCTCAACAGTGCTCT 322
              ||||  |||  || |   || ||  |||| ||  |    |  ||  |   ||  |||
Db        123 GAAAGGCCGCCTGTCCCTGCAGAATACAGCGGAGATCCAGCACTGTTTGGTCAACGCTGG 182

Qy        323 ACAGGTCGGCTGCGGGGCTTTTGCATGCCTGGAAAACTCCACCTGTGACACAGATGGGAT 382
                | || || || || |  |||| |||  | || |||  | | ||||| |     ||  |
Db        183 CGATGTGGGGTGTGGCGTGTTTGAATGTTTCGAGAACAACTCTTGTGAGATTCGGGGCTT 242

Qy        383 GTATGACATCTGTAAATCCTTCTTGTACAGCGCTGCTAAATTTGACACTCAGGGAAAAGC 442
                |||  || || |   | ||  || ||| |||||  ||||||||  | |||||  ||  |
Db        243 ACATGGGATTTGCATGACTTTTCTGCACAACGCTGGAAAATTTGATGCCCAGGGCAAGTC 302

Qy        443 ATTCGTCAAAGAGAGCTTAAAATGCATCGCCAACGGGGTCACCTCCAAGGTCTTCCTCGC 502
              ||||  |||||||   ||| |||||  |  ||| |||   |       || | ||  |  |
Db        303 ATTCATCAAAGACGCCTTGAAATGTAAGGCCCACGCTCTGCGGCACAGGTTCGGCTGCAT 362

Qy        503 CATTCGGAGGTGCTCCACTTTCCAAAGGATGATTGCTGAGGTGCAGGAAGAGTGCTACAG 562
                |  |||| |||| |  |  ||      ||| |  |  || |||||   || ||||||
Db        363 AAGCCGGAAGTGCCCGGCCATCAGGGAAATGGTGTCCCAGTTGCAGCGGGAATGCTACCT 422

Qy        563 CAAGCTGAATGTGTGCAGCATCGCCAAGCGGAACCCTGAAGCCATCACTGAGGTCGTCCA 622
              |||||   |  |||||      ||| ||  |||| |    |  ||    ||| |  ||||
Db        423 CAAGCACGACCTGTGCGCGGCTGCCCAGGAGAACACCCGGGTGATAGTGGAGATGATCCA 482

Qy        623 GCTGCCCAATCACTTCTCCAACAGATACTATAACAGACTTGTCCGAAGCCTGCTGGAATG 682
              |     |     |     ||  | |||        || ||       ||||||   ||
Db        483 TTTCAAGGACTTGCTGCTGCACGAACCCTACGTGGACCTCGTGAACTTGCTGCTGACCTG 542

Qy        683 TGATGAAGACACAGTCAGCACAATCAGAGACAGCCTGATGGAGAAAATTGGGCCTAACAT 742
              ||  || ||       | ||||   |||||.||  ||   |  || ||  |||
Db        543 TGGGGAGGAGGTGAAGGAGGCCATCACCCACAGCGTGCAGGTTCAGTGTGAGCAGAACTG 602

Qy        743 GGCCAGCCTCTTCCACATCCTG 764
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Db        603 GGGAAGCCTGTGCTCCATCTTG 624


RESULT 5
US-09-416-150-1
; Sequence 1, Application US/09416150
; Patent No. 6171822
;   GENERAL INFORMATION:
;       APPLICANT: Kuestner, Rolf E.
;                  Conklin, Darrell C.
;                  Lok, Si
;                  Buddle, Michele
;                  Downey, William
;       TITLE OF INVENTION: STANNIOCALCIN-2
;       NUMBER OF SEQUENCES: 22
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: ZymoGenetics, Inc.
;            STREET: 1201 Eastlake Avenue East
;            CITY: Seattle
;            STATE: WA
;            COUNTRY: USA
;            ZIP: 98102
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.25
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/416,150
;            FILING DATE: 11-Oct-1999
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: 08/831,132
;            FILING DATE: <Unknown>
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Sawislak, Deborah A.
;            REGISTRATION NUMBER: 37,438
;            REFERENCE/DOCKET NUMBER: 96-01
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: 206-442-6672
;            TELEFAX: 206-442-6678
;   INFORMATION FOR SEQ ID NO: 1:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 906 base pairs
;            TYPE: nucleic acid
;            STRANDEDNESS: single
;            TOPOLOGY: linear
;       MOLECULE TYPE: cDNA
;       FEATURE:
;            NAME/KEY:  sig_peptide
;            LOCATION:  1..72
;       FEATURE:
;            NAME/KEY:  mat_peptide
;            LOCATION:  73..906
;       FEATURE:
;            NAME/KEY:  CDS
;            LOCATION:  1..906
;       SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-416-150-1

  Query Match             3.3%;  Score 122.8;  DB 4;  Length 906;
  Best Local Similarity   52.8%;  Pred. No. 1.8e-24;
  Matches  265;  Conservative    0;  Mismatches  237;  Indels    0;  Gaps    0;

Qy        263 GAAATCCCGAGTGGCGGCTCAAAACTCAGCTGAAGTGGTTCGTTGCCTCAACAGTGCTCT 322
              ||||  |||  || |   || ||  |||| ||  |    |  ||  |   ||  |||
Db        123 GAAAGGCCGCCTGTCCCTGCAGAATACAGCGGAGATCCAGCACTGTTTGGTCAACGCTGG 182

Qy        323 ACAGGTCGGCTGCGGGGCTTTTGCATGCCTGGAAAACTCCACCTGTGACACAGATGGGAT 382
                | || || || || |  |||| |||  | || |||  | | ||||| |     ||  |
Db        183 CGATGTGGGGTGTGGCGTGTTTGAATGTTTCGAGAACAACTCTTGTGAGATTCGGGGCTT 242

Qy        383 GTATGACATCTGTAAATCCTTCTTGTACAGCGCTGCTAAATTTGACACTCAGGGAAAAGC 442
                |||  || || |   | ||  || ||| |||||  ||||||||  | |||||  ||  |
Db        243 ACATGGGATTTGCATGACTTTTCTGCACAACGCTGGAAAATTTGATGCCCAGGGCAAGTC 302

Qy        443 ATTCGTCAAAGAGAGCTTAAAATGCATCGCCAACGGGGTCACCTCCAAGGTCTTCCTCGC 502
              ||||  |||||||   ||| |||||  |  ||| |||   |       || | ||  |  |
Db        303 ATTCATCAAAGACGCCTTGAAATGTAAGGCCCACGCTCTGCGGCACAGGTTCGGCTGCAT 362

Qy        503 CATTCGGAGGTGCTCCACTTTCCAAAGGATGATTGCTGAGGTGCAGGAAGAGTGCTACAG 562
                |  |||| |||| |  |  ||      ||| |  |  || |||||   || ||||||
Db        363 AAGCCGGAAGTGCCCGGCCATCAGGGAAATGGTGTCCCAGTTGCAGCGGGAATGCTACCT 422

Qy        563 CAAGCTGAATGTGTGCAGCATCGCCAAGCGGAACCCTGAAGCCATCACTGAGGTCGTCCA 622
              |||||   |  |||||      ||| ||  |||| |    |  ||    ||| |  ||||
Db        423 CAAGCACGACCTGTGCGCGGCTGCCCAGGAGAACACCCGGGTGATAGTGGAGATGATCCA 482

Qy        623 GCTGCCCAATCACTTCTCCAACAGATACTATAACAGACTTGTCCGAAGCCTGCTGGAATG 682
              |     |     |     ||  | |||        || ||       ||||||   ||
Db        483 TTTCAAGGACTTGCTGCTGCACGAACCCTACGTGGACCTCGTGAACTTGCTGCTGACCTG 542

Qy        683 TGATGAAGACACAGTCAGCACAATCAGAGACAGCCTGATGGAGAAAATTGGGCCTAACAT 742
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Db        543 TGGGGAGGAGGTGAAGGAGGCCATCACCCACAGCGTGCAGGTTCAGTGTGAGCAGAACTG 602

Qy        743 GGCCAGCCTCTTCCACATCCTG 764
Db        603 GGGAAGCCTGTGCTCCATCTTG 624


RESULT 6
US-08-460-529B-1
; Sequence 1, Application US/08460529B
; Patent No. 5994103
;  GENERAL INFORMATION:
;    APPLICANT:  OLSEN, ET AL.
;    TITLE OF INVENTION:  Human Stanniocalcin-alpha
;    NUMBER OF SEQUENCES:  10
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  CARELLA, BYRNE, BAIN, GILFILLAN,
;      ADDRESSEE:  CECCHI, STEWART & OLSTEIN
;      STREET:  6 BECKER FARM ROAD
;      CITY:  ROSELAND
;      STATE:  NEW JERSEY
;      COUNTRY:  USA
;      ZIP:  07068
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5 INCH DISKETTE
;      COMPUTER:  IBM PS/2
;      OPERATING SYSTEM:  MS-DOS
;      SOFTWARE:  WORD PERFECT 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/460,529B
;      FILING DATE:  June 2, 1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US94/13206
;      FILING DATE:  10 NOV 1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  MULLINS, J.G.
;      REGISTRATION NUMBER:  33,073
;      REFERENCE/DOCKET NUMBER:  325800-334  (PF143)
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  201-994-1700
;      TELEFAX:  201-994-1744
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  892 BASE PAIRS
;      TYPE:  NUCLEIC ACID
;      STRANDEDNESS:  SINGLE
;      TOPOLOGY:  LINEAR
;    MOLECULE TYPE:  cDNA
US-08-460-529B-1

  Query Match             3.2%;  Score 121.2;  DB 2;  Length 892;
  Best Local Similarity   52.6%;  Pred. No. 5.1e-24;
  Matches  264;  Conservative    0;  Mismatches  238;  Indels    0;  Gaps    0;

Qy        263 GAAATCCCGAGTGGCGGCTCAAAACTCAGCTGAAGTGGTTCGTTGCCTCAACAGTGCTCT 322
Db        204 GAAAGGCCGCCTGTCCCTGCAGAATACAGCGGAGATCCAGCACTGTTTGGTCAACGCTGG 263

Qy        323 ACAGGTCGGCTGCGGGGCTTTTGCATGCCTGGAAAACTCCACCTGTGACACAGATGGGAT 382
Db        264 CGATGTGGGGTGTGGCGTGTTTGAATGTTTCGAGAACAACTCTTGTGAGATTCGGGGCTT 323

Qy        383 GTATGACATCTGTAAATCCTTCTTGTACAGCGCTGCTAAATTTGACACTCAGGGAAAAGC 442
Db        324 ACATGGGATTTGCATGACTTTTCTGCACAACGCTGGAAAATTTGATGCCCAGGGCAAGTC 383

Qy        443 ATTCGTCAAAGAGAGCTTAAAATGCATCGCCAACGGGGTCACCTCCAAGGTCTTCCTCGC 502
Db        384 ATTCATCAAAGACGCCTTGAAATGTAAGGCCCACGCTCTGCGGCACAGGTTCGGCTGCAT 443

Qy        503 CATTCGGAGGTGCTCCACTTTCCAAAGGATGATTGCTGAGGTGCAGGAAGAGTGCTACAG 562
Db        444 AAGCCGGAAGTGCCCGGCCATCAGGGAAATGGTGTCCCAGTTGGAGCGGGAATGCTACCT 503

Qy        563 CAAGCTGAATGTGTGCAGCATCGCCAAGCGGAACCCTGAAGCCATCACTGAGGTCGTCCA 622
Db        504 CAAGCACGACCTGTGCGCGGCTGCCCAGGAGAACACCCGGGTGATAGTGGAGATGATCCA 563

Qy        623 GCTGCCCAATCACTTCTCCAACAGATACTATAACAGACTTGTCCGAAGCCTGCTGGAATG 682
Db        564 TTTCAAGGACTTGCTGCTGCACGAACCCTACGTGGACCTCGTGAACTTGCTGCTGACCTG 623

Qy        683 TGATGAAGACACAGTCAGCACAATCAGAGACAGCCTGATGGAGAAAATTGGGCCTAACAT 742
Db        624 TGGGGAGGAGGTGAAGGAGGCCATCACCCACAGCGTGCAGGTTCAGTGTGAGCAGAACTG 683

Qy        743 GGCCAGCCTCTTCCACATCCTG 764
Db        684 GGGAAGCCTGTGCTCCATCTTG 705


RESULT 7
US-08-831-132-13
; Sequence 13, Application US/08831132
; Patent No. 6008322
;  GENERAL INFORMATION:
;    APPLICANT:  Kuestner, Rolf E.
;    APPLICANT:  Conklin, Darrell C.
;    APPLICANT:  Lok, Si
;    APPLICANT:  Buddle, Michele
;    APPLICANT:  Downey, William
;    TITLE OF INVENTION:  STANNIOCALCIN-2
;    NUMBER OF SEQUENCES:  22
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  ZymoGenetics, Inc.
;      STREET:  1201 Eastlake Avenue East
;      CITY:  Seattle
;      STATE:  WA
;      COUNTRY:  USA
;      ZIP:  98102
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/831,132
;      FILING DATE:
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Sawislak, Deborah A.
;      REGISTRATION NUMBER:  37,438
;      REFERENCE/DOCKET NUMBER:  96-01
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  206-442-6672
;      TELEFAX:  206-442-6678
;  INFORMATION FOR SEQ ID NO:  13:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  888 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  sig_peptide
;      LOCATION:  1..72
;    FEATURE:
;      NAME/KEY:  mat_peptide
;      LOCATION:  73..888
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  1..888
US-08-831-132-13
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  Query Match             2.9%;  Score 110;  DB 3;  Length 888;
  Best Local Similarity   51.2%;  Pred. No. 7e-21;
  Matches  257;  Conservative    0;  Mismatches  245;  Indels    0;  Gaps    0;

Qy        263 GAAATCCCGAGTGGCGGCTCAAAACTCAGCTGAAGTGGTTCGTTGCCTCAACAGTGCTCT 322
              ||||  |||  || |    || ||| |||| ||  |    .|  ||  |   || |||
Db        123 GAAAGGCCGTCTGTCCCTGCAGAACACAGCGGAGATCCAGCACTGTTTGGTCAATGCCGG 182

Qy        323 ACAGGTCGGCTGCGGGGCTTTTGCATGCCTGGAAAACTCCACCTGTGACACAGATGGGAT 382
                | || ||||| || |  ||||  ||  | || |||  | | ||||| |   | || |
Db        183 GGACGTGGGCTGTGGTGTGTTTGAGTGTTTCGAGAACAACTCTTGTGAAATCCAGGGTTT 242

Qy        383 GTATGACATCTGTAAATCCTTCTTGTACAGCGCTGCTAAATTTGACACTCAGGGAAAAGC 442
                |||  || || |   | ||  || ||| |||||  ||||| ||  | ||||||||  |
Db        243 ACATGGGATTTGCATGACGTTTCTGCACAACGCTGGAAAATTCGATGCCCAGGGAAAGTC 302

Qy        443 ATTCGTCAAAGAGAGCTTAAAATGCATCGCCAACGGGGTCACCTCCAAGGTCTTCCTCGC 502
              |||| |||| ||   | | |  |||| ||| | |   |        ||  |   |  |
Db        303 ATTCATCAAGGATGCCCTGAGGTGCAAGGCCCATGCCCTGCGTCATAAATTTGGCTGCAT 362

Qy        503 CATTCGGAGGTGCTCCACTTTCCAAAGGATGATTGCTGAGGTGCAGGAAGAGTGCTACAG 562
              ||   ||| |||  |  |  |        ||| ||    || |||||  || |||||
Db        363 CAGCAGGAAGTGTCCAGCAATTAGGGAAATGGTTTTCCAGTTGCAGAGGGAATGCTATCT 422

Qy        563 CAAGCTGAATGTGTGCAGCATCGCCAAGCGGAACCCTGAAGCCATCACTGAGGTCGTCCA 622
              ||||   | |||||  |   ||| ||  ||||   |  |  ||    ||| |  | ||
Db        423 GAAGCATGACCTGTGCTCCGCAGCCCAGGAGAACGTCGGTGTGATTGTGGAGATGATTCA 482

Qy        623 GCTGCCCAATCACTTCTCCAACAGATACTATAACAGACTTGTCCGAAGCCTGCTGGAATG 682
                |     ||| | |      |       ||||       |||||        ||||||   ||
Db        483 TTTCAAGGATCTCCTGCTGCATGAGCCCTATGTGGACCTTGTGAACCTGCTGCTGACCTG 542

Qy        683 TGATGAAGACACAGTCAGCACAATCAGAGACAGCCTGATGGAGAAAATTGGGCCTAACAT 742
              |  |||||           || |||    |||| |   ||   |  ||  | | |
Db        543 CGGGGAAGATGTGAAGGAGGCAGTCACCCGCAGCGTCCAGGCTCAGTGTGAACAGAGCTG 602

Qy        743 GGCCAGCCTCTTCCACATCCTG 764
              ||   |||||| |  |||||||
Db        603 GGGAGGCCTCTGCTCCATCCTG 624


RESULT 8
US-09-416-150-13
; Sequence 13, Application US/09416150
; Patent No. 6171822
;   GENERAL INFORMATION:
;        APPLICANT: Kuestner, Rolf E.
;                   Conklin, Darrell C.
;                   Lok, Si
;                   Buddle, Michele
;                   Downey, William
;        TITLE OF INVENTION: STANNIOCALCIN-2
;        NUMBER OF SEQUENCES: 22
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: ZymoGenetics, Inc.
;             STREET: 1201 Eastlake Avenue East
;             CITY: Seattle
;             STATE: WA
;             COUNTRY: USA
;             ZIP: 98102
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.25
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/416,150
;             FILING DATE: 11-Oct-1999
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 08/831,132
;             FILING DATE: <Unknown>
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Sawislak, Deborah A.
;             REGISTRATION NUMBER: 37,438
;             REFERENCE/DOCKET NUMBER: 96-01
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 206-442-6672
;             TELEFAX: 206-442-6678
;   INFORMATION FOR SEQ ID NO: 13:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 888 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: cDNA
;        FEATURE:
;             NAME/KEY:  sig_peptide
;             LOCATION:  1..72
;        FEATURE:
;             NAME/KEY:  mat_peptide
;             LOCATION:  73..888
;        FEATURE:
;             NAME/KEY:  CDS
;             LOCATION:  1..888
;        SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-09-416-150-13

  Query Match             2.9%;  Score 110;  DB 4;  Length 888;
  Best Local Similarity   51.2%;  Pred. No. 7e-21;
  Matches  257;  Conservative    0;  Mismatches  245;  Indels    0;  Gaps    0;

Qy        263 GAAATCCCGAGTGGCGGCTCAAAACTCAGCTGAAGTGGTTCGTTGCCTCAACAGTGCTCT 322
              ||||  |||  || |    || ||| |||| ||  |    |  ||  |   || |||
Db        123 GAAAGGCCGTCTGTCCCTGCAGAACACAGCGGAGATCCAGCACTGTTTGGTCAATGCCGG 182

Qy        323 ACAGGTCGGCTGCGGGGCTTTTGCATGCCTGGAAAACTCCACCTGTGACACAGATGGGAT 382
                | || ||||| || |  ||||  ||  | || |||  | | ||||| |   | || |
Db        183 GGACGTGGGCTGTGGTGTGTTTGAGTGTTTCGAGAACAACTCTTGTGAAATCCAGGGTTT 242

Qy        383 GTATGACATCTGTAAATCCTTCTTGTACAGCGCTGCTAAATTTGACACTCAGGGAAAAGC 442
                |||  || || |   | ||  || ||| |||||  ||||| ||  | ||||||||  |
Db        243 ACATGGGATTTGCATGACGTTTCTGCACAACGCTGGAAAATTCGATGCCCAGGGAAAGTC 302

Qy        443 ATTCGTCAAAGAGAGCTTAAAATGCATCGCCAACGGGGTCACCTCCAAGGTCTTCCTCGC 502
              |||| |||| ||   | | |  |||| ||| | |   |        ||  |   |  |
Db        303 ATTCATCAAGGATGCCCTGAGGTGCAAGGCCCATGCCCTGCGTCATAAATTTGGCTGCAT 362

Qy        503 CATTCGGAGGTGCTCCACTTTCCAAAGGATGATTGCTGAGGTGCAGGAAGAGTGCTACAG 562
              ||   ||| |||  |  |  |        ||| ||    || |||||  || |||||
Db        363 CAGCAGGAAGTGTCCAGCAATTAGGGAAATGGTTTTCCAGTTGCAGAGGGAATGCTATCT 422

Qy        563 CAAGCTGAATGTGTGCAGCATCGCCAAGCGGAACCCTGAAGCCATCACTGAGGTCGTCCA 622
              ||||   | |||||  |   ||| ||  ||||   |  |  ||    ||| |  | ||
Db        423 GAAGCATGACCTGTGCTCCGCAGCCCAGGAGAACGTCGGTGTGATTGTGGAGATGATTCA 482

Qy        623 GCTGCCCAATCACTTCTCCAACAGATACTATAACAGACTTGTCCGAAGCCTGCTGGAATG 682
                |     ||| | |      |       ||||       |||||        ||||||   ||
Db        483 TTTCAAGGATCTCCTGCTGCATGAGCCCTATGTGGACCTTGTGAACCTGCTGCTGACCTG 542

Qy        683 TGATGAAGACACAGTCAGCACAATCAGAGACAGCCTGATGGAGAAAATTGGGCCTAACAT 742
              |  |||||           || |||    |||| |   ||   |  ||  | | |
Db        543 CGGGGAAGATGTGAAGGAGGCAGTCACCCGCAGCGTCCAGGCTCAGTGTGAACAGAGCTG 602

Qy        743 GGCCAGCCTCTTCCACATCCTG 764
              ||   |||||| |  |||||||
Db        603 GGGAGGCCTCTGCTCCATCCTG 624


RESULT 9
US-08-232-463-14
; Sequence 14, Application US/08232463
; Patent No. 5670367
;  GENERAL INFORMATION:
;    APPLICANT:  DORNER, F.
;    APPLICANT:  SCHEIFLINGER, F.
```

```
;    APPLICANT:  FALKNER, F. G.
;    TITLE OF INVENTION:  RECOMBINANT FOWLPOX VIRUS
;    NUMBER OF SEQUENCES:  52
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Foley & Lardner
;      STREET:  1800 Diagonal Road, Suite 500
;      CITY:  Alexandria
;      STATE:  VA
;      COUNTRY:  USA
;      ZIP:  22313-0299
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/232,463
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/935,313
;      FILING DATE:
;      APPLICATION NUMBER:  EP 91 114 300.6
;      FILING DATE:  26-AUG-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  BENT, Stephen A.
;      REGISTRATION NUMBER:  29,768
;      REFERENCE/DOCKET NUMBER:  30472/114 IMMU
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (703)836-9300
;      TELEFAX:  (703)683-4109
;      TELEX:  899149
;  INFORMATION FOR SEQ ID NO:  14:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  7218 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    IMMEDIATE SOURCE:
;      CLONE:  pTZgpt-F1s
US-08-232-463-14

  Query Match             2.2%;  Score 82;  DB 1;  Length 7218;
  Best Local Similarity   5.4%;  Pred. No. 1.9e-12;
  Matches   22;  Conservative  242;  Mismatches  146;  Indels    0;  Gaps    0;

Qy       3138 TTCTCTCTTTCTTCAGTTCAGTAGATTTCCTTTTTTCTTNTCTNTTNTTTTTTNTTTTTT 3197
              |:::::::::::::  :::  :   :::::::::::::: ::: :: :::::: ::::::
Db       1066 TYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY.1125

Qy       3198 TGGCTGTGACCTCTTCAAACCGTGGTACCCCCCCTTTTCTCCCCACGATGATATCTATAT 3257
              :  :: :  :::::::   :: :  : ::::::::::::::::: :  :  : ::: : :
Db       1126 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1185

Qy       3258 ATGTATCTACAATACATATATCTACACATACAGAAAGAAGCAGTTCTCACAATGTTGCTA 3317
              : : ::: :  : : : : ::: : : : :          :  ::::: :  : :: ::
Db       1186 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1245

Qy       3318 GTTTTTTGCTTCTCTTTCCCCCACCCTACTCCCTCCAATTCCCCCTTAAACTTCCAAAGC 3377
              :::::: :::::::::::::: :::: :::::::::  :::::::::   :::::    :
Db       1246 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1305

Qy       3378 TTCGTCTTGTGTTTGCTGCAGAGTGATTCGGGGGCTGACCTAGACCAGTTTGCATGATTC 3437
              ::: :::: : ::: :: :   :  :::    ::  :::   ::  ::: : :  :::
Db       1306 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1365

Qy       3438 TTCTCTTGTGATTTGGTTGCACTTTAGACATTTTTGTGCCATTATATTTGCATTATGTAT 3497
              ::::::: :  :::  :: : ::::   : ::::: : :: :: : ::: : :: : : :
Db       1366 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1425

Qy       3498 TTATAATTTAAATGATATTTAGGTTTTTGGCTGAGTACTGGAATAAACAG 3547
              :: :  :::  |  | |||    | | |   | | |||| | ||| | ||
Db       1426 YYYYYYYYYGTACCAAATTCTTCTATCTCTTTAACTACTTGCATAGATAG 1475
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RESULT 10
5175095-4/c
;Patent No.5175095
;    APPLICANT: Martineau, Belinda M.;Houck, Catherine M.
;    TITLE OF INVENTION: OVARY TISSUE TRANSCRIPTIONAL FACTORS
;    NUMBER OF SEQUENCES: 9
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/554,195
;      FILING DATE: 17-JUL-1990
;SEQ ID NO:4:
;      LENGTH: 4383
5175095-4

  Query Match             1.2%;  Score 44;  DB 6;  Length 4383;
  Best Local Similarity   48.8%;  Pred. No. 0.064;
  Matches  119;  Conservative    0;  Mismatches  125;  Indels    0;  Gaps    0;

Qy       3493 TGTATTTATAATTTAAATGATATTTAGGTTTTTGGCTGAGTACTGGAATAAACAGTGAGC 3552
              ||||| || | || |  |  |||||   |||||   |||||||    || |  |||  |
Db       1525 TGTATATACACTTGATTTTTTATTTTATTTTTTTTGTGAGTACATCTATTAGTAGTTTGG 1466

Qy       3553 ATATCTGGTATATGTCATTATTTATTGTTAAATTACATTTTTAAGCTCCATGTGCATATA 3612
                ||        | | ||||||||     |||   ||| |||||        |      ||
Db       1465 CAATAGACATATTTTTATTATTTAAGCAAAAAAATCATCTTTAATTAATTGGGTGGAGTA 1406

Qy       3613 AAGGTTATGAAACATATCATGGTAATGACAGATGCAAGTTATTTTATTTGCTTATTTTTA 3672
                |    ||    || ||  | |  |||| |    |   | |||| | ||   || ||||
Db       1405 CATTAGATATTTCAGATTCTAGCTATGATTGTAAAATAGTTTTTTGTGTGGAAATATTTA 1346

Qy       3673 TAATTAAAGATGCCATAGCATAATATGAAGCCTTTGGTGAATTCCTTCTAAGATAAAAAT 3732
                | ||  ||  |   |   | | |||        | | |   |||||| || ||  |
Db       1345 CCCATTAATGTGAGACCACTCTACACGAATATAAATTTAATTATTTTCTAATATGAATGT 1286

Qy       3733 AATA 3736
                | |
Db       1285 CAAA 1282
```

```
RESULT 11
US-09-402-002-3/c
; Sequence 3, Application US/09402002
; Patent No. 6225453
;  GENERAL INFORMATION:
;    APPLICANT:  Ueyama, Hiroshi
;    APPLICANT:  Abe, Kanako
;    APPLICANT:  Keshi, Hiroyuki
;    APPLICANT:  Matsuhisa, Akio
;    TITLE OF INVENTION:  PROBES FOR THE DIAGNOSIS OF INFECTIONS
;    TITLE OF INVENTION:  CAUSED BY KLEBSIELLA PNEUMONIAE
;    NUMBER OF SEQUENCES:  7
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Marshall, O'Toole, Gerstein, Murray & Borun
;      STREET:  233 South Wacker Drive/6300 Sears Tower
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  United States of America
;      ZIP:  60606
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/402,002
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 1997-71082
;      FILING DATE:  25-MAR-1997
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/JP98/01286
```

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;      FILING DATE:  23-MAR-1998
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Cawley, Jr., Thomas A.
;      REGISTRATION NUMBER:  40,944
;      REFERENCE/DOCKET NUMBER:  19036/36276
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (312) 474-6300
;      TELEFAX:  (312) 474-0448
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1988 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    ORIGINAL SOURCE:
;      ORGANISM:  Klebsiella pneumoniae
;      STRAIN:  Clinical Isolate KP-98-22
;    FEATURE:
;      NAME/KEY:  misc_feature
;      LOCATION:  1930
;      OTHER INFORMATION:  /note= "N= adenine or cytosine or
;      OTHER INFORMATION:  guanine or thymine"
US-09-402-002-3

  Query Match             1.2%;  Score 43.4;  DB 4;  Length 1988;
  Best Local Similarity   50.7%;  Pred. No. 0.057;
  Matches  104;  Conservative    0;  Mismatches  101;  Indels    0;  Gaps    0;

Qy       3479 TTATATTTGCATTATGTATTTATAATTTAAATGATATTTAGGTTTTTGGCTGAGTACTGG 3538
              | || ||    |  | | |||    || |  |  || |||| |  ||     |    ||
Db        206 TCATTTTATTCTCCTTTGTTTTCTGTTCATTTATTAATTAGCTAATTAAAATATATTTGT 147

Qy       3539 AATAAACAGTGAGCATATCTGGTATATGTCATTATTTATTGTTAAATTACATTTTTAAGC 3598
              |  || | |   || |||| |  ||| | | |  || ||||     |  || | |||||
Db        146 CAATAATATTATACACATCTTGACTATATTAATTATTGTTGTATTTATTTATATGTAAGC 87

Qy       3599 TCCATGTGCATATAAAGGTTATGAAACATATCATGGTAATGACAGATGCAAGTTATTTTA 3658
                ||    |||  |||| || |||||| || |   ||   |  |  | |||||||
Db         86 CAAATAAAAATAATAAGGATACGAAACAAATAAACATACAAAATGGAGAAAGTTATGAAG 27

Qy       3659 TTTGCTTATTTTTATAATTAAAGAT 3683
                  || ||| || |  ||| |
Db         26 AAGAAAAATCTTTTTATTCTAAGCT 2


RESULT 12
US-09-014-969-14/c
; Sequence 14, Application US/09014969
; Patent No. 5965397
;  GENERAL INFORMATION:
;    APPLICANT:  Jacobs, Kenneth
;    APPLICANT:  McCoy, John M.
;    APPLICANT:  LaVallie, Edward R.
;    APPLICANT:  Racie, Lisa A.
;    APPLICANT:  Merberg, David
;    APPLICANT:  Treacy, Maurice
;    APPLICANT:  Spaulding, Vikki
;    APPLICANT:  Agostino, Michael J.
;    TITLE OF INVENTION:  SECRETED PROTEINS AND POLYNUCLEOTIDES
;    TITLE OF INVENTION:  ENCODING THEM
;    NUMBER OF SEQUENCES:  32
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Genetics Institute, Inc.
;      STREET:  87 CambridgePark Drive
;      CITY:  Cambridge
;      STATE:  MA
;      COUNTRY:  U.S.A.
;      ZIP:  02140
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/014,969
;      FILING DATE:
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Sprunger, Suzanne A.
;      REGISTRATION NUMBER:  41,323
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617) 498-8284
;      TELEFAX:  (617) 876-5851
;  INFORMATION FOR SEQ ID NO:  14:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2447 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-09-014-969-14

  Query Match             1.1%;  Score 43.2;  DB 2;  Length 2447;
  Best Local Similarity   53.2%;  Pred. No. 0.074;
  Matches   84;  Conservative    1;  Mismatches   73;  Indels    0;  Gaps    0;

Qy       3137 TTTCTCTCTTTCTTCAGTTCAGTAGATTTCCTTTTTTCTTNTCTNTTNTTTTTTNTTTTT 3196
              ||| | | ||| ||   ||   |   |||  |||||| || | | || ||||||  |:|||
Db       2315 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTYTTT 2256

Qy       3197 TTGGCTGTGACCTCTTCAAACCGTGGTACCCCCCCTTTTCTCCCCACGATGATATCTATA 3256
              ||   | |   |||   |||   |  |   | | |||       ||  || | ||  | |
Db       2255 TTTTTTTTTTTCTCCCAAAAGGTTTATTTGTCACATTTAAAGTACAAAATCAAATACACA 2196

Qy       3257 TATGTATCTACAATACATATATCTACACATACAGAAAG 3294
              ||  |  ||    |   |||| |||| ||  | | ||
Db       2195 GATCCAGATATGTGAACCATATATACATATCTATACAG 2158


RESULT 13
US-08-232-463-14/c
; Sequence 14, Application US/08232463
; Patent No. 5670367
;  GENERAL INFORMATION:
;    APPLICANT:  DORNER, F.
;    APPLICANT:  SCHEIFLINGER, F.
;    APPLICANT:  FALKNER, F. G.
;    TITLE OF INVENTION:  RECOMBINANT FOWLPOX VIRUS
;    NUMBER OF SEQUENCES:  52
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Foley & Lardner
;      STREET:  1800 Diagonal Road, Suite 500
;      CITY:  Alexandria
;      STATE:  VA
;      COUNTRY:  USA
;      ZIP:  22313-0299
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/232,463
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/935,313
;      FILING DATE:
;      APPLICATION NUMBER:  EP 91 114 300.6
;      FILING DATE:  26-AUG-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  BENT, Stephen A.
;      REGISTRATION NUMBER:  29,768
;      REFERENCE/DOCKET NUMBER:  30472/114 IMMU
;    TELECOMMUNICATION INFORMATION:
```

```
;      TELEPHONE:  (703)836-9300
;      TELEFAX:  (703)683-4109
;      TELEX:  899149
;  INFORMATION FOR SEQ ID NO:  14:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  7218 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    IMMEDIATE SOURCE:
;      CLONE:  pTZgpt-F1s
US-08-232-463-14

  Query Match             1.1%;  Score 42.8;  DB 1;  Length 7218;
  Best Local Similarity   4.5%;  Pred. No. 0.19;
  Matches   14;  Conservative  156;  Mismatches  138;  Indels    0;  Gaps    0;

Qy       2548 AAAGGTCAATGTCAAGAGAGGAAGAGAGGGAGGAGGGGTAGGACTGCAGGGGCCACTCCA 2607
              :::::  :: :  :::::::::::::::::::::::::: ::::  : :::::  :    :
Db       1348 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1289

Qy       2608 AACTCGCTTAGGTAGAAACTATTGGTGCTTGACTCTCACTAGGCTAAACTCAAGATTTGA 2667
              ::   :  ::: ::::::  :  :: :   ::      :  :::  :::   ::::   ::
Db       1288 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1229

Qy       2668 CCAAATCGAGTGATAGGGATCCTGGTGGGAGGAGAGAGGGCACATCTCCAGAAAAATGAA 2727
                :::  ::: :: :::::    :: :::::::::::::: : :     ::::::: :::
Db       1228 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1169

Qy       2728 AAGCAATACAACTTTACCATAAAGCCTTTAAAACCAGTAACGTGCTGCTCAAGGACCAAG 2787
              ::: :: : ::    :  : ::::    :::::  :: :: : :  :   :::::  :::
Db       1168 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1109

Qy       2788 AGCAATTNNNNNNNNNNNNNNNNNNNNNNNNNNNNCAAACATTGCTGCCTTTGTCCCC 2847
              :: ::                          ::: || ||   ||   ||  |
Db       1108 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRATCGCAAGCTCCCTCGAC 1049

Qy       2848 ACACAGCC 2855
                |||||
Db       1048 CTGCAGCC 1041


RESULT 14
US-08-487-826B-13/c
; Sequence 13, Application US/08487826B
; Patent No. 5993827
;  GENERAL INFORMATION:
;    APPLICANT:  Sim, Kim L.
;    APPLICANT:  Chitnis, Chetan
;    APPLICANT:  Miller, Louis H.
;    APPLICANT:  Peterson, David S.
;    APPLICANT:  Su, Xin-zhaun
;    APPLICANT:  Wellems, Thomas E.
;    TITLE OF INVENTION:  BINDING DOMAINS FROM PLASMODIUM VIVAX
;    TITLE OF INVENTION:  AND PLASMODIUM FALCIPARUM ERYTHROCYTE BINDING PROTEINS
;    NUMBER OF SEQUENCES:  45
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Knobbe Martens Olson & Bear
;      STREET:  620 Newport Center Drive  16th Floor
;      CITY:  Newport Beach
;      STATE:  California
;      COUNTRY:  US
;      ZIP:  92660
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/487,826B
;      FILING DATE:  10-SEP-1993
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Israelsen, Ned
;      REGISTRATION NUMBER:  29,655
;      REFERENCE/DOCKET NUMBER:  NIH121.001CP1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (619) 235-8550
;      TELEFAX:  (619) 235-0176
;  INFORMATION FOR SEQ ID NO:  13:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  19124 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
US-08-487-826B-13

  Query Match             1.1%;  Score 41.4;  DB 2;  Length 19124;
  Best Local Similarity   46.4%;  Pred. No. 0.88;
  Matches  135;  Conservative    0;  Mismatches  156;  Indels    0;  Gaps    0;

Qy       3431 ATGATTCTTCTCTTGTGATTTGGTTGCACTTTAGACATTTTTGTGCCATTATATTTGCAT 3490
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RESULT 15
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; Sequence 22, Application US/08953326
; Patent No. 6251872
; GENERAL INFORMATION:
;  APPLICANT: Barbet, Anthony F.
;  APPLICANT: Ganta, Roman R.
;  APPLICANT: McGuire, Travis C.
;  APPLICANT: Burridge, Michael J.
;  APPLICANT: Nyika, Aceme
;  APPLICANT: Rurangirwa, Fred R.
;  APPLICANT: Mahan, Suman M.
;  TITLE OF INVENTION: Nucleic Acid Vaccines Against Rickettsial Diseases of
;  TITLE OF INVENTION: Animals and Humans
;  FILE REFERENCE: UF-167C1
;  CURRENT APPLICATION NUMBER: US/08/953,326
;  CURRENT FILING DATE: 1997-10-17
;  EARLIER APPLICATION NUMBER: 08/953,326
;  EARLIER FILING DATE: 1997-10-17
;  EARLIER APPLICATION NUMBER: 08/733,230
;  EARLIER FILING DATE: 1996-10-17
;  NUMBER OF SEQ ID NOS: 24
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 22
;   LENGTH: 618
;   TYPE: DNA
;   ORGANISM: Ehrlichia chaffeensis
US-08-953-326-22

  Query Match             1.1%;  Score 40.4;  DB 4;  Length 618;
  Best Local Similarity   46.7%;  Pred. No. 0.19;
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Matches 128; Conservative 0; Mismatches 146; Indels 0; Gaps 0;

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Qy       3484 TTTGCATTATGTATTTATAATTTAAATGATATTTAGGTTTTTGGCTGAGTACTGGAATAA 3543
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Qy       3664 TTATTTTTATAATTAAAGATGCCATAGCATAATA 3697
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Db        276 TGCTATTCCTAATTCAGCAGGGCAGATGCTTTTA 243
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Search completed: June 9, 2003, 13:11:14
Job time : 206 secs

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: June 9, 2003, 12:58:53 ; Search time 484 Seconds
(without alignments)
10878.222 Million cell updates/sec

Title: US-09-705-500A-2
Perfect score: 3762
Sequence: 1 ggtggcagcagcagcatcac.....tgttacgttttattggtttc 3762

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 870385 seqs, 699768693 residues

Total number of hits satisfying chosen parameters: 1740770

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_NA:*
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13: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
14: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	3658	97.2	3765	12	US-10-044-090-638	Sequence 638, App
	2	3650.6	97.0	3897	9	US-10-198-846-13651	Sequence 13651, A
	3	2311.6	61.4	2572	10	US-09-925-300-486	Sequence 486, App
	4	1226	32.6	1283	10	US-09-840-989A-1	Sequence 1, Appli
	5	769.4	20.5	771	12	US-10-116-051-1	Sequence 1, Appli
	6	552	14.7	585	10	US-09-778-320-149	Sequence 149, App
	7	552	14.7	585	10	US-09-910-689-149	Sequence 149, App
	8	552	14.7	585	12	US-10-010-742-149	Sequence 149, App
c	9	482.4	12.8	510	9	US-09-736-457-4	Sequence 4, Appli
c	10	482.4	12.8	510	9	US-09-902-941-4	Sequence 4, Appli
c	11	482.4	12.8	510	9	US-09-849-626-4	Sequence 4, Appli
c	12	482.4	12.8	510	9	US-10-017-754-4	Sequence 4, Appli
c	13	471.4	12.5	473	9	US-10-060-036-2677	Sequence 2677, Ap
	14	436	11.6	436	9	US-09-918-995-33032	Sequence 33032, A
	15	320	8.5	420	10	US-09-778-320-141	Sequence 141, App
	16	320	8.5	420	10	US-09-910-689-141	Sequence 141, App
	17	320	8.5	420	12	US-10-010-742-141	Sequence 141, App
c	18	237.2	6.3	1074	9	US-10-198-846-7201	Sequence 7201, Ap
c	19	235.4	6.3	263	10	US-09-880-107-249	Sequence 249, App
	20	230.6	6.1	401	10	US-09-960-352-4108	Sequence 4108, Ap
c	21	214.8	5.7	219	10	US-09-864-761-21309	Sequence 21309, A
c	22	123.8	3.3	362	10	US-09-864-761-4563	Sequence 4563, Ap
	23	122.8	3.3	2759	9	US-10-198-846-9993	Sequence 9993, Ap
	24	122.8	3.3	4173	9	US-10-071-766-128	Sequence 128, App
	25	121.2	3.2	892	10	US-09-361-736-1	Sequence 1, Appli
c	26	120.6	3.2	879	9	US-10-198-846-5049	Sequence 5049, Ap
c	27	64.6	1.7	432	9	US-10-198-846-12603	Sequence 12603, A
	28	53.6	1.4	5689	9	US-10-239-676-90	Sequence 90, Appl
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	30	49.6	1.3	393	10	US-09-960-352-4582	Sequence 4582, Ap
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	34	46.8	1.2	6544	9	US-10-239-676-46	Sequence 46, Appl
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	36	46.4	1.2	7657	9	US-10-239-676-185	Sequence 185, App
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	38	46	1.2	516	10	US-09-960-352-5785	Sequence 5785, Ap
	39	45.8	1.2	479	10	US-09-960-352-12872	Sequence 12872, A
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c	41	45.4	1.2	335913	9	US-09-754-853A-3	Sequence 3, Appli
	42	44.8	1.2	5337	9	US-10-239-676-137	Sequence 137, App
	43	44.8	1.2	6204	9	US-10-239-676-190	Sequence 190, App
	44	44.8	1.2	6478	9	US-10-239-676-124	Sequence 124, App
	45	44.4	1.2	11036	9	US-10-239-676-117	Sequence 117, App

ALIGNMENTS

RESULT 1
US-10-044-090-638
; Sequence 638, Application US/10044090
; Patent No. US20020137081A1
; GENERAL INFORMATION:
; APPLICANT: Olga Bandman
; TITLE OF INVENTION: GENES DIFFERENTIALLY EXPRESSED IN VASCULAR TISSUE ACTIVATION
; FILE REFERENCE: PA-0028 US
; CURRENT APPLICATION NUMBER: US/10/044,090
; CURRENT FILING DATE: 2002-01-09
; NUMBER OF SEQ ID NOS: 850
; SOFTWARE: PERL Program
; SEQ ID NO 638
; LENGTH: 3765
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. US20020137081A1 331181.1
; NAME/KEY: unsure
; LOCATION: 2378, 3184, 3187, 3194
; OTHER INFORMATION: a, t, c, g, or other
US-10-044-090-638

Query Match 97.2%; Score 3658; DB 12; Length 3765;
Best Local Similarity 98.1%; Pred. No. 0;
Matches 3695; Conservative 0; Mismatches 67; Indels 3; Gaps 3;

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Qy       1981 TTGACTTAGACCTATACTGAAAGATCTCTGTCACATCCAACTGGAAATTCCAGGAACCAA 2040
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Db       2041 AAAGAGCATCCCTATGGGCTTGGACCACTTACAGTGTGATAAGGCCTACTATACATTAGG 2100

Qy       2100 AAGTGGCAGTTCTTTACTCGTCCCC-TTTCATCGGTGCCTGGTACTCTGGCAAATGATGA 2158
              |||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db       2101 AAGTGGCAGTTCTTTACTCGTCCCCTTTTCATCGGTGCCTGGTACTCTGGCAAATGATGA 2160

Qy       2159 TGGGGTGGGAGACTTTCCATTAAATCAATCAGGAATGAGTCAATCAGCCTTTAGGTCTTT 2218
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2161 TGGGGTGGGAGACTTTCCATTAAATCAATCAGGAATGAGTCAATCAGCCTTTAGGTCTTT 2220

Qy       2219 AGTCCGGGGGACTTGGGGCTGAGAGAGTATAAATAACCCTGGGCTGTCCAGCCTTAATAG 2278
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2221 AGTCCGGGGGACTTGGGGCTGAGAGAGTATAAATAACCCTGGGCTGTCCAGCCTTAATAG 2280

Qy       2279 ACTTCTCTTACATTTTCGTCCTGTAGCACGCTGCCTGCCAAAGTAGTCCTGGCAGCTGGA 2338
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2281 ACTTCTCTTACATTTTCGTCCTGTAGCACGCTGCCTGCCAAAGTAGTCCTGGCAGCTGGA 2340

Qy       2339 CCATCTCTGTAGGATCGTAAAAAAAATAGAAANNNNNNNNNNNNNNNNNNNNNNNNNNNN 2398
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Db       2341 CCATCTCTGTAGGATCGTAAAAAAAATAGAAAAAAAAGANAAAAAAAAAGAAAGAAAGAGGGA 2400
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Qy       2399 NNNNNNNCTGGTGG-TTGATCATTTCTGCCATGATGTTTACAAGATGGCGACCACCAANG 2457
Db       2401 AAAAGAGCTGGTGGTTTGATCATTTCTGCCATGATGTTTACAAGATGGCGACCACCAAAG 2460

Qy       2458 TCAAACGACTAACCTATCTATGAACAACAGTAGTTTCTCAGGGTCACTGTCCTTGAACCC 2517
Db       2461 TCAAACGACTAACCTATCTATGAACAACAGTAGTTTCTCAGGGTCACTGTCCTTGAACCC 2520

Qy       2518 AACAGTCCCTTATGAGCGTCACTGCCCACCAAAGGTCAATGTCAAGAGAGGAAGAGAGGG 2577
Db       2521 AACAGTCCCTTATGAGCGTCACTGCCCACCAAAGGTCAATGTCAAGAGAGGAAGAGAGGG 2580

Qy       2578 AGGAGGGGTAGGACTGCAGGGGCCACTCCAAACTCGCTTAGGTAGAAACTATTGGTGCTT 2637
Db       2581 AGGAGGGGTAGGACTGCAGGGGCCACTCCAAACTCGCTTAGGTAGAAACTATTGGTGCTT 2640

Qy       2638 GACTCTCACTAGGCTAAACTCAAGATTTGACCAAATCGAGTGATAGGGATCCTGGTGGGA 2697
Db       2641 GACTCTCACTAGGCTAAACTCAAGATTTGACCAAATCGAGTGATAGGGATCCTGGTGGGA 2700

Qy       2698 GGAGAGAGGGCACATCTCCAGAAAAATGAAAAGCAATACAACTTTACCATAAAGCCTTTA 2757
Db       2701 GGAGAGAGGGCACATCTCCAGAAAAATGAAAAGCAATACAACTTTACCATAAAGCCTTTA 2760

Qy       2758 AAACCAGTAACGTGCTGCTCAAGGACCAAGAGCAATTNNNNNNNNNNNNNNNNNNNNNNN 2817
Db       2761 AAACCAGTAACGTGCTGCTCAAGGACCAAGAGCAATTGCAGCAGACCCAGCAGCAGCAGC 2820

Qy       2818 NNNNNNNCAAACATTGCTGCCTTTGTCCCCACACAGCCTCTAAGCGTGCTGACATCAGAT 2877
Db       2821 AGCAGCACAAACATTGCTGCCTTTGTCCCCACACAGCCTCTAAGCGTGCTGACATCAGAT 2880

Qy       2878 TGTTAAGGGCATTTTTATACTCAGAACTGTCCCATCCCCAGGTCCCCAAACTTATGGACA 2937
Db       2881 TGTTAAGGGCATTTTTATACTCAGAACTGTCCCATCCCCAGGTCCCCAAACTTATGGACA 2940

Qy       2938 CTGCCTTAGCCTCTTGGAAATCAGGTAGACCATATTCTAAGTTAGACTCTTCCCCTCCCT 2997
Db       2941 CTGCCTTAGCCTCTTGGAAATCAGGTAGACCATATTCTAAGTTAGACTCTTCCCCTCCCT 3000

Qy       2998 CCCACACTTCCCACCCCCAGGCAAGGCTGACTTCTCTGAATCAGAAAAGCTATTAAAGTT 3057
Db       3001 CCCACACTTCCCACCCCCAGGCAAGGCTGACTTCTCTGAATCAGAAAAGCTATTAAAGTT 3060

Qy       3058 TGTGTGTTGTGTCCATTTTGCAAACCCAACTAAGCCAGGACCCCAATGCGACAAGTAGTT 3117
Db       3061 TGTGTGTTGTGTCCATTTTGCAAACCCAACTAAGCCAGGACCCCAATGCGACAAGTAGTT 3120

Qy       3118 CATGAGTATTCCTAGCAAATTTCTCTCTTTCTTCAGTTCAGTAGATTTCCTTTTTTCTTN 3177
Db       3121 CATGAGTATTCCTAGCAAATTTCTCTCTTTCTTCAGTTCAGTAGATTTCCTTTTTTCTTT 3180

Qy       3178 TCTNTTNTTTTTTNTTTTTTTGGCTGTGACCTCTTCAAACCGTGGTACCCCCCCTTTTCT 3237
Db       3181 TCTNTTNTTTTTTNTTTTTTTGGCTGTGACCTCTTCAAACCGTGGTACCCCCCCTTTTCT 3240

Qy       3238 CCCCACGATGATATCTATATATGTATCTACAATACATATATCTACACATACAGAAAGAAG 3297
Db       3241 CCCCACGATGATATCTATATATGTATCTACAATACATATATCTACACATACAGAAAGAAG 3300

Qy       3298 CAGTTCTCACAATGTTGCTAGTTTTTTGCTTCTCTTTCCCCCACCCTACTCCCTCCAATT 3357
Db       3301 CAGTTCTCACAATGTTGCTAGTTTTTTGCTTCTCTTTCCCCCACCCTACTCCCTCCAATT 3360

Qy       3358 CCCCCTTAAACTTCCAAAGCTTCGTCTTGTGTTTGCTGCAGAGTGATTCGGGGGCTGACC 3417
Db       3361 CCCCCTTAAACTTCCAAAGCTTCGTCTTGTGTTTGCTGCAGAGTGATTCGGGGGCTGACC 3420

Qy       3418 TAGACCAGTTTGCATGATTCTTCTCTTGTGATTTGGTTGCACTTTAGACATTTTTGTGCC 3477
Db       3421 TAGACCAGTTTGCATGATTCTTCTCTTGTGATTTGGTTGCACTTTAGACATTTTTGTGCC 3480

Qy       3478 ATTATATTTGCATTATGTATTTATAATTTAAATGATATTTAGGTTTTTGGCTGAGTACTG 3537
Db       3481 ATTATATTTGCATTATGTATTTATAATTTAAATGATATTTAGGTTTTTGGCTGAGTACTG 3540

Qy       3538 GAATAAACAGTGAGCATATCTGGTATATGTCATTATTTATTGTTAAATTACATTTTTAAG 3597
Db       3541 GAATAAACAGTGAGCATATCTGGTATATGTCATTATTTATTGTTAAATTACATTTTTAAG 3600

Qy       3598 CTCCATGTGCATATAAAGGTTATGAAACATATCATGGTAATGACAGATGCAAGTTATTTT 3657
Db       3601 CTCCATGTGCATATAAAGGTTATGAAACATATCATGGTAATGACAGATGCAAGTTATTTT 3660

Qy       3658 ATTTGCTTATTTTTATAATTAAAGATGCCATAGCATAATATGAAGCCTTTGGTGAATTCC 3717
Db       3661 ATTTGCTTATTTTTATAATTAAAGATGCCATAGCATAATATGAAGCCTTTGGTGAATTCC 3720

Qy       3718 TTCTAAGATAAAAATAATAATAAAGTGTTACGTTTTATTGGTTTC 3762
Db       3721 TTCTAAGATAAAAATAATAATAAAGTGTTACGTTTTATTGGTTTC 3765
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RESULT 2
US-10-198-846-13651
; Sequence 13651, Application US/10198846
; Publication No. US20030099974A1
; GENERAL INFORMATION:
; APPLICANT: Lillie, James
; APPLICANT: Xu, Yongyao
; APPLICANT: Wang, Youzhen
; APPLICANT: Steinmann, Kathleen
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS
; TITLE OF INVENTION: FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF BREAST CANCER
; FILE REFERENCE: MRI-049
; CURRENT APPLICATION NUMBER: US/10/198,846
; CURRENT FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/306,220
; PRIOR FILING DATE: 2001-07-18
; NUMBER OF SEQ ID NOS: 14084
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 13651
; LENGTH: 3897
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 3878, 3879, 3880, 3881, 3882, 3883, 3884, 3885, 3886, 3887,
; LOCATION: 3888, 3889, 3890, 3891, 3892, 3893, 3894, 3895, 3896, 3897
; OTHER INFORMATION: n = A,T,C or G
US-10-198-846-13651

Query Match 97.0%; Score 3650.6; DB 9; Length 3897;
Best Local Similarity 97.8%; Pred. No. 0;
Matches 3680; Conservative 0; Mismatches 80; Indels 4; Gaps 2;

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Qy          1 GGTGGCAGCAGCAGCATCACACGTAACAACAACAAAAAAAAATCCTCATCAAATCCTCAC 60
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Qy         61 CTAAGCTTTCAGTGTATCCAGATCCACATCTTCACTCAAGCCAGGAGAGGGAAAGAGGAA 120
Db        172 CTAAGCTTTCAGTGTATCCAGATCCACATCTTCACTCAAGCCAGGAGAGGGAAAGAGGAA 231

Qy        121 AGGGGGGCAGGAAAAAAAAAAAAACCCAACAACTTAGCGGAAACTTCTCAGAGAATGCTCC 180
Db        232 AGGGGGGCAGGAAAAAAAAAAAAACCCAACAACTTAGCGGAAACTTCTCAGAGAATGCTCC 291

Qy        181 AAAACTCAGCAGTGCTTCTGGTGCTGGTGATCAGTGCTTCTGCAACCCATGAGGCGGAGC 240
Db        292 AAAACTCAGCAGTGCTTCTGGTGCTGGTGATCAGTGCTTCTGCAACCCATGAGGCGGAGC 351

Qy        241 AGAATGACTCTGTGAGCCCCAGGAAATCCCGAGTGGCGGCTCAAAACTCAGCTGAAGTGG 300
Db        352 AGAATGACTCTGTGAGCCCCAGGAAATCCCGAGTGGCGGCTCAAAACTCAGCTGAAGTGG 411
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Qy       301 TTCGTTGCCTCAACAGTGCTCTACAGGTCGGCTGCGGGGCTTTTGCATGCCTGGAAAACT 360
Db       412 TTCGTTGCCTCAACAGTGCTCTACAGGTCGGCTGCGGGGCTTTTGCATGCCTGGAAAACT 471

Qy       361 CCACCTGTGACACAGATGGGATGTATGACATCTGTAAATCCTTCTTGTACAGCGCTGCTA 420
Db       472 CCACCTGTGACACAGATGGGATGTATGACATCTGTAAATCCTTCTTGTACAGCGCTGCTA 531

Qy       421 AATTTGACACTCAGGGAAAAGCATTCGTCAAAGAGAGCTTAAAATGCATCGCCAACGGGG 480
Db       532 AATTTGACACTCAGGGAAAAGCATTCGTCAAAGAGAGCTTAAAATGCATCGCCAACGGGG 591

Qy       481 TCACCTCCAAGGTCTTCCTCGCCATTCGGAGGTGCTCCACTTTCCAAAGGATGATTGCTG 540
Db       592 TCACCTCCAAGGTCTTCCTCGCCATTCGGAGGTGCTCCACTTTCCAAAGGATGATTGCTG 651

Qy       541 AGGTGCAGGAAGAGTGCTACAGCAAGCTGAATGTGTGCAGCATCGCCAAGCGGAACCCTG 600
Db       652 AGGTGCAGGAAGAGTGCTACAGCAAGCTGAATGTGTGCAGCATCGCCAAGCGGAACCCTG 711

Qy       601 AAGCCATCACTGAGGTCGTCCAGCTGCCCAATCACTTCTCCAACAGATACTATAACAGAC 660
Db       712 AAGCCATCACTGAGGTCGTCCAGCTGCCCAATCACTTCTCCAACAGATACTATAACAGAC 771

Qy       661 TTGTCCGAAGCCTGCTGGAATGTGATGAAGACACAGTCAGCACAATCAGAGACAGCCTGA 720
Db       772 TTGTCCGAAGCCTGCTGGAATGTGATGAAGACACAGTCAGCACAATCAGAGACAGCCTGA 831

Qy       721 TGGAGAAAATTGGGCCTAACATGGCCAGCCTCTTCCACATCCTGCAGACAGACCACTGTG 780
Db       832 TGGAGAAAATTGGGCCTAACATGGCCAGCCTCTTCCACATCCTGCAGACAGACCACTGTG 891

Qy       781 CCCAAACACACCCACGAGCTGACTTCAACAGGAGACGCACCAATGAGCCGCAGAAGCTGA 840
Db       892 CCCAAACACACCCACGAGCTGACTTCAACAGGAGACGCACCAATGAGCCGCAGAAGCTGA 951

Qy       841 AAGTCCTCCTCAGGAACCTCCGAGGTGAGGAGGACTCTCCCTCCCACATCAAACGCACAT 900
Db       952 AAGTCCTCCTCAGGAACCTCCGAGGTGAGGAGGACTCTCCCTCCCACATCAAACGCACAT 1011

Qy       901 CCCATGAGAGTGCATAACCAGGGAGAGGTTATTCACAACCTCACCAAACTAGTATCATTT 960
Db      1012 CCCATGAGAGTGCATAACCAGGGAGAGGTTATTCACAACCTCACCAAACTAGTATCATTT 1071

Qy       961 TAGGGGTGTTGACACACCAGTTTTGAGTGTACTGTGCCTGGTTTGATTTTTTTAAAGTAG 1020
Db      1072 TAGGGGTGTTGACACACCAATTTTGAGTGTACTGTGCCTGGTTTGATTTTTTTAAAGTAG 1131

Qy      1021 TTCCTATTTTCTATCCCCCTTAAAGAAAATTGCATGAAACTAGGCTTCTGTAATCAATAT 1080
Db      1132 TTCCTATTTTCTATCCCCCTTAAAGAAAATTGCATGAAACTAGGCTTCTGTAATCAATAT 1191

Qy      1081 CCCAACATTCTGCAATGGCAGCATTCCCACCAACAAAATCCATGTGACCATTCTGCCTCT 1140
Db      1192 CCCAACATTCTGCAATGGCAGCATTCCCACCAACAAAATCCATGTGACCATTCTGCCTCT 1251

Qy      1141 CCTCAGGAGAAAGTACCCTCTTTTACCAACTTCCTCTGCCATGTTTTTCCCCTGCTCCCC 1200
Db      1252 CCTCAGGAGAAAGTACCCTCTTTTACCAACTTCCTCTGCCATGTTTTTCCCCTGCTCCCC 1311

Qy      1201 TGAGACCACCCCCAAACACAAAACATTCATGTAACTCTCCAGCCATTGTAATTTGAAGAT 1260
Db      1312 TGAGACCACCCCCAAACACAAAACATTCATGTAACTCTCCAGCCATTGTAATTTGAAGAT 1371

Qy      1261 GTGGATCCCTTTAGAACGGTTGCCCCAGTAGAGTTAGCTGATAAGGAAACTTTATTTAAA 1320
Db      1372 GTGGATCCCTTTAGAACGGTTGCCCCAGTAGAGTTAGCTGATAAGGAAACTTTATTTAAA 1431

Qy      1321 TGCATGTCTTAAATGCTCATAAAGATGTTAAATGGAATTCGTGTTATGAATCTGTGCTGG 1380
Db      1432 TGCATGTCTTAAATGCTCATAAAGATGTTAAATGGAATTCGTGTTATGAATCTGTGCTGG 1491

Qy      1381 CCATGGACGAATATGAATGTCACATTTGAATTCTTGATCTCTAATGAGCTAGTGTCTTAT 1440
Db      1492 CCATGGACGAATATGAATGTCACATTTGAATTCTTGATCTCTAATGAGCTAGTGTCTTAT 1551

Qy      1441 GGTCTTGATCCTCCAATGTCTAATTTTCTTTCCGACACATTTACCAAATTGCTTGAGCCT 1500
Db      1552 GGTCTTGATCCTCCAATGTCTAATTTTCTTTCCGACACATTTACCAAATTGCTTGAGCCT 1611

Qy      1501 GGCTGTCCAACCAGACTTTGAGCCTGCATCTTCTTGCATCTAATGAAAAACAAAAAGCTA 1560
Db      1612 GGCTGTCCAACCAGACTTTGAGCCTGCATCTTCTTGCATCTAATGAAAAACAAAAAGCTA 1671

Qy      1561 ACATCTTTACGTACTGTAACTGCTCAGAGCTTTAAAAGTATCTTTAACAATTGTCTTAAA 1620
Db      1672 ACATCTTTACGTACTGTAACTGCTCAGAGCTTTAAAAGTATCTTTAACAATTGTCTTAAA 1731

Qy      1621 ACCAGAGAATCTTAAGGTCTAACTGTGGAATATAAATAGCTGAAAACTAATGTACTGTAC 1680
Db      1732 ACCAGAGAATCTTAAGGTCTAACTGTGGAATATAAATAGCTGAAAACTAATGTACTGTAC 1791

Qy      1681 ATAAATTCCAGAGGACTCTGCTTAAACAAAGCAGTATATAATAACTTTATTGCATATAGA 1740
Db      1792 ATAAATTCCAGAGGACTCTGCTTAAACAAAGCAGTATATAATAACTTTATTGCATATAGA 1851

Qy      1741 TTTAGTTTTGTAACTTAGCTTTATTTTTCTTTTCCTGGGAATGGAATAACTATCTCACTT 1800
Db      1852 TTTAGTTTTGTAACTTAGCTTTATTTTTCTTTTCCTGGGAATGGAATAACTATCTCACTT 1911

Qy      1801 CCAGATATCCACATAAATGCTCCTTGTGGCCTTTTTTATAACTAAGGGGGTAGAAGTAGT 1860
Db      1912 CCAGATATCCACATAAATGCTCCTTGTGGCCTTTTTTATAACTAAGGGGGTAGAAGTAGT 1971

Qy      1861 TTTAATTCAACATCAAAACTTAAGATGGGCCTGTATGAGACAGGAAAAACCAACAGGTTT 1920
Db      1972 TTTAATTCAACATCAAAACTTAAGATGGGCCTGTATGAGACAGGAAAAACCAACAGGTTT 2031

Qy      1921 ATCTGAAGGACCCCAGGTAAGATGTTAATCTCCCAGCCCACCTCAACCCAGAGGCTACTC 1980
Db      2032 ATCTGAAGGACCCCAGGTAAGATGTTAATCTCCCAGCCCACCTCAACCCAGAGGCTACTC 2091

Qy      1981 TTGACTTAGACCTATACTGAAAGATCTCTGTCACATCCAACTGGAAATTCCAGGAACCAA 2040
Db      2092 TTGACTTAGACCTATACTGAAAGATCTCTGTCACATCCAACTGGAAATTCCAGGAACCAA 2151

Qy      2041 AAAGAGCA-CCCTATGGGCTTGGACCACTTACAGTGTGATAAGGCCTACTATACATTAGG 2099
Db      2152 AAAGAGCATCCCTATGGGCTTGGACCACTTACAGTGTGATAAGGCCTACTATACATTAGG 2211

Qy      2100 AAGTGGCAGTTCTTTACTCGTCCCCTTTCATCGGTGCCTGGTACTCTGGCAAATGATGAT 2159
Db      2212 AAGTGGCAGTTCTTTACTCGTCCCCTTTCATCGGTGCCTGGTACTCTGGCAAATGATGAT 2271

Qy      2160 GGGGTGGGAGACTTTCCATTAAATCAATCAGGAATGAGTCAATCAGCCTTTAGGTCTTTA 2219
Db      2272 GGGGTGGGAGACTTTCCATTAAATCAATCAGGAATGAGTCAATCAGCCTTTAGGTCTTTA 2331

Qy      2220 GTCCGGGGGACTTGGGGCTGAGAGAGTATAAATAACCCTGGGCTGTCCAGCCTTAATAGA 2279
Db      2332 GTCCGGGGGACTTGGGGCTGAGAGAGTATAAATAACCCTGGGCTGTCCAGCCTTAATAGA 2391

Qy      2280 CTTCTCTTACATTTTCGTCCTGTAGCACGCTGCCTGCCAAAGTAGTCCTGGCAGCTGGAC 2339
Db      2392 CTTCTCTTACATTTTCGTCCTGTAGCACGCTGCCTGCCAAAGTAGTCCTGGCAGCTGGAC 2451

Qy      2340 CATCTCTGTAGGATCGTAAAAAAAATAGAAANNNNNNNNNNNNNNNNNNNNNNNNNNNN 2399
Db      2452 CATCTCTGTAGGATCGTAAAAAAAATAGAAAAAAAAAAAAAAAAAAGAAAGAAAGAGGGAAA 2511

Qy      2400 NNNNNNCTGGTGGTTGATCATTTCTGCCATGATGTTTACAAGATGGCGACCACCAANGTC 2459
Db      2512 AAGAGCTGGTGGTTTGATCATTTCTGCCATGATGTTTACAAGATGGCGACCACCAAAGTC 2571

Qy      2460 AAACGACTAACCTATCTATGAACAACAGTAGTTTCTCAGGGTCACTGTCCTTGAACCCAA 2519
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Db       2572 AAACGACTAACCTATCTATGAACAACAGTAGTTTCTCAGGGTCACTGTCCTTGAACCCAA 2631

Qy       2520 CAGTCCCTTATGAGCGTCACTGCCCACCAAAGGTCAATGTCAAGAGAGGAAGAGAGGGAG 2579

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Qy       2580 GAGGGGTAGGACTGCAGGGGCCACTCCAAACTCGCTTAGGTAGAAACTATTGGTGCTTGA 2639

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Db       2812 AGAGAGGGCACATCTCCAGAAAAATGAAAAGCAATACAACTTTACCATAAAGCCTTTAAA 2871

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Qy       2880 TTAAGGGCATTTTTATACTCAGAACTGTCCCATCCCCAGGTCCCCAAACTTATGGACACT 2939

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Qy       2940 GCCTTAGCCTCTTGGAAATCAGGTAGACCATATTCTAAGTTAGACTCTTCCCCTCCCTCC 2999

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Qy       3000 CACACTTCCCACCCCCAGGCAAGGCTGACTTCTCTGAATCAGAAAAGCTATTAAAGTTTG 3059

Db       3112 CACACTTCCCACCCCCAGGCAAGGCTGACTTCTCTGAATCAGAAAAGCTATTAAAGTTTG 3171

Qy       3060 TGTGTTGTGTCCATTTTGCAAACCCAACTAAGCCAGGACCCCAATGCGACAAGTAGTTCA 3119

Db       3172 TGTGTTGTGTCCATTTTGCAAACCCAACTAAGCCAGGACCCCAATGCGACAAGTAGTTCA 3231

Qy       3120 TGAGTATTCCTAGCAAATTTCTCTCTTTCTTCAGTTCAGTAGATTTCCTTTTTTCTTNTC 3179

Db       3232 TGAGTATTCCTAGCAAATTTCTCTCTTTCTTCAGTTCAGTAGATTTCCTTTTTTCTTTTC 3291

Qy       3180 ---TNTTNTTTTTTNTTTTTTTGGCTGTGACCTCTTCAAACCGTGGTACCCCCCCTTTTC 3236

Db       3292 TTTTTTTTTTTTTTTTTTTTTTTGGCTGTGACCTCTTCAAACCGTGGTACCCCCCCTTTTC 3351

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Db       3472 TCCCCCTTAAACTTCCAAAGCTTCGTCTTGTGTTTGCTGCAGAGTGATTCGGGGGCTGAC 3531

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Qy       3717 CTTCTAAGATAAAAATAATAATAAAGTGTTACGTTTTATTGGTT 3760

Db       3832 CTTCTAAGATAAAAATAATAATAAAGTGTTACGTTTTATTGGTT 3875
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RESULT 3
US-09-925-300-486
; Sequence 486, Application US/09925300
; Patent No. US20020151681A1
; GENERAL INFORMATION:
; APPLICANT: Craig Rosen,
; APPLICANT: Steve Ruben
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA101
; CURRENT APPLICATION NUMBER: US/09/925,300
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05988
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1890
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 486
; LENGTH: 2572
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (823)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-925-300-486

Query Match 61.4%; Score 2311.6; DB 10; Length 2572;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 2344; Conservative 4; Mismatches 3; Indels 3; Gaps 3;

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Qy          1 GGTGGCAGCAGCAGCATCACACGTAACAACAACAAAAAAAAATCCTCATCAAATCCTCAC 60

Db         92 GGTGGCAGCAGCAGCATCACCAGCAACAACAACAAMAAAAAATCCTCATCAAATCCTCAC 151

Qy         61 CTAAGCTTTCAGTGTATCCAGATCCACATCTTCACTCAAGCCAGGAGAGGGAAAGAGGAA 120

Db        152 CTAAGCTTTCAGTGTATCCAGATCCACATCTTCACTCAAGCCAGGAGAGGGAAAGAGGAA 211

Qy        121 AGGGGGGCAGGAAAAAAAAAAAACCCAACAACTTAGCGGAAACTTCTCAGAGAATGCTCC 180

Db        212 AGGGGGGCAGGAAAAAAAAAAAACCCAACAACTTAGCGGAAACTTCTCAGAGAATGCTCC 271

Qy        181 AAAACTCAGCAGTGCTTCTGGTGCTGGTGATCAGTGCTTCTGCAACCCATGAGGCGGAGC 240

Db        272 AAAACTCAGCAGTGCTTCTGGTGCTGGTGATCAGTGCTTCTGCAACCCATGAGGCGGAGC 331

Qy        241 AGAATGACTCTGTGAGCCCCAGGAAATCCCGAGTGGCGGCTCAAAACTCAGCTGAAGTGG 300

Db        332 AGAATGACTCTGTGAGCCCCAGGAAATCCCGAGTGGCGGCTCAAAACTCAGCTGAAGTGG 391

Qy        301 TTCGTTGCCTCAACAGTGCTCTACAGGTCGGCTGCGGGGCTTTTGCATGCCTGGAAAACT 360

Db        392 TTCGTTGCCTCAACAGTGCTCTACAGGTCGGCTGCGGGGCTTTTGCATGCCTGGAAAACT 451

Qy        361 CCACCTGTGACACAGATGGGATGTATGACATCTGTAAATCCTTCTTGTACAGCGCTGCTA 420

Db        452 CCACCTGTGACACAGATGGGATGTATGACATCTGTAAATCCTTCTTGTACAGCGCTGCTA 511
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Qy       421 AATTTGACACTCAGGGAAAAGCATTCGTCAAAGAGAGCTTAAAATGCATCGCCAACGGGG 480
Db       512 AATTTGACACTCAGGGAAAAGCATTCGTCAAAGAGAGCTTAAAATGCATCGCCAACGGGG 571

Qy       481 TCACCTCCAAGGTCTTCCTCGCCATTCGGAGGTGCTCCACTTTCCAAAGGATGATTGCTG 540
Db       572 TCACCTCCAAGGTCTTCCTCGCCATTCGGAGGTGCTCCACTTTCCAAAGGATGATTGCTG 631

Qy       541 AGGTGCAGGAAGAGTGCTACAGCAAGCTGAATGTGTGCAGCATCGCCAAGCGGAACCCTG 600
Db       632 AGGTGCAGGAAGAGTGCTACAGCAAGCTGAATGTGTGCAGCATCGCCAAGCGGAACCCTG 691

Qy       601 AAGCCATCACTGAGGTCGTCCAGCTGCCCAATCACTTCTCCAACAGATACTATAACAGAC 660
Db       692 AAGCCATCACTGAGGTCGTCCAGCTGCCCAATCACTTCTCCAACAGATACTATAACAGAC 751

Qy       661 TTGTCCGAAGCCTGCTGGAATGTGATGAAGACACAGTCAGCACAATCAGAGACAGCCTGA 720
Db       752 TTGTCCGAAGCCTGCTGGAATGTGATGAAGACACAGTCAGCACAATCAGAGACAGCCTGA 811

Qy       721 TGGAGAAAATT-GGGCCTAACATGGCCAGCCTCTTCCACATCCTGCAGACAGACCACTGT 779
Db       812 TGGAGRAAATTNGGGCCTAACATGGCCAGCCTCTTCCACATCCTGCAGACAGACCACTGT 871

Qy       780 GCCCAAACACACCCACGAGCTGACTTCAACAGGAGACGCACCAATGAGCCGCAGAAGCTG 839
Db       872 GCCCAAACACACCCACGAGCTGACTTCAACAGGAGACGCACCAATGAGCCGCAGAAGCTG 931

Qy       840 AAAGTCCTCCTCAGGAACCTCCGAGGTGAGGAGGACTCTCCCTCCCACATCAAACGCACA 899
Db       932 AAAGTCCTCCTCAGGAACCTCCGAGGTGAGGAGGACTCTCCCTCCCACATCAAACGCACA 991

Qy       900 TCCCATGAGAGTGCATAACCAGGGAGAGGTTATTCACAACCTCACCAAACTAGTATCATT 959
Db       992 TCCCATGAGAGTGCATAACCAGGGAGAGGTTATTCACAACCTCACCAAACTAGTATCATT 1051

Qy       960 TTAGGGGTGTTGACACACCAGTTTTGAGTGTACTGTGCCTGGTTTGATTTTTTTAAAGTA 1019
Db      1052 TTAGGGGTGTTGACACACCARTTTTGAGTGTACTGTGCCTGGTTTGATTTTTTTAAAGTA 1111

Qy      1020 GTTCCTATTTTCTATCCCCCTTAAAGAAAATTGCATGAAACTAGGCTTCTGTAATCAATA 1079
Db      1112 GTTCCTATTTTCTATCCCCCTTAAAGAAAATTGCATGAAACTAGGCTTCTGTAATCAATA 1171

Qy      1080 TCCCAACATTCTGCAATGGCAGCATTCCCACCAACAAAATCCATGTGACCATTCTGCCTC 1139
Db      1172 TCCCAACATTCTGCAATGGCAGCATTCCCACCAACAAAATCCATGTGACCATTCTGCCTC 1231

Qy      1140 TCCTCAGGAGAAAGTACCCTCTTTTACCAACTTCCTCTGCCATGTTTTTCCCCTGCTCCC 1199
Db      1232 TCCTCAGGAGAAAGTACCCTCTTTTACCAACTTCCTCTGCCATGTTTTTCCCCTGCTCCC 1291

Qy      1200 CTGAGACCACCCCCAAACACAAAACATTCATGTAACTCTCCAGCCATTGTAATTTGAAGA 1259
Db      1292 CTGAGACCACCCCCAAACACAAAACATTCATGTAACTCTCCAGCCATTGTAATTTGAAGA 1351

Qy      1260 TGTGGATCCCTTTAGAACGGTTGCCCCAGTAGAGTTAGCTGATAAGGAAACTTTATTTAA 1319
Db      1352 TGTGGATCCCTTTAGAACGGTTGCCCCAGTAGAGTTAGCTGATAAGGAAACTTTATTTAA 1411

Qy      1320 ATGCATGTCTTAAATGCTCATAAAGATGTTAAATGGAATTCGTGTTATGAATCTGTGCTG 1379
Db      1412 ATGCATGTCTTAAATGCTCATAAAGATGTTAAATGGAATTCGTGTTATGAATCTGTGCTG 1471

Qy      1380 GCCATGGACGAATATGAATGTCACATTTGAATTCTTGATCTCTAATGAGCTAGTGTCTTA 1439
Db      1472 GCCATGGACGAATATGAATGTCACATTTGAATTCTTGATCTCTAATGAGCTAGTGTCTTA 1531

Qy      1440 TGGTCTTGATCCTCCAATGTCTAATTTTCTTTCCGACACATTTACCAAATTGCTTGAGCC 1499
Db      1532 TGGTCTTGATCCTCCAATGTCTAATTTTCTTTCCGACACATTTACCAAATTGCTTGAGCC 1591

Qy      1500 TGGCTGTCCAACCAGACTTTGAGCCTGCATCTTCTTGCATCTAATGAAAAACAAAAAGCT 1559
Db      1592 TGGCTGTCCAACCAGACTTTGAGCCTGCATCTTCTTGCATCTAATGAAAAACAAAAAGCT 1651

Qy      1560 AACATCTTTACGTACTGTAACTGCTCAGAGCTTTAAAAGTATCTTTAACAATTGTCTTAA 1619
Db      1652 AACATCTTTACGTACTGTAACTGCTCAGAGCTTTAAAAGTATCTTTAACAATTGTCTTAA 1711

Qy      1620 AACCAGAGAATCTTAAGGTCTAACTGTGGAATATAAATAGCTGAAAACTAATGTACTGTA 1679
Db      1712 AACCAGAGAATCTTAAGGTCTAACTGTGGAATATAAATAGCTGAAAACTAATGTACTGTA 1771

Qy      1680 CATAAATTCCAGAGGACTCTGCTTAAACAAAGCAGTATATAATAACTTTATTGCATATAG 1739
Db      1772 CATAAATTCCAGAGGACTCTGCTTAAACAAAGCAGTATATAATAACTTTATTGCATATAG 1831

Qy      1740 ATTTAGTTTTGTAACTTAGCTTTATTTTTCTTTTCCTGGGAATGGAATAACTATCTCACT 1799
Db      1832 ATTTAGTTTTGTAACTTAGCTTTATTTTTCTTTTCCTGGGAATGGAATAACTATCTCACT 1891

Qy      1800 TCCAGATATCCACATAAATGCTCCTTGTGGCCTTTTTTATAACTAAGGGGGTAGAAGTAG 1859
Db      1892 TCCAGATATCCACATAAATGCTCCTTGTGGCCTTTTTTATAACTAAGGGGGTAGAAGTAG 1951

Qy      1860 TTTTAATTCAACATCAAAACTTAAGATGGGCCTGTATGAGACAGGAAAAACCAACAGGTT 1919
Db      1952 TTTTAATTCAACATCAAAACTTAAGATGGGCCTGTATGAGACAGGAAAAACCAACAGGTT 2011

Qy      1920 TATCTGAAGGACCCCAGGTAAGATGTTAATCTCCCAGCCCACCTCAACCCAGAGGCTACT 1979
Db      2012 TATCTGAAGGACCCCAGGTAAGATGTTAATCTCCCAGCCCACCTCAACCCAGAGGCTACT 2071

Qy      1980 CTTGACTTAGACCTATACTGAAAGATCTCTGTCACATCCAACTGGAAATTCCAGGAACCA 2039
Db      2072 CTTGACTTAGACCTATACTGAAAGATCTCTGTCACATCCAACTGGRAATTCCAGGAACCA 2131

Qy      2040 AAAAGAGCA-CCCTATGGGCTTGGACCACTTACAGTGTGATAAGGCCTACTATACATTAG 2098
Db      2132 AAAAGAGCATCCCTATGGGCTTGGACCACTTACAGTGTGATAAGGCCTACTATACATTAG 2191

Qy      2099 GAAGTGGCAGTTCTTTACTCGTCCCCTTTCATCGGTGCCTGGTACTCTGGCAAATGATGA 2158
Db      2192 GAAGTGGCAGTTCTTTACTCGTCCCCTTTCATCGGTGCCTGGTACTCTGGCAAATGATGA 2251

Qy      2159 TGGGGTGGGAGACTTTCCATTAAATCAATCAGGAATGAGTCAATCAGCCTTTAGGTCTTT 2218
Db      2252 TGGGGTGGGAGACTTTCCATTAAATCAATCAGGAATGAGTCAATCAGCCTTTAGGTCTTT 2311

Qy      2219 AGTCCGGGGGACTTGGGGCTGAGAGAGTATAAATAACCCTGGGCTGTCCAGCCTTAATAG 2278
Db      2312 AGTCCGGGGGACTTGGGGCTGAGAGAGTATAAATAACCCT-GGCTGTCCAGCCTTAATAG 2370

Qy      2279 ACTTCTCTTACATTTTCGTCCTGTAGCACGCTGCCTGCCAAAGTAGTCCTGGCAGCTGGA 2338
Db      2371 ACTTCTCTTACATTTTCGTCCTGTAGCACGCTGCCTGCCAAAGTAGTCCTGGCAGCTGGA 2430

Qy      2339 CCATCTCTGTAGGA 2352
Db      2431 CCATCTCTGTAGGA 2444
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RESULT 4
US-09-840-989A-1
; Sequence 1, Application US/09840989A
; Patent No. US20020042372A1
; GENERAL INFORMATION:
; APPLICANT: Olsen et al.
; TITLE OF INVENTION: Stanniocalcin Polynucleotides, Polypeptides, and Methods Based The
; FILE REFERENCE: PF108P2
; CURRENT APPLICATION NUMBER: US/09/840,989A
; CURRENT FILING DATE: 2001-04-25
; PRIOR APPLICATION NUMBER: PCT/US00/29432
; PRIOR FILING DATE: 2000-10-26

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;  PRIOR APPLICATION NUMBER: US 60/161,740
;  PRIOR FILING DATE: 1999-10-27
;  NUMBER OF SEQ ID NOS: 12
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
;   LENGTH: 1283
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (45)..(788)
;   OTHER INFORMATION:
;   NAME/KEY: misc_feature
;   LOCATION: (857)..(857)
;   OTHER INFORMATION: n is equal to a, t, c, or g.
;   NAME/KEY: misc_feature
;   LOCATION: (1254)..(1254)
;   OTHER INFORMATION: n is equal to a, t, c, or g.
;   NAME/KEY: misc_feature
;   LOCATION: (1279)..(1279)
;   OTHER INFORMATION: n is equal to a, t, c, or g.
US-09-840-989A-1

  Query Match           32.6%;  Score 1226;  DB 10;  Length 1283;
  Best Local Similarity   98.9%;  Pred. No. 6.8e-315;
  Matches 1254;  Conservative    0;  Mismatches   12;  Indels    2;  Gaps    2;

Qy        132 AAAAAAAAAAAAACCCAACAACTTAGCGGAAACTTCTCAGAGAATGCTCCAAAACTCAGCA 191
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          3 AAAAAAAAAAAAACCCAACAACTTAGCGGAAACTTCTCAGAGAATGCTCCAAAACTCAGCA 62

Qy        192 GTGCTTCTGGTGCTGGTGATCAGTGCTTCTGCAACCCATGAGGCGGAGCAGAATGACTCT 251
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         63 GTGCTTCTGGTGCTGGTGATCAGTGCTTCTGCAACCCATGAGGCGGAGCAGAATGACTCT 122

Qy        252 GTGAGCCCCAGGAAATCCCGAGTGGCGGCTCAAAACTCAGCTGAAGTGGTTCGTTGCCTC 311
              ||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db        123 GTGAGCCCCAGGAAATCCCGAGTGGCGGCCCAAAACTCAGCTGAAGTGGTTCGTTGCCTC 182

Qy        312 AACAGTGCTCTACAGGTCGGCTGCGGGGCTTTTGCATGCCTGGAAAACTCCACCTGTGAC 371
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        183 AACAGTGCTCTACAGGTCGGCTGCGGGGCTTTTGCATGCCTGGAAAACTCCACCTGTGAC 242

Qy        372 ACAGATGGGATGTATGACATCTGTAAATCCTTCTTGTACAGCGCTGCTAAATTTGACACT 431
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        243 ACAGATGGGATGTATGACATCTGTAAATCCTTCTTGTACAGCGCTGCTAAATTTGACACT 302

Qy        432 CAGGGAAAAGCATTCGTCAAAGAGAGCTTAAAATGCATCGCCAACGGGGTCACCTCCAAG 491
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        303 CAGGGAAAAGCATTCGTCAAAGAGAGCTTAAAATGCATCGCCAACGGGGTCACCTCCAAG 362

Qy        492 GTCTTCCTCGCCATTCGGAGGTGCTCCACTTTCCAAAGGATGATTGCTGAGGTGCAGGAA 551
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        363 GTCTTCCTCGCCATTCGGAGGTGCTCCACTTTCCAAAGGATGATTGCTGAGGTGCAGGAA 422

Qy        552 GAGTGCTACAGCAAGCTGAATGTGTGCAGCATCGCCAAGCGGAACCCTGAAGCCATCACT 611
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        423 GAGTGCTACAGCAAGCTGAATGTGTGCAGCATCGCCAAGCGGAACCCTGAAGCCATCACT 482

Qy        612 GAGGTCGTCCAGCTGCCCAATCACTTCTCCAACAGATACTATAACAGACTTGTCCGAAGC 671
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        483 GAGGTCGTCCAGCTGCCCAATCACTTCTCCAACAGATACTATAACAGACTTGTCCGAAGC 542

Qy        672 CTGCTGGAATGTGATGAAGACACAGTCAGCACAATCAGAGACAGCCTGATGGAGAAAATT 731
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        543 CTGCTGGAATGTGATGAAGACACAGTCAGCACAATCAGAGACAGCCTGATGGAGAAAATT 602

Qy        732 GGGCCTAACATGGCCAGCCTCTTCCACATCCTGCAGACAGACCACTGTGCCCAAACACAC 791
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        603 GGGCCTAACATGGCCAGCCTCTTCCACATCCTGCAGACAGACCACTGTGCCCAAACACAC 662

Qy        792 CCACGAGCTGACTTCAACAGGAGACGCACCAATGAGCCGCAGAAGCTGAAAGTCCTCCTC 851
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        663 CCACGAGCTGACTTCAACAGGAGACGCACCAATGAGCCGCAGAAGCTGAAAGTCCTCCTC 722

Qy        852 AGGAACCTCCGAGGTGAGGAGGACTCTCCCTCCCACATCAAACGCACATCCCATGAGAGT 911
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        723 AGGAACCTCCGAGGTGAGGAGGACTCTCCCTCCCACATCAAACGCACATCCCATGAGAGT 782

Qy        912 GCATAACCAGGGAGAGGTTATTCACAACCTCACCAAACTAGTATCATTTTAGGGGTGTTG 971
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        783 GCATAACCAGGGAGAGGTTATTCACAACCTCACCAAACTAGTATCATTTTAGGGGTGTTG 842

Qy        972 ACACACCAGTTTTGAGTGTACTGTGCCTGGTTTGATTTTTTTAAAGTAGTTCCTATTTTC 1031
              ||||||||||||||| |||||||||||||||||||| ||||||||||||||||||||||||
Db        843 ACACACCAGTTTTGNGTGTACTGTGCCTGGTTTGGTTTTTTTAAAGTAGTTCCTATTTTC 902

Qy       1032 TATCCCCCTTAAAGAAAATTGCATGAAACTAGGCTTCTGTAATCAATATCCCAACATTCT 1091
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        903 TATCCCCCTTAAAGAAAATTGCATGAAACTAGGCTTCTGTAATCAATATCCCAACATTCT 962

Qy       1092 GCAATGGCAGCATTCCCACCAACAAAATCCATGTGACCATTCTGCCTCTCCTCAGGAGAA 1151
              ||||||| || |||||||||||||||||||||||| ||||||  ||||||||||||||||
Db        963 GCAATGGGAGGATTCCCACCAACAAAATCCATGTGAACATTCTTGCTCTCCTCAGGAGAA 1022

Qy       1152 AGTACCCTC-TTTTACCAACTTCCTCTGCCATGTTTTTCCCCTGCTCCCCTGAGACCACC 1210
              ||||||||| |||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1023 AGTACCCTCTTTTTACCAACTTCCTCTGCCATGTTTTTCCCCTGCTCCCCTGAGACCACC 1082

Qy       1211 CCCAAACACAAAACATTCATGTAACTCTCCAGCCATTGTAATTTGAAGATGTGGATCCCT 1270
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1083 CCCAAACACAAAACATTCATGTAACTCTCCAGCCATTGTAATTTGAAGATGTGGATCCCT 1142

Qy       1271 TTAG-AACGGTTGCCCCAGTAGAGTTAGCTGATAAGGAAACTTTATTTAAATGCATGTCT 1329
              |||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1143 TTAGAAACGGTTGCCCCAGTAGAGTTAGCTGATAAGGAAACTTTATTTAAATGCATGTCT 1202

Qy       1330 TAAATGCTCATAAAGATGTTAAATGGAATTCGTGTTATGAATCTGTGCTGGCCATGGACG 1389
              |||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||
Db       1203 TAAATGCTCATAAAGATGTTAAATGGAATTCGTGTTATGAATCTGTGCTGGNCATGGACG 1262

Qy       1390 AATATGAA 1397
              || |  ||
Db       1263 AAAAAAAA 1270


RESULT 5
US-10-116-051-1
; Sequence 1, Application US/10116051
; Patent No. US20020146791A1
; GENERAL INFORMATION:
;  APPLICANT: Olsen et al.
;  TITLE OF INVENTION: CORPUSCLES OF STANNIUS PROTEIN, STANNIOCALCIN
;  FILE REFERENCE: PF108P1D1C1
;  CURRENT APPLICATION NUMBER: US/10/116,051
;  CURRENT FILING DATE:  2002-04-05
;  PRIOR APPLICATION NUMBER: 09/312,610
;  PRIOR FILING DATE: 1999-05-17
;  PRIOR APPLICATION NUMBER: 08/431,117
;  PRIOR FILING DATE: 1995-04-28
;  PRIOR APPLICATION NUMBER: 08/208,005
;  PRIOR FILING DATE: 1994-03-08
;  NUMBER OF SEQ ID NOS: 10
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
;   LENGTH: 771
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-116-051-1

  Query Match           20.5%;  Score 769.4;  DB 12;  Length 771;
  Best Local Similarity   99.9%;  Pred. No. 7.1e-194;
  Matches  770;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        159 GAAACTTCTCAGAGAATGCTCCAAAACTCAGCAGTGCTTCTGGTGCTGGTGATCAGTGCT 218
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db          1 GAAACTTCTCAGAGAATGCTCCAAAACTCAGCAGTGCTTCTGGTGCTGGTGATCAGTGCT 60

Qy        219 TCTGCAACCCATGAGGCGGAGCAGAATGACTCTGTGAGCCCCAGGAAATCCCGAGTGGCG 278
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TCTGCAACCCATGAGGCGGAGCAGAATGACTCTGTGAGCCCCAGGAAATCCCGAGTGGCG 120

Qy        279 GCTCAAAACTCAGCTGAAGTGGTTCGTTGCCTCAACAGTGCTCTACAGGTCGGCTGCGGG 338
              || ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GCCCAAAACTCAGCTGAAGTGGTTCGTTGCCTCAACAGTGCTCTACAGGTCGGCTGCGGG 180

Qy        339 GCTTTTGCATGCCTGGAAAACTCCACCTGTGACACAGATGGGATGTATGACATCTGTAAA 398
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GCTTTTGCATGCCTGGAAAACTCCACCTGTGACACAGATGGGATGTATGACATCTGTAAA 240

Qy        399 TCCTTCTTGTACAGCGCTGCTAAATTTGACACTCAGGGAAAAGCATTCGTCAAAGAGAGC 458
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TCCTTCTTGTACAGCGCTGCTAAATTTGACACTCAGGGAAAAGCATTCGTCAAAGAGAGC 300

Qy        459 TTAAAATGCATCGCCAACGGGGTCACCTCCAAGGTCTTCCTCGCCATTCGGAGGTGCTCC 518
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TTAAAATGCATCGCCAACGGGGTCACCTCCAAGGTCTTCCTCGCCATTCGGAGGTGCTCC 360

Qy        519 ACTTTCCAAAGGATGATTGCTGAGGTGCAGGAAGAGTGCTACAGCAAGCTGAATGTGTGC 578
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 ACTTTCCAAAGGATGATTGCTGAGGTGCAGGAAGAGTGCTACAGCAAGCTGAATGTGTGC 420

Qy        579 AGCATCGCCAAGCGGAACCCTGAAGCCATCACTGAGGTCGTCCAGCTGCCCAATCACTTC 638
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 AGCATCGCCAAGCGGAACCCTGAAGCCATCACTGAGGTCGTCCAGCTGCCCAATCACTTC 480

Qy        639 TCCAACAGATACTATAACAGACTTGTCCGAAGCCTGCTGGAATGTGATGAAGACACAGTC 698
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 TCCAACAGATACTATAACAGACTTGTCCGAAGCCTGCTGGAATGTGATGAAGACACAGTC 540

Qy        699 AGCACAATCAGAGACAGCCTGATGGAGAAAATTGGGCCTAACATGGCCAGCCTCTTCCAC 758
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 AGCACAATCAGAGACAGCCTGATGGAGAAAATTGGGCCTAACATGGCCAGCCTCTTCCAC 600

Qy        759 ATCCTGCAGACAGACCACTGTGCCCAAACACACCCACGAGCTGACTTCAACAGGAGACGC 818
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 ATCCTGCAGACAGACCACTGTGCCCAAACACACCCACGAGCTGACTTCAACAGGAGACGC 660

Qy        819 ACCAATGAGCCGCAGAAGCTGAAAGTCCTCCTCAGGAACCTCCGAGGTGAGGAGGACTCT 878
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 ACCAATGAGCCGCAGAAGCTGAAAGTCCTCCTCAGGAACCTCCGAGGTGAGGAGGACTCT 720

Qy        879 CCCTCCCACATCAAACGCACATCCCATGAGAGTGCATAACCAGGGAGAGGT 929
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 CCCTCCCACATCAAACGCACATCCCATGAGAGTGCATAACCAGGGAGAGGT 771


RESULT 6
US-09-778-320-149
; Sequence 149, Application US/09778320
; Patent No. US20010034052A1
; GENERAL INFORMATION:
;  APPLICANT:  Dillon, Davin C.
;  APPLICANT:  Day, Craig H.
;  APPLICANT:  Jiang, Yuqiu
;  APPLICANT:  Houghton, Raymond L.
;  APPLICANT:  Mitcham, Jennifer
;  APPLICANT:  Wang, TongTong
;  APPLICANT:  McNeill, Patricia D.
;  TITLE OF INVENTION:  COMPOSITIONS AND METHODS FOR THE THERAPY AND
;  TITLE OF INVENTION:  DIAGNOSIS OF BREAST CANCER
;  FILE REFERENCE:  210121.491C5
;  CURRENT APPLICATION NUMBER: US/09/778,320
;  CURRENT FILING DATE:  2001-02-06
;  NUMBER OF SEQ ID NOS:  301
;  SOFTWARE:  FastSEQ for Windows Version 3.0
; SEQ ID NO 149
;   LENGTH: 585
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(585)
;   OTHER INFORMATION: n=A,T,C or G
US-09-778-320-149

  Query Match             14.7%;  Score 552;  DB 10;  Length 585;
  Best Local Similarity   96.6%;  Pred. No. 3.7e-136;
  Matches  561;  Conservative    0;  Mismatches   20;  Indels    0;  Gaps    0;

Qy        407 GTACAGCGCTGCTAAATTTGACACTCAGGGAAAAGCATTCGTCAAAGAGAGCTTAAAATG 466
              ||||| | |||||||||||||||| | ||||||||||||||||||||||||||||||||
Db          5 GTACANCACTGCTAAATTTGACACTNANGGAAAAGCATTCGTCAAAGAGAGCTTAAAATG 64

Qy        467 CATCGCCAACGGGGTCACCTCCAAGGTCTTCCTCGCCATTCGGAGGTGCTCCACTTTCCA 526
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         65 CATCGCCAACGGGGTCACCTCCAAGGTCTTCCTCGCCATTCGGAGGTGCTCCACTTTCCA 124

Qy        527 AAGGATGATTGCTGAGGTGCAGGAAGAGTGCTACAGCAAGCTGAATGTGTGCAGCATCGC 586
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        125 AAGGATGATTGCTGAGGTGCAGGAAGAGTGCTACAGCAAGCTGAATGTGTGCAGCATCGC 184

Qy        587 CAAGCGGAACCCTGAAGCCATCACTGAGGTCGTCCAGCTGCCCAATCACTTCTCCAACAG 646
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        185 CAAGCGGAACCCTGAAGCCATCACTGAGGTCGTCCAGCTGCCCAATCACTTCTCCAACAG 244

Qy        647 ATACTATAACAGACTTGTCCGAAGCCTGCTGGAATGTGATGAAGACACAGTCAGCACAAT 706
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        245 ATACTATAACAGACTTGTCCGAAGCCTGCTGGAATGTGATGAAGACACAGTCAGCACAAT 304

Qy        707 CAGAGACAGCCTGATGGAGAAAATTGGGCCTAACATGGCCAGCCTCTTCCACATCCTGCA 766
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        305 CAGAGACAGCCTGATGGAGAAAATTGGGCCTAACATGGCCAGCCTCTTCCACATCCTGCA 364

Qy        767 GACAGACCACTGTGCCCAAACACACCCACGAGCTGACTTCAACAGGAGACGCACCAATGA 826
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        365 GACAGACCACTGTGCCCAAACACACCCACGAGCTGACTTCAACAGGAGACGCACCAATGA 424

Qy        827 GCCGCAGAAGCTGAAAGTCCTCCTCAGGAACCTCCGAGGTGAGGAGGACTCTCCCTCCCA 886
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        425 GCCGCAGAAGCTGAAAGTCCTCCTCAGGAACCTCCGAGGTGAGGAGGACTCTCCCTCCCA 484

Qy        887 CATCAAACGCACATCCCATGAGAGTGCATAACCAGGGAGAGGTTATTCACAACCTCACCA 946
              |||||||||||||||||||||||||||||||||||||||| ||||||||||||| | |
Db        485 CATCAAACGCACATCCCATGAGAGTGCATAACCAGGGAGAGGNTATTCACAACCTCCCAA 544

Qy        947 AACTAGTATCATTTTAGGGGTGTTGACACACCAGTTTTGAG 987
              |          |||  |||| ||||||||||||||||||
Db        545 ACTAGTATCATTTTAGGGGGNGTTGACACACCAGTTTTGAG 585


RESULT 7
US-09-910-689-149
; Sequence 149, Application US/09910689
; Patent No. US20020081609A1
; GENERAL INFORMATION:
;  APPLICANT: Dillon, Davin C.
;  APPLICANT:  Day, Craig H.
;  APPLICANT:  Jiang, Yuqiu
;  APPLICANT:  Houghton, Raymond L.
;  APPLICANT:  Mitcham, Jennifer
;  APPLICANT:  Wang, Tongtong
;  APPLICANT:  McNeill, Patricia D.
;  APPLICANT:  Harlocker, Susan L.
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
;  TITLE OF INVENTION:  DIAGNOSIS OF BREAST CANCER
;  FILE REFERENCE: 210121.491C6
;  CURRENT APPLICATION NUMBER: US/09/910,689
;  CURRENT FILING DATE:  2001-07-20
;  NUMBER OF SEQ ID NOS: 307
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 149
```

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;   LENGTH: 585
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: 10, 30, 32, 527, 565
;   OTHER INFORMATION: n = A,T,C or G
US-09-910-689-149

  Query Match             14.7%;  Score 552;  DB 10;  Length 585;
  Best Local Similarity   96.6%;  Pred. No. 3.7e-136;
  Matches  561;  Conservative    0;  Mismatches   20;  Indels    0;  Gaps    0;

Qy        407 GTACAGCGCTGCTAAATTTGACACTCAGGGAAAAGCATTCGTCAAAGAGAGCTTAAAATG 466
              ||||| | |||||||||||||||| | ||||||||||||||||||||||||||||||||
Db          5 GTACANCACTGCTAAATTTGACACTNANGGAAAAGCATTCGTCAAAGAGAGCTTAAAATG 64

Qy        467 CATCGCCAACGGGGTCACCTCCAAGGTCTTCCTCGCCATTCGGAGGTGCTCCACTTTCCA 526
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         65 CATCGCCAACGGGGTCACCTCCAAGGTCTTCCTCGCCATTCGGAGGTGCTCCACTTTCCA 124

Qy        527 AAGGATGATTGCTGAGGTGCAGGAAGAGTGCTACAGCAAGCTGAATGTGTGCAGCATCGC 586
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        125 AAGGATGATTGCTGAGGTGCAGGAAGAGTGCTACAGCAAGCTGAATGTGTGCAGCATCGC 184

Qy        587 CAAGCGGAACCCTGAAGCCATCACTGAGGTCGTCCAGCTGCCCAATCACTTCTCCAACAG 646
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        185 CAAGCGGAACCCTGAAGCCATCACTGAGGTCGTCCAGCTGCCCAATCACTTCTCCAACAG 244

Qy        647 ATACTATAACAGACTTGTCCGAAGCCTGCTGGAATGTGATGAAGACACAGTCAGCACAAT 706
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        245 ATACTATAACAGACTTGTCCGAAGCCTGCTGGAATGTGATGAAGACACAGTCAGCACAAT 304

Qy        707 CAGAGACAGCCTGATGGAGAAAATTGGGCCTAACATGGCCAGCCTCTTCCACATCCTGCA 766
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        305 CAGAGACAGCCTGATGGAGAAAATTGGGCCTAACATGGCCAGCCTCTTCCACATCCTGCA 364

Qy        767 GACAGACCACTGTGCCCAAACACACCCACGAGCTGACTTCAACAGGAGACGCACCAATGA 826
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        365 GACAGACCACTGTGCCCAAACACACCCACGAGCTGACTTCAACAGGAGACGCACCAATGA 424

Qy        827 GCCGCAGAAGCTGAAAGTCCTCCTCAGGAACCTCCGAGGTGAGGAGGACTCTCCCTCCCA 886
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        425 GCCGCAGAAGCTGAAAGTCCTCCTCAGGAACCTCCGAGGTGAGGAGGACTCTCCCTCCCA 484

Qy        887 CATCAAACGCACATCCCATGAGAGTGCATAACCAGGGAGAGGTTATTCACAACCTCACCA 946
              |||||||||||||||||||||||||||||||||||||| |||||||||||| | |
Db        485 CATCAAACGCACATCCCATGAGAGTGCATAACCAGGGAGAGGNTATTCACAACCTCCCAA 544

Qy        947 AACTAGTATCATTTTAGGGGTGTTGACACACCAGTTTTGAG 987
              |          |||  |||| ||||||||||||||||||||
Db        545 ACTAGTATCATTTTAGGGGGNGTTGACACACCAGTTTTGAG 585


RESULT 8
US-10-010-742-149
; Sequence 149, Application US/10010742
; Patent No. US20020146727A1
; GENERAL INFORMATION:
;  APPLICANT: Dillon, Davin C.
;  APPLICANT:  Day, Craig H.
;  APPLICANT:  Jiang, Yuqiu
;  APPLICANT:  Houghton, Raymond L.
;  APPLICANT:  Mitcham, Jennifer L.
;  APPLICANT:  Wang, Tongtong
;  APPLICANT:  McNeill, Patricia D.
;  APPLICANT:  Harlocker, Susan L.
;  APPLICANT:  Bennington, Angela Ann
;  APPLICANT:  Zehentner, Barbara
;  APPLICANT:  Fanger, Gary R.
;  APPLICANT:  Retter, Marc W.
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
;  TITLE OF INVENTION:  DIAGNOSIS OF BREAST CANCER
;  FILE REFERENCE: 210121.491C7
;  CURRENT APPLICATION NUMBER: US/10/010,742
;  CURRENT FILING DATE:  2001-11-30
;  NUMBER OF SEQ ID NOS: 307
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 149
;   LENGTH: 585
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: 10, 30, 32, 527, 565
;   OTHER INFORMATION: n = A,T,C or G
US-10-010-742-149

  Query Match             14.7%;  Score 552;  DB 12;  Length 585;
  Best Local Similarity   96.6%;  Pred. No. 3.7e-136;
  Matches  561;  Conservative    0;  Mismatches   20;  Indels    0;  Gaps    0;

Qy        407 GTACAGCGCTGCTAAATTTGACACTCAGGGAAAAGCATTCGTCAAAGAGAGCTTAAAATG 466
              ||||| | |||||||||||||||| | ||||||||||||||||||||||||||||||||
Db          5 GTACANCACTGCTAAATTTGACACTNANGGAAAAGCATTCGTCAAAGAGAGCTTAAAATG 64

Qy        467 CATCGCCAACGGGGTCACCTCCAAGGTCTTCCTCGCCATTCGGAGGTGCTCCACTTTCCA 526
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         65 CATCGCCAACGGGGTCACCTCCAAGGTCTTCCTCGCCATTCGGAGGTGCTCCACTTTCCA 124

Qy        527 AAGGATGATTGCTGAGGTGCAGGAAGAGTGCTACAGCAAGCTGAATGTGTGCAGCATCGC 586
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        125 AAGGATGATTGCTGAGGTGCAGGAAGAGTGCTACAGCAAGCTGAATGTGTGCAGCATCGC 184

Qy        587 CAAGCGGAACCCTGAAGCCATCACTGAGGTCGTCCAGCTGCCCAATCACTTCTCCAACAG 646
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        185 CAAGCGGAACCCTGAAGCCATCACTGAGGTCGTCCAGCTGCCCAATCACTTCTCCAACAG 244

Qy        647 ATACTATAACAGACTTGTCCGAAGCCTGCTGGAATGTGATGAAGACACAGTCAGCACAAT 706
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        245 ATACTATAACAGACTTGTCCGAAGCCTGCTGGAATGTGATGAAGACACAGTCAGCACAAT 304

Qy        707 CAGAGACAGCCTGATGGAGAAAATTGGGCCTAACATGGCCAGCCTCTTCCACATCCTGCA 766
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        305 CAGAGACAGCCTGATGGAGAAAATTGGGCCTAACATGGCCAGCCTCTTCCACATCCTGCA 364

Qy        767 GACAGACCACTGTGCCCAAACACACCCACGAGCTGACTTCAACAGGAGACGCACCAATGA 826
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        365 GACAGACCACTGTGCCCAAACACACCCACGAGCTGACTTCAACAGGAGACGCACCAATGA 424

Qy        827 GCCGCAGAAGCTGAAAGTCCTCCTCAGGAACCTCCGAGGTGAGGAGGACTCTCCCTCCCA 886
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        425 GCCGCAGAAGCTGAAAGTCCTCCTCAGGAACCTCCGAGGTGAGGAGGACTCTCCCTCCCA 484

Qy        887 CATCAAACGCACATCCCATGAGAGTGCATAACCAGGGAGAGGTTATTCACAACCTCACCA 946
              |||||||||||||||||||||||||||||||||||||| |||||||||||| | |
Db        485 CATCAAACGCACATCCCATGAGAGTGCATAACCAGGGAGAGGNTATTCACAACCTCCCAA 544

Qy        947 AACTAGTATCATTTTAGGGGTGTTGACACACCAGTTTTGAG 987
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Db        545 ACTAGTATCATTTTAGGGGGNGTTGACACACCAGTTTTGAG 585


RESULT 9
US-09-736-457-4/c
; Sequence 4, Application US/09736457
; Patent No. US20020168637A1
; GENERAL INFORMATION:
;  APPLICANT:  Wang, Tongtong
;  APPLICANT:  Bangur, Chaitanya S.
;  APPLICANT:  Lodes, Michael A.
;  APPLICANT:  Fanger, Gary
;  APPLICANT:  Vedvick, Tom
;  APPLICANT:  Carter, Darrick
;  APPLICANT:  Retter, Marc
;  APPLICANT:  Mannion, Jane
```

```
;  APPLICANT:  Fan, Liqun
;  APPLICANT:  Wang, Aijun
;  TITLE OF INVENTION:  COMPOSITIONS AND METHODS FOR THE THERAPY AND
;  TITLE OF INVENTION:  DIAGNOSIS OF LUNG CANCER
;  FILE REFERENCE:  210121.478C15
;  CURRENT APPLICATION NUMBER: US/09/736,457
;  CURRENT FILING DATE:  2000-12-13
;  NUMBER OF SEQ ID NOS:  1864
;  SOFTWARE:  FastSEQ for Windows Version 3.0
; SEQ ID NO 4
;   LENGTH: 510
;   TYPE: DNA
;   ORGANISM: Homo sapien
US-09-736-457-4

  Query Match             12.8%;  Score 482.4;  DB 9;  Length 510;
  Best Local Similarity   99.4%;  Pred. No. 1.1e-117;
  Matches  505;  Conservative    0;  Mismatches    1;  Indels    2;  Gaps    2;

Qy       1578 AACTGCTCAGAGCTTTAAAAGTATCTTTAACAATTGTCTTAAAACCAGAGAATCTTAAGG 1637
             |||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db        508 AACTGCTCAGAGCTTTAGAAGTATCTTTAACAATTGTCTTAAAACCAGAGAATCTTAAGG 449

Qy       1638 TCTAAC-TGTGGAATATAAATAGCTGAAAACTAATGTACTGTACATAAATTCCAGAGGAC 1696
             |||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        448 TCTAACTTGTGGAATATAAATAGCTGAAAACTAATGTACTGTACATAAATTCCAGAGGAC 389

Qy       1697 TCTGCTTAAACAAAGCAGTATATAATAACTTTATTGCATATAGATTTAGTTTTGTAACTT 1756
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        388 TCTGCTTAAACAAAGCAGTATATAATAACTTTATTGCATATAGATTTAGTTTTGTAACTT 329

Qy       1757 AGCTTTATTTTTCTTTTCCTGGGAATGGAATAACTATCTCACTTCCAGATATCCACATAA 1816
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        328 AGCTTTATTTTTCTTTTCCTGGGAATGGAATAACTATCTCACTTCCAGATATCCACATAA 269

Qy       1817 ATGCTCCTTGTGGCCTTTTTTATAACTAAGGGGGTAGAAGTAGTTTTAATTCAACATCAA 1876
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        268 ATGCTCCTTGTGGCCTTTTTTATAACTAAGGGGGTAGAAGTAGTTTTAATTCAACATCAA 209

Qy       1877 AACTTAAGATGGGCCTGTATGAGACAGGAAAAACCAACAGGTTTATCTGAAGGACCCCAG 1936
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        208 AACTTAAGATGGGCCTGTATGAGACAGGAAAAACCAACAGGTTTATCTGAAGGACCCCAG 149

Qy       1937 GTAAGATGTTAATCTCCCAGCCCACCTCAACCCAGAGGCTACTCTTGACTTAGACCTATA 1996
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        148 GTAAGATGTTAATCTCCCAGCCCACCTCAACCCAGAGGCTACTCTTGACTTAGACCTATA 89

Qy       1997 CTGAAAGATCTCTGTCACATCCAACTGGAAATTCCAGGAACCAAAAAGAGCA-CCCTATG 2055
             ||||||||||||||||||||||||||||||||||||||||||||||||||| |||||||
Db          88 CTGAAAGATCTCTGTCACATCCAACTGGAAATTCCAGGAACCAAAAAGAGCATCCCTATG 29

Qy       2056 GGCTTGGACCACTTACAGTGTGATAAGG 2083
             ||||||||||||||||||||||||||||
Db          28 GGCTTGGACCACTTACAGTGTGATAAGG 1


RESULT 10
US-09-902-941-4/c
; Sequence 4, Application US/09902941
; Patent No. US20020172952A1
; GENERAL INFORMATION:
;  APPLICANT: Henderson, Robert A.
;  APPLICANT:  Wang, Tongtong
;  APPLICANT:  Watanabe, Yoshihiro
;  APPLICANT:  Johnson, Jeffrey C.
;  APPLICANT:  Retter, Marc W.
;  APPLICANT:  Marnerakis, Margarita
;  APPLICANT:  Carter, Darrick
;  APPLICANT:  Fanger, Gary R.
;  APPLICANT:  Vedvick, Thomas S.
;  APPLICANT:  Bangur, Chaitanya S.
;  APPLICANT:  McNabb, Andria
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
;  TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
;  FILE REFERENCE: 210121.478C17
;  CURRENT APPLICATION NUMBER: US/09/902,941
;  CURRENT FILING DATE:  2001-07-10
;  NUMBER OF SEQ ID NOS: 2002
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
;   LENGTH: 510
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-902-941-4

  Query Match             12.8%;  Score 482.4;  DB 9;  Length 510;
  Best Local Similarity   99.4%;  Pred. No. 1.1e-117;
  Matches  505;  Conservative    0;  Mismatches    1;  Indels    2;  Gaps    2;

Qy       1578 AACTGCTCAGAGCTTTAAAAGTATCTTTAACAATTGTCTTAAAACCAGAGAATCTTAAGG 1637
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Db        508 AACTGCTCAGAGCTTTAGAAGTATCTTTAACAATTGTCTTAAAACCAGAGAATCTTAAGG 449

Qy       1638 TCTAAC-TGTGGAATATAAATAGCTGAAAACTAATGTACTGTACATAAATTCCAGAGGAC 1696
             |||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        448 TCTAACTTGTGGAATATAAATAGCTGAAAACTAATGTACTGTACATAAATTCCAGAGGAC 389

Qy       1697 TCTGCTTAAACAAAGCAGTATATAATAACTTTATTGCATATAGATTTAGTTTTGTAACTT 1756
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        388 TCTGCTTAAACAAAGCAGTATATAATAACTTTATTGCATATAGATTTAGTTTTGTAACTT 329

Qy       1757 AGCTTTATTTTTCTTTTCCTGGGAATGGAATAACTATCTCACTTCCAGATATCCACATAA 1816
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        328 AGCTTTATTTTTCTTTTCCTGGGAATGGAATAACTATCTCACTTCCAGATATCCACATAA 269

Qy       1817 ATGCTCCTTGTGGCCTTTTTTATAACTAAGGGGGTAGAAGTAGTTTTAATTCAACATCAA 1876
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        268 ATGCTCCTTGTGGCCTTTTTTATAACTAAGGGGGTAGAAGTAGTTTTAATTCAACATCAA 209

Qy       1877 AACTTAAGATGGGCCTGTATGAGACAGGAAAAACCAACAGGTTTATCTGAAGGACCCCAG 1936
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        208 AACTTAAGATGGGCCTGTATGAGACAGGAAAAACCAACAGGTTTATCTGAAGGACCCCAG 149

Qy       1937 GTAAGATGTTAATCTCCCAGCCCACCTCAACCCAGAGGCTACTCTTGACTTAGACCTATA 1996
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        148 GTAAGATGTTAATCTCCCAGCCCACCTCAACCCAGAGGCTACTCTTGACTTAGACCTATA 89

Qy       1997 CTGAAAGATCTCTGTCACATCCAACTGGAAATTCCAGGAACCAAAAAGAGCA-CCCTATG 2055
             ||||||||||||||||||||||||||||||||||||||||||||||||||| |||||||
Db          88 CTGAAAGATCTCTGTCACATCCAACTGGAAATTCCAGGAACCAAAAAGAGCATCCCTATG 29

Qy       2056 GGCTTGGACCACTTACAGTGTGATAAGG 2083
             ||||||||||||||||||||||||||||
Db          28 GGCTTGGACCACTTACAGTGTGATAAGG 1


RESULT 11
US-09-849-626-4/c
; Sequence 4, Application US/09849626
; Publication No. US20020197669A1
; GENERAL INFORMATION:
;  APPLICANT: Bangur, Chaitanya
;  APPLICANT:  Fanger, Gary
;  APPLICANT:  Wang, Aijun
;  APPLICANT:  Wang, Tongtong
;  APPLICANT:  Switzer, Anne
;  APPLICANT:  McNeill, Patricia
;  APPLICANT:  Clapper, Jonathan
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
;  TITLE OF INVENTION:  DIAGNOSIS OF LUNG CANCER
;  FILE REFERENCE: 210121.478C16
;  CURRENT APPLICATION NUMBER: US/09/849,626
;  CURRENT FILING DATE:  2001-05-03
;  NUMBER OF SEQ ID NOS: 1926
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 4
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;   LENGTH: 510
;   TYPE: DNA
;   ORGANISM: Homo sapien
US-09-849-626-4

  Query Match            12.8%;  Score 482.4;  DB 9;  Length 510;
  Best Local Similarity   99.4%;  Pred. No. 1.1e-117;
  Matches  505;  Conservative    0;  Mismatches    1;  Indels    2;  Gaps    2;

Qy       1578 AACTGCTCAGAGCTTTAAAAGTATCTTTAACAATTGTCTTAAAACCAGAGAATCTTAAGG 1637
             |||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db        508 AACTGCTCAGAGCTTTAGAAGTATCTTTAACAATTGTCTTAAAACCAGAGAATCTTAAGG 449

Qy       1638 TCTAAC-TGTGGAATATAAATAGCTGAAAACTAATGTACTGTACATAAATTCCAGAGGAC 1696
             |||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        448 TCTAACTTGTGGAATATAAATAGCTGAAAACTAATGTACTGTACATAAATTCCAGAGGAC 389

Qy       1697 TCTGCTTAAACAAAGCAGTATATAATAACTTTATTGCATATAGATTTAGTTTTGTAACTT 1756
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        388 TCTGCTTAAACAAAGCAGTATATAATAACTTTATTGCATATAGATTTAGTTTTGTAACTT 329

Qy       1757 AGCTTTATTTTTCTTTTCCTGGGAATGGAATAACTATCTCACTTCCAGATATCCACATAA 1816
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        328 AGCTTTATTTTTCTTTTCCTGGGAATGGAATAACTATCTCACTTCCAGATATCCACATAA 269

Qy       1817 ATGCTCCTTGTGGCCTTTTTTATAACTAAGGGGGTAGAAGTAGTTTTAATTCAACATCAA 1876
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        268 ATGCTCCTTGTGGCCTTTTTTATAACTAAGGGGGTAGAAGTAGTTTTAATTCAACATCAA 209

Qy       1877 AACTTAAGATGGGCCTGTATGAGACAGGAAAAACCAACAGGTTTATCTGAAGGACCCCAG 1936
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        208 AACTTAAGATGGGCCTGTATGAGACAGGAAAAACCAACAGGTTTATCTGAAGGACCCCAG 149

Qy       1937 GTAAGATGTTAATCTCCCAGCCCACCTCAACCCAGAGGCTACTCTTGACTTAGACCTATA 1996
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        148 GTAAGATGTTAATCTCCCAGCCCACCTCAACCCAGAGGCTACTCTTGACTTAGACCTATA 89

Qy       1997 CTGAAAGATCTCTGTCACATCCAACTGGAAATTCCAGGAACCAAAAAGAGCA-CCCTATG 2055
             ||||||||||||||||||||||||||||||||||||||||||||||||||| |||||||
Db          88 CTGAAAGATCTCTGTCACATCCAACTGGAAATTCCAGGAACCAAAAAGAGCATCCCTATG 29

Qy       2056 GGCTTGGACCACTTACAGTGTGATAAGG 2083
             ||||||||||||||||||||||||||||
Db          28 GGCTTGGACCACTTACAGTGTGATAAGG 1


RESULT 12
US-10-017-754-4/c
; Sequence 4, Application US/10017754
; Publication No. US20030054363A1
; GENERAL INFORMATION:
;  APPLICANT: Henderson, Robert A.
;  APPLICANT:  Wang, Tongtong
;  APPLICANT:  Watanabe, Yoshihiro
;  APPLICANT:  Johnson, Jeffrey C.
;  APPLICANT:  Retter, Marc W.
;  APPLICANT:  Marnerakis, Margarita
;  APPLICANT:  Carter, Darrick
;  APPLICANT:  Fanger, Gary R.
;  APPLICANT:  Vedvick, Thomas S.
;  APPLICANT:  Bangur, Chaitanya S.
;  APPLICANT:  McNabb, Andria
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
;  TITLE OF INVENTION:  AND DIAGNOSIS OF LUNG CANCER
;  FILE REFERENCE: 210121.478C18
;  CURRENT APPLICATION NUMBER: US/10/017,754
;  CURRENT FILING DATE:  2001-10-29
;  NUMBER OF SEQ ID NOS: 2004
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
;   LENGTH: 510
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-017-754-4

  Query Match            12.8%;  Score 482.4;  DB 9;  Length 510;
  Best Local Similarity   99.4%;  Pred. No. 1.1e-117;
  Matches  505;  Conservative    0;  Mismatches    1;  Indels    2;  Gaps    2;

Qy       1578 AACTGCTCAGAGCTTTAAAAGTATCTTTAACAATTGTCTTAAAACCAGAGAATCTTAAGG 1637
             |||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db        508 AACTGCTCAGAGCTTTAGAAGTATCTTTAACAATTGTCTTAAAACCAGAGAATCTTAAGG 449

Qy       1638 TCTAAC-TGTGGAATATAAATAGCTGAAAACTAATGTACTGTACATAAATTCCAGAGGAC 1696
             |||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        448 TCTAACTTGTGGAATATAAATAGCTGAAAACTAATGTACTGTACATAAATTCCAGAGGAC 389

Qy       1697 TCTGCTTAAACAAAGCAGTATATAATAACTTTATTGCATATAGATTTAGTTTTGTAACTT 1756
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        388 TCTGCTTAAACAAAGCAGTATATAATAACTTTATTGCATATAGATTTAGTTTTGTAACTT 329

Qy       1757 AGCTTTATTTTTCTTTTCCTGGGAATGGAATAACTATCTCACTTCCAGATATCCACATAA 1816
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Db        328 AGCTTTATTTTTCTTTTCCTGGGAATGGAATAACTATCTCACTTCCAGATATCCACATAA 269

Qy       1817 ATGCTCCTTGTGGCCTTTTTTATAACTAAGGGGGTAGAAGTAGTTTTAATTCAACATCAA 1876
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        268 ATGCTCCTTGTGGCCTTTTTTATAACTAAGGGGGTAGAAGTAGTTTTAATTCAACATCAA 209

Qy       1877 AACTTAAGATGGGCCTGTATGAGACAGGAAAAACCAACAGGTTTATCTGAAGGACCCCAG 1936
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        208 AACTTAAGATGGGCCTGTATGAGACAGGAAAAACCAACAGGTTTATCTGAAGGACCCCAG 149

Qy       1937 GTAAGATGTTAATCTCCCAGCCCACCTCAACCCAGAGGCTACTCTTGACTTAGACCTATA 1996
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        148 GTAAGATGTTAATCTCCCAGCCCACCTCAACCCAGAGGCTACTCTTGACTTAGACCTATA 89

Qy       1997 CTGAAAGATCTCTGTCACATCCAACTGGAAATTCCAGGAACCAAAAAGAGCA-CCCTATG 2055
             ||||||||||||||||||||||||||||||||||||||||||||||||||| |||||||
Db          88 CTGAAAGATCTCTGTCACATCCAACTGGAAATTCCAGGAACCAAAAAGAGCATCCCTATG 29

Qy       2056 GGCTTGGACCACTTACAGTGTGATAAGG 2083
             ||||||||||||||||||||||||||||
Db          28 GGCTTGGACCACTTACAGTGTGATAAGG 1


RESULT 13
US-10-060-036-2677/c
; Sequence 2677, Application US/10060036
; Publication No. US20030073144A1
; GENERAL INFORMATION:
;  APPLICANT: Benson, Darin R.
;  APPLICANT:  Kalos, Michael D.
;  APPLICANT:  Lodes, Michael J.
;  APPLICANT:  Persing, David H.
;  APPLICANT:  Hepler, William T.
;  APPLICANT:  Jiang, Yuqiu
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
;  TITLE OF INVENTION:  AND DIAGNOSIS OF PANCREATIC CANCER
;  FILE REFERENCE: 210121.566
;  CURRENT APPLICATION NUMBER: US/10/060,036
;  CURRENT FILING DATE:  2002-01-30
;  NUMBER OF SEQ ID NOS: 4560
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2677
;   LENGTH: 473
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-060-036-2677

  Query Match            12.5%;  Score 471.4;  DB 9;  Length 473;
  Best Local Similarity   99.8%;  Pred. No. 8.4e-115;
  Matches  472;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        518 CACTTTCCAAAGGATGATTGCTGAGGTGCAGGAAGAGTGCTACAGCAAGCTGAATGTGTG 577
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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```
Db        473 CACTTTCCAAAGGATGATTGCTGAGGTGCAGGAAGAGTGCTACAGCAAGCTGAATGTGTG 414

Qy        578 CAGCATCGCCAAGCGGAACCCTGAAGCCATCACTGAGGTCGTCCAGCTGCCCAATCACTT 637
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        413 CAGCATCGCCAAGCGGAACCCTGAAGCCATCACTGAGGTCGTCCAGCTGCCCAATCACTT 354

Qy        638 CTCCAACAGATACTATAACAGACTTGTCCGAAGCCTGCTGGAATGTGATGAAGACACAGT 697
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        353 CTCCAACAGATACTATAACAGACTTGTCCGAAGCCTGCTGGAATGTGATGAAGACACAGT 294

Qy        698 CAGCACAATCAGAGACAGCCTGATGGAGAAAATTGGGCCTAACATGGCCAGCCTCTTCCA 757
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        293 CAGCACAATCAGAGACAGCCTGATGGAGAAAATTGGGCCTAACATGGCCAGCCTCTTCCA 234

Qy        758 CATCCTGCAGACAGACCACTGTGCCCAAACACACCCACGAGCTGACTTCAACAGGAGACG 817
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        233 CATCCTGCAGACAGACCACTGTGCCCAAACACACCCACGAGCTGACTTCAACAGGAGACG 174

Qy        818 CACCAATGAGCCGCAGAAGCTGAAAGTCCTCCTCAGGAACCTCCGAGGTGAGGAGGACTC 877
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        173 CACCAATGAGCCGCAGAAGCTGAAAGTCCTCCTCAGGAACCTCCGAGGTGAGGAGGACTC 114

Qy        878 TCCCTCCCACATCAAACGCACATCCCATGAGAGTGCATAACCAGGGAGAGGTTATTCACA 937
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        113 TCCCTCCCACATCAAACGCACATCCCATGAGAGTGCATAACCAGGGAGAGGTTATTCACA 54

Qy        938 ACCTCACCAAACTAGTATCATTTTAGGGGTGTTGACACACCAGTTTTGAGTGT 990
              |||||||||||||||||||||||||||||||||||||||||| ||||||||||
Db         53 ACCTCACCAAACTAGTATCATTTTAGGGGTGTTGACACACCAATTTTGAGTGT 1
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RESULT 14
US-09-918-995-33032
; Sequence 33032, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; TITLE OF INVENTION: FROM VARIOUS cDNA LIBRARIES
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918,995
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/235,076
; PRIOR FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 33032
; LENGTH: 436
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-918-995-33032

Query Match 11.6%; Score 436; DB 9; Length 436;
Best Local Similarity 100.0%; Pred. No. 2.1e-105;
Matches 436; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy        686 TGAAGACACAGTCAGCACAATCAGAGACAGCCTGATGGAGAAAATTGGGCCTAACATGGC 745
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 TGAAGACACAGTCAGCACAATCAGAGACAGCCTGATGGAGAAAATTGGGCCTAACATGGC 60

Qy        746 CAGCCTCTTCCACATCCTGCAGACAGACCACTGTGCCCAAACACACCCACGAGCTGACTT 805
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CAGCCTCTTCCACATCCTGCAGACAGACCACTGTGCCCAAACACACCCACGAGCTGACTT 120

Qy        806 CAACAGGAGACGCACCAATGAGCCGCAGAAGCTGAAAGTCCTCCTCAGGAACCTCCGAGG 865
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CAACAGGAGACGCACCAATGAGCCGCAGAAGCTGAAAGTCCTCCTCAGGAACCTCCGAGG 180

Qy        866 TGAGGAGGACTCTCCCTCCCACATCAAACGCACATCCCATGAGAGTGCATAACCAGGGAG 925
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TGAGGAGGACTCTCCCTCCCACATCAAACGCACATCCCATGAGAGTGCATAACCAGGGAG 240

Qy        926 AGGTTATTCACAACCTCACCAAACTAGTATCATTTTAGGGGTGTTGACACACCAGTTTTG 985
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AGGTTATTCACAACCTCACCAAACTAGTATCATTTTAGGGGTGTTGACACACCAGTTTTG 300

Qy        986 AGTGTACTGTGCCTGGTTTGATTTTTTTAAAGTAGTTCCTATTTTCTATCCCCCTTAAAG 1045
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 AGTGTACTGTGCCTGGTTTGATTTTTTTAAAGTAGTTCCTATTTTCTATCCCCCTTAAAG 360

Qy       1046 AAAATTGCATGAAACTAGGCTTCTGTAATCAATATCCCAACATTCTGCAATGGCAGCATT 1105
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AAAATTGCATGAAACTAGGCTTCTGTAATCAATATCCCAACATTCTGCAATGGCAGCATT 420

Qy       1106 CCCACCAACAAAATCC 1121
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Db        421 CCCACCAACAAAATCC 436
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RESULT 15
US-09-778-320-141
; Sequence 141, Application US/09778320
; Patent No. US20010034052A1
; GENERAL INFORMATION:
; APPLICANT: Dillon, Davin C.
; APPLICANT: Day, Craig H.
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Mitcham, Jennifer
; APPLICANT: Wang, TongTong
; APPLICANT: McNeill, Patricia D.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER
; FILE REFERENCE: 210121.491C5
; CURRENT APPLICATION NUMBER: US/09/778,320
; CURRENT FILING DATE: 2001-02-06
; NUMBER OF SEQ ID NOS: 301
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 141
; LENGTH: 420
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(420)
; OTHER INFORMATION: n = A,T,C or G
US-09-778-320-141

Query Match 8.5%; Score 320; DB 10; Length 420;
Best Local Similarity 92.4%; Pred. No. 1.4e-74;
Matches 379; Conservative 0; Mismatches 25; Indels 6; Gaps 5;

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Qy        426 GACACTCAGGGAAAAGCATTCGTCAAAGAGAGCTTAAAATGCATCGCCAACGGGGTCACC 485
              |||||||||||||||||  | |||| ||||||||||||||||||||||||||||||||||
Db          1 GACACTCAGGGAAAAGCATNNGNCAAANAGAGCTTAAAATGCATCGCCAACGGGGTCACC 60

Qy        486 TCCAAGGTCTTCCTCGCCATTCGGAGGTGCTCCACTTTCCAAAGGATGATTGCTGAGGTG 545
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TCCAAGGTCTTCCTCGCCATTCGGAGGTGCTCCACTTTCCAAAGGATGATTGCTGAGGTG 120

Qy        546 CAGGAAGAGTGCTACAGCAAGCTGAATGTGTGCAGCATCGCCAAGCGGAACCCTGAAGCC 605
              |||||||||||||||||||||||||||||| ||| ||||||||||||||||| ||||||
Db        121 CAGGAAGAGTGCTACAGCAAGCTGAATGTGCGCANCATCGCCAAGCGGAACCCNGAAGCC 180

Qy        606 ATCACTGAGGTCGTCCAGCTGCCCAATCACTTCTCCAACAGATACTATAACAGACTTGTC 665
              ||||||||||||| |||||||||||||||||||||| |||||||||||||||||||
Db        181 ATCACTGAGGTCGTGCAGCTGCCCAATCACTTCTCCAACANATACTATAACAGACTTGNN 240

Qy        666 CGAAGCCTGCTGGAATGTGATGAAGACACA-GTCAGCACAATCA-GAGACAGCCTGATGG 723
              |||||||||||||||| |||||| ||||| | |||||||||||| ||||||||||||||
Db        241 CGAAGCCTGCTGGAATGNGATGAANACACAGGGCAGCACAATCAGGAGACAGCCTGATGG 300

Qy        724 AGAAAATTGGGCCTAACATGGCCA-GCCTCTTCCACATCCTG--CAGACAGACCACTGTG 780
              | |||| |||||||| |||||||| ||||||||||||||||     ||||||||||||||
Db        301 ANAAAANTGGGCCTANCATGGCCAGGCCTCTTCCACATCCTNGCANGACAGACCACTGTG 360
```

```
Qy        781 CCCAAACACACCCAC-GAGCTGACTTCAACAGGAGACGCACCAATGAGCC 829
              ||||||||||||| | ||||||||||  |||||||||||| || |||||
Db        361 CCCAAACACACCCNCTGAGCTGACTTNNACAGGAGACGCACNAAGGAGCC 410
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Search completed: June 9, 2003, 15:59:33
Job time : 488 secs

GenCore version 5.1.6

OM protein - nucleic search, using frame_plus_p2n model

Run on: June 12, 2003, 21:15:35 ; Search time 1994 Seconds
(without alignments)
3605.012 Million cell updates/sec

Title: US-09-705-500A-3
Perfect score: 247
Sequence: 1 MLQNSAVLLVLVISASATHE.....NLRGEEDSPSHIKRTSHESA 247

Scoring table: OLIGO
Xgapop 60.0 , Xgapext 60.0
Ygapop 60.0 , Ygapext 60.0
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2054640 seqs, 14551402878 residues

Word size: 1

Total number of hits satisfying chosen parameters: 4106482

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Command line parameters:
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-Q=/cgn2_1/USPTO_spool/US09705500/runat_06062003_113644_7975/app_query.fasta_1.391
-DB=GenEmbl -QFMT=fastap -SUFFIX=oligo.rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=oligo -TRANS=human40.cdi -LIST=1000
-DOCALIGN=200 -THR_SCORE=quality -THR_MIN=1 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto
-NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09705500_@CGN_1_1_1420_@runat_06062003_113644_7975 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7

Database : GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_or:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sts:*
28: em_un:*
29: em_vi:*
30: em_htg_hum:*
31: em_htg_inv:*
32: em_htg_other:*
33: em_htg_mus:*
34: em_htg_pln:*
35: em_htg_rod:*
36: em_htg_mam:*
37: em_htg_vrt:*
38: em_sy:*
39: em_htgo_hum:*
40: em_htgo_mus:*
41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	247	100.0	741	6	E37712	E37712 Osteogenesi
	2	247	100.0	741	6	E39295	E39295 Novel prote
	3	247	100.0	771	6	AR055558	AR055558 Sequence
	4	247	100.0	771	6	AR091578	AR091578 Sequence
	5	247	100.0	840	9	HSU46768	U46768 Human stann
	6	247	100.0	2481	9	BC029044	BC029044 Homo sapi
	7	247	100.0	3901	9	HSU25997	U25997 Homo sapien
	8	160	64.8	585	6	AX156292	AX156292 Sequence
	9	90	36.4	18216	9	AF242179	AF242179 Homo sapi
	10	90	36.4	154898	9	AC012119	AC012119 Homo sapi
	11	86	34.8	834	4	AF257506	AF257506 Bos tauru
	12	84	34.0	1004	10	RNU62667	U62667 Rattus norv
	13	84	34.0	1232	10	MMU47815	U47815 Mus musculu
	14	84	34.0	2341	10	BC021425	BC021425 Mus muscu
	15	84	34.0	4183	10	AF099098	AF099098 Mus muscu
	16	75	30.4	177104	10	AC091237	AC091237 Mus muscu
	17	73	29.6	4479	9	AF098463	AF098463 Homo sapi
	18	40	16.2	420	6	AX156284	AX156284 Sequence
	19	17	6.9	314	11	G60515	G60515 SHGC-35548
	20	15	6.1	2807	5	AB060558	AB060558 Osteoglos
	21	14	5.7	555	5	S80134	S80134 Oncorhynchu
	22	14	5.7	1743	5	AF326317	AF326317 Oncorhync
	23	14	5.7	1850	5	AF326318	AF326318 Oncorhync
	24	14	5.7	1934	5	S59519	S59519 stanniocalc
	25	12	4.9	2190	6	A05174	A05174 Synthetic n
	26	12	4.9	2192	5	ANGCSPA	M36967 Anguilla au
	27	10	4.0	90019	8	TM021B04	AF007271 Arabidops
c	28	9	3.6	227	8	AY023639	AY023639 Oryza sat
	29	9	3.6	436	6	AX309100	AX309100 Sequence
	30	9	3.6	647	5	TCA309137	AJ309137 Triturus
	31	9	3.6	6440	3	AF040989	AF040989 Drosophil
c	32	9	3.6	16652	2	AC014298	AC014298 Drosophil
	33	9	3.6	39104	6	AX059498	AX059498 Sequence
c	34	9	3.6	81877	8	T32B20	AF262041 Arabidops
	35	9	3.6	88200	9	AC023061	AC023061 Homo sapi
c	36	9	3.6	89938	3	AC006469	AC006469 Drosophil
	37	9	3.6	92113	9	AC108070	AC108070 Homo sapi
c	38	9	3.6	94993	9	AC117534	AC117534 Homo sapi
	39	9	3.6	96583	8	ATAC009992	AC009992 Arabidops
	40	9	3.6	99643	8	ATT6K21	AL021889 Arabidops
c	41	9	3.6	103563	9	AC006979	AC006979 Homo sapi
	42	9	3.6	105854	2	AC129397	AC129397 Rattus no
	43	9	3.6	107183	8	AC002983	AC002983 Arabidops
	44	9	3.6	109238	9	AL133538	AL133538 Human DNA
c	45	9	3.6	109659	2	AC111442	AC111442 Rattus no
	46	9	3.6	113578	2	AC019916	AC019916 Drosophil
	47	9	3.6	116416	2	AC130801	AC130801 Medicago
	48	9	3.6	121584	2	AC008232	AC008232 Drosophil
	49	9	3.6	126087	8	T3E15	AF147264 Arabidops
c	50	9	3.6	139848	10	AC122904	AC122904 Mus muscu

c	51	9	3.6	142994	2	CNS08C7P	AL731740 Oryza sat
	52	9	3.6	147174	8	AP000492	AP000492 Oryza sat
	53	9	3.6	149384	9	AC006318	AC006318 Homo sapi
	54	9	3.6	157903	8	AP000570	AP000570 Oryza sat
c	55	9	3.6	163650	9	AL445932	AL445932 Human DNA
c	56	9	3.6	167227	9	AC020602	AC020602 Homo sapi
c	57	9	3.6	169534	3	AC008350	AC008350 Drosophil
	58	9	3.6	174364	2	AC094843	AC094843 Rattus no
c	59	9	3.6	174877	2	AC095529	AC095529 Rattus no
	60	9	3.6	180825	2	AC094133	AC094133 Rattus no
	61	9	3.6	190540	2	AC092086	AC092086 Bos tauru
c	62	9	3.6	191923	10	AL691469	AL691469 Mouse DNA
	63	9	3.6	194746	2	AC123544	AC123544 Lemur cat
	64	9	3.6	197064	8	ATCHRIV18	AL161506 Arabidops
	65	9	3.6	197994	3	AC097445	AC097445 Drosophil
	66	9	3.6	198067	8	ATCHRIV47	AL161547 Arabidops
c	67	9	3.6	199362	8	ATCHRIV24	AL161512 Arabidops
	68	9	3.6	208927	2	AC125366	AC125366 Rattus no
c	69	9	3.6	230965	3	AE003842	AE003842 Drosophil
	70	9	3.6	253389	2	AC008605	AC008605 Homo sapi
	71	9	3.6	257887	2	AC092193	AC092193 Bos tauru
c	72	9	3.6	302225	3	AE003458	AE003458 Drosophil
c	73	8	3.2	139	11	G35135	G35135 craig Crypt
	74	8	3.2	324	6	AX188630	AX188630 Sequence
	75	8	3.2	416	6	AX321867	AX321867 Sequence
c	76	8	3.2	461	11	PCU64658	U64658 Paracharter
c	77	8	3.2	519	5	AY030188	AY030188 Geothlypi
	78	8	3.2	666	9	HSA340760	AJ340760 Homo sapi
c	79	8	3.2	1000	6	AX244759	AX244759 Sequence
	80	8	3.2	1748	14	U01069	U01069 African hor
	81	8	3.2	1800	1	MLTRTRXHP	X87899 M.leprae TR
c	82	8	3.2	2441	4	BTU88551	U88551 Bos taurus
c	83	8	3.2	2443	9	HSM800406	AL050079 Homo sapi
c	84	8	3.2	3006	6	AX415094	AX415094 Sequence
c	85	8	3.2	3024	6	AX413688	AX413688 Sequence
	86	8	3.2	3153	6	AR177273	AR177273 Sequence
	87	8	3.2	3538	8	AF200530	AF200530 Zea mays
c	88	8	3.2	3750	14	AF027657	AF027657 Choriston
	89	8	3.2	3928	3	AB023491	AB023491 Stichopus
c	90	8	3.2	4515	9	HSM802584	AL162055 Homo sapi
	91	8	3.2	4552	8	ATU93308	U93308 Arabidopsis
	92	8	3.2	5388	14	OPU39145	U39145 Orgyia pseu
c	93	8	3.2	6668	8	AB037664	AB037664 Oryza sat
	94	8	3.2	6687	9	AB037748	AB037748 Homo sapi
c	95	8	3.2	7215	1	SMABIO	D17468 S. marcesce
	96	8	3.2	7525	6	AX090483	AX090483 Sequence
c	97	8	3.2	8558	3	CEU95074	U95074 Caenorhabdi
c	98	8	3.2	10302	9	HSMUPS	X69086 H.sapiens m
	99	8	3.2	10556	1	AE006559	AE006559 Streptoco
	100	8	3.2	10636	1	AE001014	AE001014 Archaeogl
	101	8	3.2	10793	1	AE004283	AE004283 Vibrio ch
	102	8	3.2	10832	1	AE010039	AE010039 Streptoco
c	103	8	3.2	10925	1	U32738	U32738 Haemophilus
	104	8	3.2	12156	1	AE000759	AE000759 Aquifex a
	105	8	3.2	12256	1	AE013810	AE013810 Yersinia
c	106	8	3.2	12997	1	AE006061	AE006061 Pasteurel
c	107	8	3.2	14598	1	AE009622	AE009622 Brucella
c	108	8	3.2	19176	9	AL162381	AL162381 Human DNA
	109	8	3.2	29350	3	CEC14B1	Z37139 Caenorhabdi
	110	8	3.2	30916	8	AP004979	AP004979 Lotus jap
	111	8	3.2	33448	3	AF043693	AF043693 Caenorhab
c	112	8	3.2	34084	2	AC015075	AC015075 Drosophil
	113	8	3.2	35654	3	CER05D7	Z81105 Caenorhabdi
c	114	8	3.2	36864	3	AF022980	AF022980 Caenorhab
c	115	8	3.2	37913	10	AL662808	AL662808 Mouse DNA
c	116	8	3.2	38270	3	AC012524	AC012524 Leishmani
c	117	8	3.2	39580	3	CEF45H7	Z34800 Caenorhabdi
c	118	8	3.2	39971	3	U13875	U13875 Caenorhabdi
	119	8	3.2	40498	2	AC017296	AC017296 Drosophil
	120	8	3.2	40571	1	MSGDNAB	L39923 Mycobacteri
	121	8	3.2	42651	3	CEC37A5	Z92828 Caenorhabdi
	122	8	3.2	44983	9	AL606913	AL606913 Human DNA
c	123	8	3.2	46083	2	AC117555	AC117555 Ciona sav
	124	8	3.2	49293	3	U88314	U88314 Caenorhabdi
	125	8	3.2	50221	9	AC092441	AC092441 Homo sapi
	126	8	3.2	50946	1	AE014153	AE014153 Streptoco
c	127	8	3.2	55514	9	AC097525	AC097525 Homo sapi
c	128	8	3.2	57678	2	AC108393	AC108393 Mus muscu
	129	8	3.2	58581	2	AC104990	AC104990 Homo sapi
	130	8	3.2	61349	2	AC117543	AC117543 Mus muscu
c	131	8	3.2	61926	2	AC113184	AC113184 Mus muscu
	132	8	3.2	63247	9	AC007695	AC007695 Homo sapi
	133	8	3.2	64759	2	AC121744	AC121744 Rattus no
c	134	8	3.2	64871	2	AC009674	AC009674 Homo sapi
	135	8	3.2	65239	2	AC019844	AC019844 Drosophil
	136	8	3.2	65816	2	AC105194	AC105194 Homo sapi
	137	8	3.2	65884	2	AC122777	AC122777 Mus muscu
c	138	8	3.2	70082	2	AC127492	AC127492 Homo sapi
c	139	8	3.2	70236	2	AC015634	AC015634 Homo sapi
	140	8	3.2	71894	2	AC027754	AC027754 Homo sapi
	141	8	3.2	72007	2	AC101336	AC101336 Mus muscu
	142	8	3.2	73377	2	AC125822	AC125822 Rattus no
	143	8	3.2	76083	2	AC101411	AC101411 Mus muscu
	144	8	3.2	76336	9	AL445529	AL445529 Human DNA
	145	8	3.2	77685	3	AC005444	AC005444 Drosophil
	146	8	3.2	79917	9	AC010721	AC010721 Homo sapi
c	147	8	3.2	81507	2	AC128346	AC128346 Rattus no
c	148	8	3.2	81905	1	LISINP100	AL592102 Listeria
c	149	8	3.2	81905	6	AX415066	AX415066 Sequence
c	150	8	3.2	82010	8	AB023042	AB023042 Arabidops
c	151	8	3.2	82689	6	AX413020	AX413020 Sequence
c	152	8	3.2	83351	8	AC010657	AC010657 Genomic s
c	153	8	3.2	84915	2	HSDJ84J3	AL117343 Homo sapi
	154	8	3.2	88000	2	AC098844	AC098844 Leishmani
	155	8	3.2	88001	2	AC111428	AC111428 Rattus no
	156	8	3.2	88218	2	AC095700	AC095700 Rattus no
	157	8	3.2	89517	8	ATF17J16	AL163527 Arabidops
	158	8	3.2	90840	8	AB073158	AB073158 Arabidops
c	159	8	3.2	93475	5	AL672088	AL672088 Zebrafish
	160	8	3.2	94409	2	AC096217	AC096217 Rattus no
c	161	8	3.2	94850	9	AC025275	AC025275 Homo sapi
c	162	8	3.2	95643	8	F6N15	AF069299 Arabidops
	163	8	3.2	96743	9	AL358174	AL358174 Human DNA
	164	8	3.2	96877	2	AC017776	AC017776 Drosophil
	165	8	3.2	97364	2	AC114024	AC114024 Rattus no
c	166	8	3.2	99056	2	AC127623	AC127623 Rattus no
c	167	8	3.2	99147	2	AC128606	AC128606 Rattus no
	168	8	3.2	99995	9	AC091157	AC091157 Homo sapi
	169	8	3.2	101282	2	AC121474	AC121474 Rattus no
	170	8	3.2	101971	9	AC011114	AC011114 Homo sapi
c	171	8	3.2	102564	9	AL627427	AL627427 Human DNA
	172	8	3.2	102722	2	AC110684	AC110684 Rattus no
c	173	8	3.2	102818	9	AC003042	AC003042 Homo sapi
c	174	8	3.2	104037	9	HSAF002992	AF002992 Homo sapi
c	175	8	3.2	104287	9	AC005905	AC005905 Homo sapi
c	176	8	3.2	104808	3	AE003567	AE003567 Drosophil
c	177	8	3.2	105145	2	AC091670	AC091670 Oryza sat
c	178	8	3.2	106057	9	AC012195	AC012195 Homo sapi
c	179	8	3.2	106444	2	AC080103	AC080103 Homo sapi
	180	8	3.2	106556	9	HSDJ512E2	AL121787 Human DNA
c	181	8	3.2	108090	9	AC009533	AC009533 Homo sapi
c	182	8	3.2	108443	2	AC118153	AC118153 Rattus no
	183	8	3.2	108534	9	HS124O9	AL021327 Human DNA
	184	8	3.2	109501	10	AC084213	AC084213 Mus muscu
	185	8	3.2	110000	2	CEY105E8_0	AL022594 Caenorhab
	186	8	3.2	110000	2	AC021072_0	AC021072 Homo sapi
	187	8	3.2	110000	2	AC021072_1	Continuation (2 of
	188	8	3.2	110000	2	AC048347_1	Continuation (2 of
c	189	8	3.2	110444	9	AL391667	AL391667 Human DNA
c	190	8	3.2	110653	2	AC098630	AC098630 Rattus no
	191	8	3.2	110909	9	AC117510	AC117510 Homo sapi
	192	8	3.2	111500	9	AC121344	AC121344 Homo sapi
	193	8	3.2	111934	9	AF281074	AF281074 Homo sapi
	194	8	3.2	112211	9	AC108929	AC108929 Homo sapi
	195	8	3.2	112662	9	AC104453	AC104453 Homo sapi
	196	8	3.2	113592	2	AC095942	AC095942 Rattus no

c 197	8	3.2 113905	2	AC122604	AC122604	Rattus no
c 198	8	3.2 114097	2	AL672171	AL672171	Danio rer
c 199	8	3.2 114367	8	ATF10M10	AL035521	Arabidops
200	8	3.2 114631	9	AC006010	AC006010	Homo sapi
201	8	3.2 115079	2	CNS08C9M	AL732647	Oryza sat
202	8	3.2 115787	8	AF466202	AF466202	Zea mays
203	8	3.2 116039	9	AC007362	AC007362	Homo sapi
c 204	8	3.2 116597	8	AB073155	AB073155	Arabidops
c 205	8	3.2 118564	9	AL162501	AL162501	Human DNA
c 206	8	3.2 120507	9	AL136358	AL136358	Human DNA
c 207	8	3.2 122025	9	AC022334	AC022334	Homo sapi
c 208	8	3.2 122139	2	AC084796	AC084796	Homo sapi
c 209	8	3.2 122232	2	AC094303	AC094303	Rattus no
c 210	8	3.2 122736	2	AP004080	AP004080	Oryza sat
211	8	3.2 124050	8	AF474373	AF474373	Hordeum v
212	8	3.2 126140	3	AC007329	AC007329	Drosophil
c 213	8	3.2 128403	2	AC017472	AC017472	Drosophil
214	8	3.2 129024	2	AP004185	AP004185	Oryza sat
c 215	8	3.2 129271	8	AC005687	AC005687	Arabidops
c 216	8	3.2 129479	9	AL590488	AL590488	Human DNA
217	8	3.2 129723	2	AC120316	AC120316	Rattus no
c 218	8	3.2 129867	2	AF130866	AF130866	Homo sapi
c 219	8	3.2 130010	2	AC025292	AC025292	Homo sapi
c 220	8	3.2 131270	2	AC113793	AC113793	Rattus no
221	8	3.2 131530	9	HUAC002303	AC002303	Homo sapi
222	8	3.2 131995	14	OPU75930	U75930	Orgyia pseu
223	8	3.2 133810	2	AC130750	AC130750	Rattus no
c 224	8	3.2 134743	9	HUAC002300	AC002300	Homo sapi
c 225	8	3.2 135398	2	AC130452	AC130452	Homo sapi
c 226	8	3.2 135834	2	AP005253	AP005253	Oryza sat
227	8	3.2 137068	2	AC118314	AC118314	Rattus no
228	8	3.2 137299	2	AC121666	AC121666	Rattus no
c 229	8	3.2 137436	9	AL159986	AL159986	Human DNA
230	8	3.2 137904	10	AL645857	AL645857	Mouse DNA
c 231	8	3.2 138707	2	AC119710	AC119710	Rattus no
c 232	8	3.2 138814	30	AC068997	Ac068997	Homo sapi
233	8	3.2 139111	2	AC114281	AC114281	Homo sapi
234	8	3.2 139144	2	AC124863	AC124863	Homo sapi
235	8	3.2 139173	9	AC009140	AC009140	Homo sapi
c 236	8	3.2 140108	2	AP004125	AP004125	Oryza sat
c 237	8	3.2 141594	9	AC068302	AC068302	Homo sapi
c 238	8	3.2 141690	2	AC097013	AC097013	Schistoso
c 239	8	3.2 143405	2	AC062023	AC062023	Homo sapi
240	8	3.2 143512	2	AC087632	AC087632	Homo sapi
c 241	8	3.2 143814	2	AC126086	AC126086	Rattus no
242	8	3.2 144201	10	AC087218	AC087218	Rattus no
243	8	3.2 144480	2	AP004276	AP004276	Oryza sat
c 244	8	3.2 145614	2	AC006872	AC006872	Caenorhab
245	8	3.2 145628	2	AC021730	AC021730	Homo sapi
c 246	8	3.2 145945	2	AC119369	AC119369	Rattus no
247	8	3.2 147670	9	AC026617	AC026617	Homo sapi
248	8	3.2 147676	2	AC098065	AC098065	Rattus no
249	8	3.2 147699	2	AC116277	AC116277	Rattus no
250	8	3.2 148726	2	AC116935	AC116935	Papio cyn
251	8	3.2 148792	2	AC129245	AC129245	Rattus no
252	8	3.2 149001	9	AC107909	AC107909	Homo sapi
c 253	8	3.2 150840	2	AC121211	AC121211	Rattus no
254	8	3.2 151037	9	AC092620	AC092620	Homo sapi
255	8	3.2 151083	2	AC128618	AC128618	Rattus no
c 256	8	3.2 151338	2	AC126577	AC126577	Rattus no
257	8	3.2 151359	8	AC025098	AC025098	Oryza sat
c 258	8	3.2 151479	2	AC012278	AC012278	Homo sapi
c 259	8	3.2 151778	2	AC113646	AC113646	Rattus no
c 260	8	3.2 152106	2	AC123198	AC123198	Rattus no
261	8	3.2 152444	2	AC107570	AC107570	Rattus no
262	8	3.2 152547	9	AC104701	AC104701	Homo sapi
263	8	3.2 152688	2	AC123325	AC123325	Rattus no
c 264	8	3.2 153705	9	AL445650	AL445650	Human DNA
c 265	8	3.2 153787	2	AC023037	AC023037	Homo sapi
266	8	3.2 154277	2	AP003943	AP003943	Oryza sat
267	8	3.2 154433	10	AL732447	AL732447	Mouse DNA
c 268	8	3.2 154939	9	AC022537	AC022537	Homo sapi
c 269	8	3.2 155043	2	AC102878	AC102878	Mus muscu
c 270	8	3.2 155156	9	AF241727	AF241727	Homo sapi
c 271	8	3.2 155827	9	AC046136	AC046136	Homo sapi
272	8	3.2 156177	9	AC093896	AC093896	Homo sapi
273	8	3.2 156671	2	AC027431	AC027431	Homo sapi
c 274	8	3.2 156842	2	AC069318	AC069318	Homo sapi
275	8	3.2 157199	2	AC106479	AC106479	Rattus no
c 276	8	3.2 157317	2	AC118094	AC118094	Rattus no
c 277	8	3.2 157356	2	AC021376	AC021376	Homo sapi
c 278	8	3.2 157636	9	AL360011	AL360011	Human DNA
c 279	8	3.2 157684	10	AC004093	AC004093	Mus muscu
280	8	3.2 157803	9	AC006256	AC006256	Homo sapi
281	8	3.2 158034	2	AC019275	AC019275	Homo sapi
282	8	3.2 158863	2	AC007777	AC007777	Homo sapi
283	8	3.2 159007	2	AC012578	AC012578	Homo sapi
c 284	8	3.2 159065	3	AC091634	AC091634	Drosophil
285	8	3.2 159447	2	HS373D10	AL357615	Homo sapi
286	8	3.2 159933	2	AC109935	AC109935	Rattus no
c 287	8	3.2 160200	10	AC091605	AC091605	Mus muscu
288	8	3.2 160524	2	AC121620	AC121620	Rattus no
289	8	3.2 160763	9	AC097482	AC097482	Homo sapi
c 290	8	3.2 161188	2	AC097669	AC097669	Rattus no
291	8	3.2 161844	2	AC097562	AC097562	Rattus no
292	8	3.2 161990	2	AL357313	AL357313	Homo sapi
293	8	3.2 162513	2	AC127466	AC127466	Atelerix
294	8	3.2 162558	2	AP004880	AP004880	Oryza sat
295	8	3.2 163057	2	AC012419	AC012419	Homo sapi
c 296	8	3.2 163391	2	AC114862	AC114862	Rattus no
297	8	3.2 163466	3	AC010921	AC010921	Drosophil
298	8	3.2 163852	9	AC015971	AC015971	Homo sapi
299	8	3.2 163978	2	AC126066	AC126066	Rattus no
300	8	3.2 164533	2	AC106061	AC106061	Rattus no
301	8	3.2 164857	9	AC110054	AC110054	Homo sapi
302	8	3.2 164863	2	AC026517	AC026517	Homo sapi
303	8	3.2 165948	9	AC018616	AC018616	Homo sapi
304	8	3.2 166061	2	AC096002	AC096002	Rattus no
305	8	3.2 166357	9	AC091559	AC091559	Homo sapi
c 306	8	3.2 166395	5	AL627383	AL627383	Zebrafish
307	8	3.2 166504	9	AC008275	AC008275	Homo sapi
c 308	8	3.2 166507	9	AC018523	AC018523	Homo sapi
c 309	8	3.2 166802	2	AC016253	AC016253	Homo sapi
310	8	3.2 167834	9	AC105195	AC105195	Homo sapi
c 311	8	3.2 168036	2	AC021294	AC021294	Homo sapi
312	8	3.2 168147	9	AL139092	AL139092	Human DNA
c 313	8	3.2 168495	2	AL807759	AL807759	Mus muscu
314	8	3.2 168986	9	AC008013	AC008013	Homo sapi
c 315	8	3.2 168992	2	AC103568	AC103568	Rattus no
c 316	8	3.2 169047	9	AL357935	AL357935	Human DNA
c 317	8	3.2 169387	2	AC096181	AC096181	Rattus no
318	8	3.2 169405	10	AL596256	AL596256	Mouse DNA
319	8	3.2 169529	9	AC064834	AC064834	Homo sapi
c 320	8	3.2 169713	2	AC015919	AC015919	Homo sapi
321	8	3.2 169862	2	AC025530	AC025530	Homo sapi
c 322	8	3.2 170033	9	AC099538	AC099538	Homo sapi
c 323	8	3.2 170290	2	AC102476	AC102476	Mus muscu
324	8	3.2 170508	2	AC022450	AC022450	Homo sapi
325	8	3.2 170814	2	AL844565	AL844565	Mus muscu
326	8	3.2 170952	9	HS501N12	AL022170	Human DNA
c 327	8	3.2 171771	2	AC128110	AC128110	Rattus no
c 328	8	3.2 172069	3	AC012160	AC012160	Drosophil
c 329	8	3.2 172158	2	AP005444	AP005444	Oryza sat
c 330	8	3.2 173911	9	AL354992	AL354992	Human DNA
c 331	8	3.2 174293	2	AC068787	AC068787	Homo sapi
332	8	3.2 174547	9	AC006445	AC006445	Homo sapi
333	8	3.2 174568	2	AC115917	AC115917	Mus muscu
334	8	3.2 174612	9	CNS07EF6	AL512357	Human chr
335	8	3.2 174770	2	AC110408	AC110408	Rattus no
c 336	8	3.2 174919	2	AC102468	AC102468	Mus muscu
337	8	3.2 174933	9	CNS01DRL	AL117355	Human chr
338	8	3.2 175916	2	AC007747	AC007747	Homo sapi
339	8	3.2 176787	2	AC016864	AC016864	Homo sapi
c 340	8	3.2 177082	2	AL807812	AL807812	Mus muscu
341	8	3.2 177428	2	AC113946	AC113946	Mus muscu
c 342	8	3.2 177921	9	AL353752	AL353752	Human DNA

c 343	8	3.2	178563	3	AC098801	AC098801 Drosophil
c 344	8	3.2	178630	2	AC103450	AC103450 Rattus no
345	8	3.2	179704	2	AC026627	AC026627 Homo sapi
346	8	3.2	179822	9	AC103753	AC103753 Homo sapi
c 347	8	3.2	179833	9	AL162233	AL162233 Human DNA
c 348	8	3.2	179979	2	AC024965	AC024965 Homo sapi
349	8	3.2	180104	9	DJ526N18	AF123462 Homo sapi
350	8	3.2	180236	9	AP004294	AP004294 Homo sapi
351	8	3.2	180500	2	AC107362	AC107362 Rattus no
c 352	8	3.2	181609	9	AC079385	AC079385 Homo sapi
353	8	3.2	181721	9	AC010879	AC010879 Homo sapi
354	8	3.2	181735	2	AC101728	AC101728 Mus muscu
c 355	8	3.2	181948	2	AC079008	AC079008 Homo sapi
c 356	8	3.2	182434	2	AC121754	AC121754 Homo sapi
357	8	3.2	183626	2	AC026648	AC026648 Homo sapi
c 358	8	3.2	183901	2	AL356425	AL356425 Homo sapi
359	8	3.2	184021	3	AC093048	AC093048 Drosophil
c 360	8	3.2	184164	9	AC093515	AC093515 Homo sapi
361	8	3.2	184443	2	AC114853	AC114853 Rattus no
c 362	8	3.2	184509	2	AC113237	AC113237 Canis fam
363	8	3.2	184906	2	CNS01DUQ	AL133313 Homo sapi
c 364	8	3.2	185049	9	AL365495	AL365495 Human DNA
365	8	3.2	185437	9	AC012075	AC012075 Homo sapi
c 366	8	3.2	185711	2	AC107087	AC107087 Rattus no
c 367	8	3.2	186107	2	AC023132	AC023132 Homo sapi
c 368	8	3.2	186315	8	OSJN00188	AL662987 Oryza sat
369	8	3.2	186325	2	AC074244	AC074244 Homo sapi
c 370	8	3.2	186428	9	AC016355	AC016355 Homo sapi
c 371	8	3.2	186880	2	AC114849	AC114849 Rattus no
372	8	3.2	187131	10	AL365317	AL365317 Mouse DNA
c 373	8	3.2	187520	9	AC027684	AC027684 Homo sapi
374	8	3.2	187847	2	AC023155	AC023155 Homo sapi
375	8	3.2	187983	2	AC026210	AC026210 Homo sapi
c 376	8	3.2	188091	2	AC106351	AC106351 Rattus no
c 377	8	3.2	188425	10	AL606967	AL606967 Mouse DNA
c 378	8	3.2	188478	9	CNS05TF4	AL365294 Human chr
c 379	8	3.2	188509	2	AC112621	AC112621 Rattus no
c 380	8	3.2	188670	2	AC127606	AC127606 Rattus no
381	8	3.2	188996	2	AC020747	AC020747 Homo sapi
382	8	3.2	189131	10	AL645477	AL645477 Mouse DNA
c 383	8	3.2	189305	2	AC111625	AC111625 Rattus no
c 384	8	3.2	189509	9	AC099564	AC099564 Homo sapi
c 385	8	3.2	189545	9	AC067746	AC067746 Homo sapi
c 386	8	3.2	189570	2	AC019120	AC019120 Homo sapi
387	8	3.2	190588	2	AC009861	AC009861 Homo sapi
c 388	8	3.2	190610	2	AC130419	AC130419 Homo sapi
c 389	8	3.2	190696	2	AC125753	AC125753 Rattus no
c 390	8	3.2	191603	10	AL713974	AL713974 Mouse DNA
391	8	3.2	191923	9	AC087886	AC087886 Homo sapi
392	8	3.2	192063	9	AC099665	AC099665 Homo sapi
393	8	3.2	192758	2	AC115326	AC115326 Rattus no
394	8	3.2	193228	2	AL844510	AL844510 Mus muscu
c 395	8	3.2	193237	2	AC127161	AC127161 Rattus no
c 396	8	3.2	193268	2	AC111263	AC111263 Rattus no
397	8	3.2	193551	10	AL646055	AL646055 Mouse DNA
c 398	8	3.2	193981	2	AC122465	AC122465 Mus muscu
399	8	3.2	194713	2	AC113794	AC113794 Rattus no
c 400	8	3.2	194809	4	AC091506	AC091506 Sus scrof
401	8	3.2	194944	10	AL672012	AL672012 Mouse DNA
c 402	8	3.2	195085	2	AC113815	AC113815 Rattus no
c 403	8	3.2	195541	2	AC124365	AC124365 Mus muscu
c 404	8	3.2	195766	9	CNS01DVC	AL135744 Human chr
c 405	8	3.2	195921	8	ATCHRIV81	AL161585 Arabidops
406	8	3.2	196117	9	AC110078	AC110078 Homo sapi
407	8	3.2	196725	2	AL844513	AL844513 Mus muscu
408	8	3.2	197023	2	AC101902	AC101902 Mus muscu
c 409	8	3.2	197119	8	ATCHRIV1	AL161471 Arabidops
410	8	3.2	197406	2	AC110594	AC110594 Homo sapi
411	8	3.2	198226	2	AC118908	AC118908 Rattus no
412	8	3.2	200000	2	AC006294	AC006294 Homo sapi
413	8	3.2	200698	2	AL672060	AL672060 Mus muscu
414	8	3.2	200799	2	AL445648	AL445648 Homo sapi
c 415	8	3.2	200833	9	AL390738	AL390738 Human DNA
c 416	8	3.2	201699	9	AC079844	AC079844 Homo sapi
c 417	8	3.2	202251	2	AC104472	AC104472 Homo sapi
418	8	3.2	202387	2	AC129700	AC129700 Rattus no
419	8	3.2	202843	9	CNS01DVM	AL135961 Human chr
c 420	8	3.2	204505	9	AC089983	AC089983 Homo sapi
421	8	3.2	204814	2	AC091456	AC091456 Mus muscu
422	8	3.2	205886	9	AC012504	AC012504 Homo sapi
c 423	8	3.2	206199	2	AC117045	AC117045 Rattus no
424	8	3.2	207221	2	AC107831	AC107831 Mus muscu
c 425	8	3.2	207761	3	AC093546	AC093546 Drosophil
c 426	8	3.2	208164	2	AC113194	AC113194 Homo sapi
427	8	3.2	208396	9	AC003101	AC003101 Homo sapi
c 428	8	3.2	210145	2	AC114314	AC114314 Homo sapi
429	8	3.2	211096	2	AC127309	AC127309 Mus muscu
c 430	8	3.2	211403	2	AC117260	AC117260 Mus muscu
431	8	3.2	213278	2	AC103314	AC103314 Rattus no
c 432	8	3.2	214219	10	AL691418	AL691418 Mouse DNA
c 433	8	3.2	214706	2	AC126436	AC126436 Mus muscu
434	8	3.2	215004	2	AC068146	AC068146 Homo sapi
435	8	3.2	218061	2	AC099293	AC099293 Rattus no
436	8	3.2	219753	2	AC108723	AC108723 Homo sapi
c 437	8	3.2	219973	2	AC092906	AC092906 Homo sapi
438	8	3.2	220606	2	AC005958	AC005958 Homo sapi
439	8	3.2	220631	10	AL671493	AL671493 Mouse DNA
440	8	3.2	221842	2	AC108907	AC108907 Mus muscu
441	8	3.2	222176	2	AL845357	AL845357 Danio rer
442	8	3.2	222291	2	AC020880	AC020880 Mus muscu
c 443	8	3.2	223782	2	AL808018	AL808018 Mus muscu
444	8	3.2	224954	2	AL845156	AL845156 Mus muscu
c 445	8	3.2	226460	10	AC098730	AC098730 Mus muscu
446	8	3.2	227061	2	AC125360	AC125360 Mus muscu
447	8	3.2	228031	2	AL732396	AL732396 Mus muscu
c 448	8	3.2	228960	2	AC125969	AC125969 Rattus no
449	8	3.2	229410	2	AC094515	AC094515 Rattus no
450	8	3.2	232004	2	AC023584	AC023584 Homo sapi
c 451	8	3.2	232004	2	AC023584	AC023584 Homo sapi
452	8	3.2	232200	2	AC106263	AC106263 Rattus no
453	8	3.2	232929	2	AC102528	AC102528 Mus muscu
c 454	8	3.2	233642	2	AC119846	AC119846 Mus muscu
c 455	8	3.2	234491	2	AL671118	AL671118 Mus muscu
456	8	3.2	235085	2	AC094364	AC094364 Rattus no
c 457	8	3.2	237378	2	AC087038	AC087038 Mus muscu
458	8	3.2	238817	2	AC125526	AC125526 Mus muscu
c 459	8	3.2	239667	2	AL731811	AL731811 Mus muscu
460	8	3.2	240307	2	AL805950	AL805950 Mus muscu
461	8	3.2	243508	2	AC078914	AC078914 Mus muscu
c 462	8	3.2	244978	9	AF241726	AF241726 Homo sapi
c 463	8	3.2	249403	2	AC123072	AC123072 Mus muscu
c 464	8	3.2	253794	2	AC099280	AC099280 Rattus no
465	8	3.2	256010	3	AE003657	AE003657 Drosophil
c 466	8	3.2	266902	2	AL732435	AL732435 Mus muscu
467	8	3.2	267315	2	AC099279	AC099279 Rattus no
468	8	3.2	269203	1	MLEPRTN10	AL583926 Mycobacte
c 469	8	3.2	271729	3	AE003539	AE003539 Drosophil
470	8	3.2	273658	2	AC079423	AC079423 Mus muscu
471	8	3.2	278206	2	AL513471	AL513471 Homo sapi
472	8	3.2	291923	3	AE003818	AE003818 Drosophil
c 473	8	3.2	292550	1	AP001513	AP001513 Bacillus
c 474	8	3.2	298514	3	AE003504	AE003504 Drosophil
475	8	3.2	298750	1	AP005375	AP005375 Thermosyn
476	8	3.2	299670	2	AC006845	AC006845 Caenorhab
477	8	3.2	302718	2	AC027292	AC027292 Homo sapi
478	8	3.2	303014	2	AC117448	AC117448 Homo sapi
c 479	8	3.2	332635	1	AP003005	AP003005 Mesorhizo
480	8	3.2	334050	1	AJ414151	AJ414151 Yersinia
481	8	3.2	337261	2	AC096079	AC096079 Rattus no
c 482	8	3.2	347400	1	AP003591	AP003591 Nostoc sp
c 483	8	3.2	347726	2	AC098521	AC098521 Rattus no
484	8	3.2	349050	1	AP003586	AP003586 Nostoc sp
485	8	3.2	349980	6	AX344568	AX344568 Sequence
486	7	2.8	27	6	AR055559	AR055559 Sequence
487	7	2.8	27	6	AR091579	AR091579 Sequence
c 488	7	2.8	27	6	I23812	I23812 Sequence 30

489	7	2.8	28	6	AX478553	AX478553 Sequence
490	7	2.8	28	6	AX478556	AX478556 Sequence
491	7	2.8	28	6	AX478558	AX478558 Sequence
492	7	2.8	28	6	AX478560	AX478560 Sequence
c 493	7	2.8	31	6	AR055560	AR055560 Sequence
c 494	7	2.8	31	6	AR091580	AR091580 Sequence
495	7	2.8	37	6	AR091581	AR091581 Sequence
496	7	2.8	37	6	AR091583	AR091583 Sequence
c 497	7	2.8	62	9	AF016218	AF016218 Homo sapi
498	7	2.8	110	11	G37868	G37868 Pf9607 Plas
c 499	7	2.8	120	8	PHALIGH8P	M21913 Phanerochae
500	7	2.8	129	1	HEA39NU	M33440 H.influenza
501	7	2.8	137	11	HUMSWX876	L41122 Human chrom
c 502	7	2.8	147	7	BKVP125	X96782 Bacteriopha
503	7	2.8	154	6	E15260	E15260 Rice pyruva
504	7	2.8	175	3	AF180221	AF180221 Plasmodiu
505	7	2.8	175	3	AF180244	AF180244 Plasmodiu
506	7	2.8	186	6	AX063248	AX063248 Sequence
507	7	2.8	186	8	RICS77	D10413 Rice mRNA f
c 508	7	2.8	188	14	BVDE2B	L38700 Bovine vira
c 509	7	2.8	188	14	BVDE2D	L38702 Bovine vira
c 510	7	2.8	188	14	BVDE2E	L38703 Bovine vira
511	7	2.8	213	6	A85415	A85415 Sequence 74
512	7	2.8	213	6	AR154908	AR154908 Sequence
513	7	2.8	213	6	E65433	E65433 Genome DNA
514	7	2.8	226	8	U50490	U50490 Astragalus
c 515	7	2.8	247	9	HS78D3R	Z63110 H.sapiens C
516	7	2.8	249	6	AX413101	AX413101 Sequence
c 517	7	2.8	278	8	AF146069	AF146069 Nicotiana
518	7	2.8	290	8	LUS310169	AJ310169 Linum usi
c 519	7	2.8	292	3	TCFL160B	X71868 T.cruzi mRN
c 520	7	2.8	294	6	AX439084	AX439084 Sequence
c 521	7	2.8	295	3	TCFL160C	X71869 T.cruzi mRN
522	7	2.8	297	6	AR109884	AR109884 Sequence
523	7	2.8	297	6	AR150702	AR150702 Sequence
c 524	7	2.8	297	6	AX413178	AX413178 Sequence
c 525	7	2.8	306	1	MC332	Z33244 M.capricolu
526	7	2.8	309	3	AB040842	AB040842 Donax cun
c 527	7	2.8	313	5	S48571	S48571 (fingerprin
528	7	2.8	324	11	G00734	G00734 fruit fly S
c 529	7	2.8	325	1	UGU85136	U85136 Unidentifie
c 530	7	2.8	331	8	AF061818	AF061818 Vigna rad
c 531	7	2.8	332	11	AU049638	AU049638 Rattus no
532	7	2.8	334	8	RICYK14	D29702 Rice mRNA,
533	7	2.8	338	11	G27599	G27599 human STS S
534	7	2.8	344	4	AF174691	AF174691 Ovis arie
c 535	7	2.8	354	11	HUMUT5043B	L30982 Human STS U
c 536	7	2.8	359	1	CBDAPDE	AJ001638 Coxiella
c 537	7	2.8	360	10	AB085944	AB085944 Rattus no
c 538	7	2.8	360	10	AB085945	AB085945 Mus muscu
539	7	2.8	360	11	G13079	G13079 sWSS3126 Er
c 540	7	2.8	367	11	G65440	G65440 stdJ388M5_1
541	7	2.8	371	8	AF025509	AF025509 Bosistoa
c 542	7	2.8	375	3	AF246585	AF246585 Cethosia
c 543	7	2.8	378	4	AF442925	AF442925 Lama glam
544	7	2.8	381	6	AX121611	AX121611 Sequence
c 545	7	2.8	391	8	HOR131507	AJ131507 Heloniops
c 546	7	2.8	399	9	F191594S25	AF191618 Homo sapi
c 547	7	2.8	401	7	PL2REP2	L24808 Bacteriopha
c 548	7	2.8	401	8	AY028663	AY028663 Candida a
c 549	7	2.8	403	3	BPA224969	AJ224969 Brugia pa
550	7	2.8	405	6	AX241555	AX241555 Sequence
551	7	2.8	411	9	HUMPRC5	M12686 Human prote
c 552	7	2.8	414	14	HCU14270	U14270 Hepatitis C
c 553	7	2.8	431	11	AL806573	AL806573 Arabidops
c 554	7	2.8	439	5	XLCMYC1M	X56869 X.laevis c-
c 555	7	2.8	440	10	MUSGSTYA5	M19254 Mouse gluta
c 556	7	2.8	447	3	AF499094	AF499094 Coenonymp
c 557	7	2.8	451	9	HSNLM215S	X87538 H.sapiens g
c 558	7	2.8	466	6	AX440244	AX440244 Sequence
c 559	7	2.8	471	6	AX088612	AX088612 Sequence
560	7	2.8	475	9	HUMCGBEL03	K03189 Human chori
561	7	2.8	475	10	AF121981	AF121981 Mus muscu
562	7	2.8	478	3	AF135982	AF135982 Engaewa s
c 563	7	2.8	486	6	AX337477	AX337477 Sequence
c 564	7	2.8	486	11	G22132	G22132 human STS W
565	7	2.8	494	8	STU60071	U60071 Solanum tub
566	7	2.8	495	1	AF090144	AF090144 Klebsiell
567	7	2.8	495	1	EAU02272	U02272 Enterobacte
568	7	2.8	495	1	SMU02276	U02276 Serratia ma
569	7	2.8	495	11	G27494	G27494 human STS S
c 570	7	2.8	497	4	BTMISATE	X65206 B.taurus mi
571	7	2.8	511	11	G72025	G72025 At-9B-148 A
572	7	2.8	512	8	AF291282	AF291282 Exidiopsi
c 573	7	2.8	515	8	AY028665	AY028665 Candida a
c 574	7	2.8	516	5	AY030187	AY030187 Dendroica
c 575	7	2.8	518	11	G57526	G57526 SHGC-103222
c 576	7	2.8	519	5	AY030186	AY030186 Basileute
c 577	7	2.8	519	5	AY030190	AY030190 Vermivora
c 578	7	2.8	519	8	AY028664	AY028664 Candida a
c 579	7	2.8	526	6	AX094238	AX094238 Sequence
580	7	2.8	528	9	HUMR301R	D31757 Homo sapien
c 581	7	2.8	530	8	AY028666	AY028666 Candida a
582	7	2.8	533	11	G71953	G71953 A60057334FM
c 583	7	2.8	533	14	PVE2GP11	Y12174 Pestivirus
584	7	2.8	534	3	AF502075	AF502075 Bombyx mo
c 585	7	2.8	534	5	AY030185	AY030185 Passer mo
c 586	7	2.8	534	8	AY028661	AY028661 Candida a
c 587	7	2.8	544	1	RPZ82349	Z82349 R.prowazeki
588	7	2.8	546	1	AF472560	AF472560 Wolbachia
c 589	7	2.8	554	8	AY028660	AY028660 Candida a
c 590	7	2.8	560	9	HSA323545	AJ323545 Homo sapi
c 591	7	2.8	570	8	ADA286621	AJ286621 Agathis d
c 592	7	2.8	571	8	AY028662	AY028662 Candida a
c 593	7	2.8	573	11	G15864	G15864 human STS C
c 594	7	2.8	575	8	AY028669	AY028669 Candida a
595	7	2.8	576	1	AF521148	AF521148 Wolbachia
596	7	2.8	576	1	AF521149	AF521149 Wolbachia
597	7	2.8	576	1	AF521150	AF521150 Wolbachia
598	7	2.8	576	1	AF521152	AF521152 Wolbachia
599	7	2.8	580	1	AF507779	AF507779 Unculture
600	7	2.8	583	8	AF207557	AF207557 Brassica
601	7	2.8	583	8	AF207558	AF207558 Brassica
602	7	2.8	597	8	AF121684	AF121684 Astragalu
603	7	2.8	597	8	AF121686	AF121686 Astragalu
604	7	2.8	600	8	AF121685	AF121685 Astragalu
c 605	7	2.8	601	8	PLA224828	AJ224828 Posoqueri
c 606	7	2.8	603	14	AF176462	AF176462 PRRS isol
c 607	7	2.8	603	14	AF339495	AF339495 Porcine r
c 608	7	2.8	605	6	AX321283	AX321283 Sequence
c 609	7	2.8	607	5	AF383080	AF383080 Catharope
c 610	7	2.8	613	5	AF018105	AF018105 Dendroica
c 611	7	2.8	613	5	AF018106	AF018106 Dendroica
c 612	7	2.8	613	5	AF018107	AF018107 Dendroica
c 613	7	2.8	613	5	AF018108	AF018108 Dendroica
c 614	7	2.8	613	5	AF018109	AF018109 Dendroica
c 615	7	2.8	613	5	AF018110	AF018110 Dendroica
c 616	7	2.8	613	5	AF018111	AF018111 Dendroica
c 617	7	2.8	613	5	AF018112	AF018112 Dendroica
c 618	7	2.8	613	5	AF018113	AF018113 Dendroica
c 619	7	2.8	613	5	AF018114	AF018114 Dendroica
c 620	7	2.8	613	5	AF018115	AF018115 Dendroica
c 621	7	2.8	613	5	AF018116	AF018116 Dendroica
c 622	7	2.8	613	5	AF140366	AF140366 Dendroica
c 623	7	2.8	613	5	AF140367	AF140367 Dendroica
c 624	7	2.8	613	5	AF140368	AF140368 Dendroica
c 625	7	2.8	613	5	AF140370	AF140370 Dendroica
c 626	7	2.8	613	5	AF140371	AF140371 Dendroica
c 627	7	2.8	613	5	AF140372	AF140372 Dendroica
c 628	7	2.8	613	5	AF140374	AF140374 Dendroica
c 629	7	2.8	613	5	AF140381	AF140381 Dendroica
c 630	7	2.8	613	5	AF140382	AF140382 Dendroica
c 631	7	2.8	613	5	AF140383	AF140383 Dendroica
c 632	7	2.8	613	5	AF140384	AF140384 Dendroica
c 633	7	2.8	613	5	AF140385	AF140385 Dendroica
c 634	7	2.8	613	5	AF140386	AF140386 Dendroica

c 635	7	2.8	613	5	AF140387	AF140387 Dendroica
c 636	7	2.8	613	5	AF140388	AF140388 Dendroica
c 637	7	2.8	613	5	AF140389	AF140389 Dendroica
c 638	7	2.8	613	5	AF140390	AF140390 Dendroica
c 639	7	2.8	613	5	AF140391	AF140391 Dendroica
c 640	7	2.8	613	5	AF140392	AF140392 Dendroica
c 641	7	2.8	613	5	AF140393	AF140393 Dendroica
c 642	7	2.8	613	5	AF140394	AF140394 Dendroica
c 643	7	2.8	613	5	AF140395	AF140395 Dendroica
c 644	7	2.8	613	5	AF256515	AF256515 Parula su
c 645	7	2.8	613	5	AF256516	AF256516 Parula gu
c 646	7	2.8	613	5	AF256517	AF256517 Parula gu
c 647	7	2.8	613	5	AF256519	AF256519 Vermivora
c 648	7	2.8	613	5	AF281027	AF281027 Basileute
c 649	7	2.8	613	5	AF383068	AF383068 Dendroica
c 650	7	2.8	613	5	AF383070	AF383070 Geothlypi
c 651	7	2.8	613	5	AF383074	AF383074 Xenoligea
c 652	7	2.8	613	5	AF383075	AF383075 Dendroica
c 653	7	2.8	613	5	AF383081	AF383081 Euthlypis
c 654	7	2.8	613	5	AF383082	AF383082 Mniotilta
c 655	7	2.8	613	5	AF383089	AF383089 Limnothly
c 656	7	2.8	613	5	AF383090	AF383090 Ergaticus
c 657	7	2.8	613	5	AF383093	AF383093 Myioborus
c 658	7	2.8	613	5	AF383094	AF383094 Wilsonia
c 659	7	2.8	613	5	AF383104	AF383104 Protonota
c 660	7	2.8	613	5	AF383105	AF383105 Myioborus
c 661	7	2.8	617	5	TIU91959	U91959 Tangara ino
662	7	2.8	619	11	G57837	G57837 SHGC-103590
c 663	7	2.8	624	5	AF109426	AF109426 Icterus l
c 664	7	2.8	624	5	AF109427	AF109427 Icterus l
c 665	7	2.8	626	5	DAU91961	U91961 Dendroica a
666	7	2.8	631	3	AF385067	AF385067 Menacanth
667	7	2.8	631	3	AF423797	AF423797 Menacanth
668	7	2.8	636	8	AF318264	AF318264 Alexandri
669	7	2.8	637	8	AF318262	AF318262 Alexandri
c 670	7	2.8	640	8	AY028667	AY028667 Candida a
671	7	2.8	644	8	AF033533	AF033533 Alexandri
c 672	7	2.8	646	9	HSA325984	AJ325984 Homo sapi
c 673	7	2.8	648	6	AX406589	AX406589 Sequence
c 674	7	2.8	648	8	AY028670	AY028670 Candida a
c 675	7	2.8	649	8	AY028671	AY028671 Candida a
c 676	7	2.8	649	8	AY028672	AY028672 Candida a
c 677	7	2.8	659	6	A85417	A85417 Sequence 76
c 678	7	2.8	659	6	AR154910	AR154910 Sequence
c 679	7	2.8	659	6	E65435	E65435 Genome DNA
680	7	2.8	661	6	I31643	I31643 Sequence 44
681	7	2.8	661	8	AF033532	AF033532 Alexandri
682	7	2.8	663	9	HSA334957	AJ334957 Homo sapi
683	7	2.8	664	8	ALXRGNA	L38623 Alexandrium
684	7	2.8	664	8	ALXRGND	L38626 Alexandrium
c 685	7	2.8	664	8	AY028668	AY028668 Candida a
686	7	2.8	667	1	AF320945S1	AF320945 Unculture
c 687	7	2.8	671	6	AX415963	AX415963 Sequence
c 688	7	2.8	673	8	AY028673	AY028673 Candida a
689	7	2.8	676	6	I31640	I31640 Sequence 41
690	7	2.8	676	6	I31641	I31641 Sequence 42
691	7	2.8	676	6	I31642	I31642 Sequence 43
c 692	7	2.8	679	8	AF234344	AF234344 Aloe glau
c 693	7	2.8	680	8	AF234327	AF234327 Aloe dist
694	7	2.8	685	8	AB036828	AB036828 Chlorella
695	7	2.8	690	3	CGA269828	AJ269828 Cristaser
696	7	2.8	695	14	AY100135	AY100135 Hepatitis
c 697	7	2.8	699	8	AF425185	AF425185 Pseudophe
698	7	2.8	701	8	AAU44937	U44937 Alexandrium
699	7	2.8	704	9	HSA327214	AJ327214 Homo sapi
c 700	7	2.8	707	1	AF399285	AF399285 Unculture
c 701	7	2.8	707	8	JNI278455	AJ278455 Juglans n
c 702	7	2.8	708	10	BC027817	BC027817 Mus muscu
703	7	2.8	712	9	HSA332676	AJ332676 Homo sapi
704	7	2.8	713	1	ECPAL	X05123 E. coli pal
c 705	7	2.8	713	1	XCATTLA	X70329 X.campestri
706	7	2.8	716	8	AF318222	AF318222 Alexandri
707	7	2.8	716	8	AF318231	AF318231 Alexandri
708	7	2.8	716	8	AF318232	AF318232 Alexandri
709	7	2.8	716	8	AMU44936	U44936 Alexandrium
710	7	2.8	717	8	AF318221	AF318221 Alexandri
711	7	2.8	717	8	AF318233	AF318233 Alexandri
c 712	7	2.8	720	6	AX436792	AX436792 Sequence
713	7	2.8	722	8	AF141659	AF141659 Arabidops
714	7	2.8	737	3	AB006203	AB006203 Sparganum
c 715	7	2.8	738	6	AX488951	AX488951 Sequence
c 716	7	2.8	739	1	UAR236510	AJ236510 unculture
717	7	2.8	741	11	G51725	G51725 SHGC-84489
c 718	7	2.8	743	9	HSA328779	AJ328779 Homo sapi
719	7	2.8	754	8	AF254933	AF254933 Cunningha
c 720	7	2.8	758	6	AX339071	AX339071 Sequence
c 721	7	2.8	758	10	S62638	S62638 alpha 2u-gl
722	7	2.8	761	8	LLCHS1	X78096 L.laccata c
723	7	2.8	786	8	OSRNACB5	X75670 O.sativa mR
c 724	7	2.8	793	11	G41947	G41947 SHGC-68963
725	7	2.8	796	9	HSLIPA5	X75492 H.sapiens L
726	7	2.8	798	8	AF440390	AF440390 Orychophr
727	7	2.8	802	11	G72761	G72761 MARC 4357-4
c 728	7	2.8	809	8	MSNOD25A	X13288 M.sativa mR
729	7	2.8	825	11	CNS06EQA	AL395432 T7 end of
c 730	7	2.8	827	6	AX109536	AX109536 Sequence
731	7	2.8	835	9	AK024761	AK024761 Homo sapi
c 732	7	2.8	845	1	BRUOMP16A	L27996 Brucella ab
733	7	2.8	845	8	AF089846	AF089846 Funaria h
734	7	2.8	847	3	TCZEN	X97819 T.castaneum
c 735	7	2.8	849	10	MUSGSTB	J03958 Mouse, glut
736	7	2.8	855	6	A85702	A85702 Sequence 36
737	7	2.8	855	6	AR155195	AR155195 Sequence
738	7	2.8	855	6	E65720	E65720 Genome DNA
739	7	2.8	857	3	AF153976	AF153976 Schistoso
c 740	7	2.8	863	14	BPLPATTP	X70328 Filamentous
c 741	7	2.8	871	9	HSCPH167	X52858 Human cyclo
742	7	2.8	872	10	AF287738S7	AF287744 Mus muscu
c 743	7	2.8	874	8	BLYGLUCB	M13237 Barley beta
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746	7	2.8	885	1	AB074808	AB074808 Leptolyng
c 747	7	2.8	885	14	AF314147	AF314147 Garlic la
748	7	2.8	888	6	AR199618	AR199618 Sequence
c 749	7	2.8	897	8	AF206287	AF206287 Candida a
750	7	2.8	898	11	CNS06KPX	AL403195 T3 end of
c 751	7	2.8	899	10	BC030173	BC030173 Mus muscu
c 752	7	2.8	903	8	COTSPG	M19388 G.hirsutum
c 753	7	2.8	908	1	XCATTRA	X70330 X.campestri
c 754	7	2.8	910	11	CNS06EFG	AL395042 T7 end of
c 755	7	2.8	912	3	DME426996	AJ426996 Drosophil
756	7	2.8	917	9	HSA325387	AJ325387 Homo sapi
757	7	2.8	918	3	AF385059	AF385059 Haematopi
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c 760	7	2.8	918	6	AX454708	AX454708 Sequence
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c 762	7	2.8	918	11	CNS06K31	AL402371 T7 end of
763	7	2.8	920	3	AF385061	AF385061 Neohaemat
764	7	2.8	920	3	AF423799	AF423799 Neohaemat
765	7	2.8	929	7	PL2REP1	L24807 Bacteriopha
766	7	2.8	933	4	OCU05203	U05203 Oryctolagus
767	7	2.8	939	6	AX241554	AX241554 Sequence
c 768	7	2.8	939	8	AY047606	AY047606 Sorghum b
c 769	7	2.8	944	1	HACCSR3	D83748 Haloarcula
c 770	7	2.8	949	10	MINR12SRR	X99462 N.rufus mit
771	7	2.8	955	10	AY073963	AY073963 Mus muscu
772	7	2.8	960	10	AY073043	AY073043 Mus muscu
c 773	7	2.8	961	8	MSNOD25R	X13289 Medicago sa
c 774	7	2.8	962	11	G67672	G67672 MARC3599-36
775	7	2.8	964	5	BOBGRP	M83737 Toad gastri
c 776	7	2.8	978	3	AF249871	AF249871 Panulirus
c 777	7	2.8	984	8	AY052674	AY052674 Arabidops
778	7	2.8	994	6	AX414146	AX414146 Sequence
c 779	7	2.8	999	8	AF385719	AF385719 Arabidops
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801	7	2.8	1111	10	AF035156	AF035156 Rattus no
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808	7	2.8	1176	6	AX196104	AX196104 Sequence
809	7	2.8	1179	6	AX338970	AX338970 Sequence
810	7	2.8	1180	1	LMU66186	U66186 Listeria mo
c 811	7	2.8	1183	8	AF004112	AF004112 Schizosac
812	7	2.8	1191	3	DHU65119	U65119 Dennyus hir
813	7	2.8	1194	3	USP307445	AJ307445 Ussurohel
814	7	2.8	1194	8	AY072009	AY072009 Arabidops
815	7	2.8	1195	3	MSU65110	U65110 Megarcys st
816	7	2.8	1200	1	AF082865	AF082865 Streptoco
c 817	7	2.8	1200	6	AX439290	AX439290 Sequence
818	7	2.8	1206	6	AX432490	AX432490 Sequence
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c 820	7	2.8	1224	6	AR070947	AR070947 Sequence
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c 822	7	2.8	1228	8	AF077340	AF077340 Lycopersi
823	7	2.8	1231	8	AY087570	AY087570 Arabidops
c 824	7	2.8	1236	10	AF390544	AF390544 Rattus no
825	7	2.8	1245	10	MUSACD44A	L13611 Mus musculu
826	7	2.8	1245	10	MMCD44P	X69724 M.musculus
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828	7	2.8	1248	8	AY124853	AY124853 Arabidops
c 829	7	2.8	1251	8	AF173647	AF173647 Beta vulg
c 830	7	2.8	1260	8	SCYGL005C	Z72527 S.cerevisia
831	7	2.8	1270	4	AF323790	AF323790 Oryctolag
832	7	2.8	1277	6	AR165139	AR165139 Sequence
833	7	2.8	1280	3	AF286946	AF286946 Anchistro
834	7	2.8	1304	8	MSY16672	Y16672 Medicago sa
835	7	2.8	1314	3	AF311451	AF311451 Nemurella
836	7	2.8	1314	10	AF014365	AF014365 Rattus no
837	7	2.8	1316	3	AF311459	AF311459 Scopura m
838	7	2.8	1317	3	AF311452	AF311452 Amphinemu
c 839	7	2.8	1320	6	AX414541	AX414541 Sequence
840	7	2.8	1327	3	AF311456	AF311456 Brachypte
841	7	2.8	1329	8	AF295669	AF295669 Arabidops
842	7	2.8	1330	3	AF311442	AF311442 Paracapni
c 843	7	2.8	1332	10	RNGLA2U3	X05614 Rat alpha2
c 844	7	2.8	1340	8	PCLIGR	Y00262 Phanerochae
845	7	2.8	1342	9	AB065818	AB065818 Homo sapi
846	7	2.8	1344	8	AF110342	AF110342 Roccella
847	7	2.8	1345	3	AF311439	AF311439 Acruroper
c 848	7	2.8	1345	10	AF295402	AF295402 Mus muscu
849	7	2.8	1346	3	AF311443	AF311443 Allocapni
850	7	2.8	1347	3	AF311458	AF311458 Leuctra h
851	7	2.8	1355	3	AF311457	AF311457 Leuctra n
852	7	2.8	1356	10	AF029216	AF029216 Mus muscu
853	7	2.8	1357	10	MUSERVGG1	M26005 Mouse endog
854	7	2.8	1364	3	AF311447	AF311447 Zelandope
855	7	2.8	1376	3	AF311441	AF311441 Tasmanope
856	7	2.8	1380	3	AF311445	AF311445 Stenoperl
857	7	2.8	1383	3	AF311440	AF311440 Diamphipn
858	7	2.8	1386	3	AF311444	AF311444 Cosmoperl
859	7	2.8	1386	3	AF311446	AF311446 Leptoperl
c 860	7	2.8	1386	6	AR194172	AR194172 Sequence
861	7	2.8	1387	3	AF311448	AF311448 Newmanope
862	7	2.8	1388	3	AF311462	AF311462 Austrocer
863	7	2.8	1393	3	AF311461	AF311461 Notonemou
864	7	2.8	1396	4	OCU05204	U05204 Oryctolagus
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866	7	2.8	1398	9	BC007218	BC007218 Homo sapi
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c 874	7	2.8	1428	10	AY029194	AY029194 Mus muscu
875	7	2.8	1429	3	AF311472	AF311472 Isoperla
c 876	7	2.8	1429	10	BC024538	BC024538 Mus muscu
c 877	7	2.8	1434	8	TABETGLUA	Z22873 T.aestivum
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879	7	2.8	1434	9	AF169007	AF169007 Homo sapi
c 880	7	2.8	1437	3	AF390553	AF390553 Plasmodiu
c 881	7	2.8	1437	8	POPSAMPDPT	M73430 Populus x g
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883	7	2.8	1446	1	HECFLAA	L38478 Helicobacte
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885	7	2.8	1459	3	AF385065	AF385065 Dennyus h
886	7	2.8	1461	3	TMU65159	U65159 Triozocera
887	7	2.8	1462	3	AF311466	AF311466 Sierraper
888	7	2.8	1466	3	AF311464	AF311464 Pteronarc
889	7	2.8	1471	6	AX427452	AX427452 Sequence
890	7	2.8	1471	8	AY099484	AY099484 Tagetes e
c 891	7	2.8	1472	3	AB036850	AB036850 Ciona int
892	7	2.8	1472	3	AF139486	AF139486 Pediculus
893	7	2.8	1476	3	AF311463	AF311463 Siphonope
894	7	2.8	1477	3	AF311471	AF311471 Megarcys
895	7	2.8	1479	3	AF139483	AF139483 Pediculus
896	7	2.8	1479	3	AF139484	AF139484 Pediculus
897	7	2.8	1479	8	AY093133	AY093133 Arabidops
898	7	2.8	1480	3	AF385071	AF385071 Colimenop
899	7	2.8	1481	3	AY058287	AY058287 Drosophil
900	7	2.8	1487	3	AF139478	AF139478 Pediculus
901	7	2.8	1487	3	AF139479	AF139479 Pediculus
902	7	2.8	1487	3	AF139480	AF139480 Pediculus
903	7	2.8	1487	3	AF139481	AF139481 Pediculus
904	7	2.8	1492	3	AF139488	AF139488 Pediculus
905	7	2.8	1494	8	AB044442	AB044442 Platydori
906	7	2.8	1496	3	AF139482	AF139482 Pediculus
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c 909	7	2.8	1503	9	HS845O242	AL049681 Human gen
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913	7	2.8	1530	3	AF385069	AF385069 Machaeril
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c 915	7	2.8	1534	6	AX339072	AX339072 Sequence
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933	7	2.8	1588	5	AB032769	AB032769 Seriola q
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936	7	2.8	1609	14	AB079651	AB079651 Ornithoga
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938	7	2.8	1630	9	AK021902	AK021902 Homo sapi
939	7	2.8	1634	3	AY119612	AY119612 Drosophil
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968	7	2.8	1731	3	AF375261	AF375261 Scolytus
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970	7	2.8	1741	3	AY069365	AY069365 Drosophil
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c 972	7	2.8	1748	9	AK096880	AK096880 Homo sapi
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974	7	2.8	1753	9	BC022390	BC022390 Homo sapi
c 975	7	2.8	1757	8	AY090342	AY090342 Arabidops
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977	7	2.8	1761	8	AF360224	AF360224 Arabidops
978	7	2.8	1766	6	AX402389	AX402389 Sequence
979	7	2.8	1767	6	AX402404	AX402404 Sequence
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981	7	2.8	1775	9	AK024862	AK024862 Homo sapi
982	7	2.8	1781	9	H009384S19	AF218907 Homo sapi
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984	7	2.8	1784	8	TCA313384	AJ313384 Theobroma
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993	7	2.8	1854	3	AF250097	AF250097 Myrmex fl
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c 995	7	2.8	1857	17	AF119909	Af119909 Homo sapi
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c 997	7	2.8	1859	9	AF064867	AF064867 Homo sapi
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999	7	2.8	1863	9	AB070143	AB070143 Macaca fa
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ALIGNMENTS

RESULT 1
E37712
LOCUS E37712 741 bp DNA linear PAT 31-JAN-2002
DEFINITION Osteogenesis promoter.
ACCESSION E37712
VERSION E37712.1 GI:18626798
KEYWORDS JP 2000229880-A/3.
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 741)
AUTHORS Kinozaki,M., Goto,M., Yamaguchi,K., Morita,S. and Nakagawa,N.
TITLE Osteogenesis promoter
JOURNAL Patent: JP 2000229880-A 3 22-AUG-2000;
SNOW BRAND MILK PROD CO LTD
COMMENT OS Homo sapiens (human)
PN JP 2000229880-A/3
PD 22-AUG-2000
PF 10-FEB-1999 JP 1999033262
PR
PI MASAHIKO KINOZAKI,MASAAKI GOTO,KYOJI YAMAGUCHI,SHUJI MORITA,
PI NOBUAKI NAKAGAWA
PC A61K38/00,A61K31/00,A61K31/00,A61K31/00,C07K14/47 CC
FH Key Location/Qualifiers
FT source 1. .741
FT /organism='Homo sapiens (human)'.
FEATURES Location/Qualifiers
source 1. .741
/organism="Homo sapiens"
/db_xref="taxon:9606"
BASE COUNT 201 a 209 c 183 g 148 t
ORIGIN

Alignment Scores:

Pred. No.:	2.58e-274	Length:	741
Score:	247.00	Matches:	247
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	6	Gaps:	0

US-09-705-500A-3 (1-247) x E37712 (1-741)

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Qy          1 MetLeuGlnAsnSerAlaValLeuLeuValLeuValIleSerAlaSerAlaThrHisGlu 20
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Db          1 ATGCTCCAAAACTCAGCAGTGCTTCTGGTGCTGGTGATCAGTGCTTCTGCAACCCATGAG 60

Qy         21 AlaGluGlnAsnAspSerValSerProArgLysSerArgValAlaAlaGlnAsnSerAla 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GCGGAGCAGAATGACTCTGTGAGCCCCAGGAAATCCCGAGTGGCGGCCCAAAACTCAGCT 120

Qy         41 GluValValArgCysLeuAsnSerAlaLeuGlnValGlyCysGlyAlaPheAlaCysLeu 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GAAGTGGTTCGTTGCCTCAACAGTGCTCTACAGGTCGGCTGCGGGGCTTTTGCATGCCTG 180

Qy         61 GluAsnSerThrCysAspThrAspGlyMetTyrAspIleCysLysSerPheLeuTyrSer 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GAAAACTCCACCTGTGACACAGATGGGATGTATGACATCTGTAAATCCTTCTTGTACAGC 240

Qy         81 AlaAlaLysPheAspThrGlnGlyLysAlaPheValLysGluSerLeuLysCysIleAla 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GCTGCTAAATTTGACACTCAGGGAAAAGCATTCGTCAAAGAGAGCTTAAAATGCATCGCC 300

Qy        101 AsnGlyValThrSerLysValPheLeuAlaIleArgArgCysSerThrPheGlnArgMet 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 AACGGGGTCACCTCCAAGGTCTTCCTCGCCATTCGGAGGTGCTCCACTTTCCAAAGGATG 360
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Qy        121 IleAlaGluValGlnGluGluCysTyrSerLysLeuAsnValCysSerIleAlaLysArg 140
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Db        361 ATTGCTGAGGTGCAGGAAGAGTGCTACAGCAAGCTGAATGTGTGCAGCATCGCCAAGCGG 420

Qy        141 AsnProGluAlaIleThrGluValValGlnLeuProAsnHisPheSerAsnArgTyrTyr 160
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Db        421 AACCCTGAAGCCATCACTGAGGTCGTCCAGCTGCCCAATCACTTCTCCAACAGATACTAT 480

Qy        161 AsnArgLeuValArgSerLeuLeuGluCysAspGluAspThrValSerThrIleArgAsp 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 AACAGACTTGTCCGAAGCCTGCTGGAATGTGATGAAGACACAGTCAGCACAATCAGAGAC 540

Qy        181 SerLeuMetGluLysIleGlyProAsnMetAlaSerLeuPheHisIleLeuGlnThrAsp 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 AGCCTGATGGAGAAAATTGGGCCTAACATGGCCAGCCTCTTCCACATCCTGCAGACAGAC 600

Qy        201 HisCysAlaGlnThrHisProArgAlaAspPheAsnArgArgArgThrAsnGluProGln 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CACTGTGCCCAAACACACCCACGAGCTGACTTCAACAGGAGACGCACCAATGAGCCGCAG 660

Qy        221 LysLeuLysValLeuLeuArgAsnLeuArgGlyGluGluAspSerProSerHisIleLys 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 AAGCTGAAAGTCCTCCTCAGGAACCTCCGAGGTGAGGAGGACTCTCCCTCCCACATCAAA 720

Qy        241 ArgThrSerHisGluSerAla 247
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Db        721 CGCACATCCCATGAGAGTGCA 741

RESULT 2
E39295
LOCUS       E39295                   741 bp    DNA     linear   PAT 31-JAN-2002
DEFINITION  Novel protein and process for producing the same.
ACCESSION   E39295
VERSION     E39295.1  GI:18628926
KEYWORDS    JP 2000239299-A/12.
SOURCE      Homo sapiens.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 741)
  AUTHORS   Goto,M., Tomoyasu,M., Yamaguchi,K., Kinozaki,M., Shima,N.,
            Yasuda,N. and Nakagawa,N.
  TITLE     Novel protein and process for producing the same
  JOURNAL   Patent: JP 2000239299-A 12 05-SEP-2000;
            SNOW BRAND MILK PROD CO LTD
COMMENT     OS   Homo sapiens (human)
            PN   JP 2000239299-A/12
            PD   05-SEP-2000
            PF   15-FEB-1999 JP 1999036225
            PR
            PI   MASAAKI GOTO,MASAAKI TOMOYASU,KYOJI YAMAGUCHI, PI   MASAHIKO
            KINOZAKI,
            PI   NOBUYUKI SHIMA,NAOTAKA YASUDA,NOBUAKI NAKAGAWA PC
            C07K14/47,C12N5/10,C12N15/09,C12P21/02//A61K31/00,A61K31/00, PC
            A61K38/00,
            PC   (C12P21/02,C12R1:91),C12N5/00,C12N15/00,A61K37/02 CC
            FH   Key             Location/Qualifiers
            FT   source          1. .741
            FT                   /organism='Homo sapiens (human)'.
FEATURES             Location/Qualifiers
     source          1. .741
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
BASE COUNT      201 a    209 c    183 g    148 t
ORIGIN

Alignment Scores:
Pred. No.:              2.58e-274       Length:         741
Score:                  247.00          Matches:        247
Percent Similarity:     100.00%         Conservative:   0
Best Local Similarity:  100.00%         Mismatches:     0
Query Match:            100.00%         Indels:         0
DB:                     6               Gaps:           0

US-09-705-500A-3 (1-247) x E39295 (1-741)

Qy          1 MetLeuGlnAsnSerAlaValLeuLeuValLeuValIleSerAlaSerAlaThrHisGlu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGCTCCAAAACTCAGCAGTGCTTCTGGTGCTGGTGATCAGTGCTTCTGCAACCCATGAG 60

Qy         21 AlaGluGlnAsnAspSerValSerProArgLysSerArgValAlaAlaGlnAsnSerAla 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GCGGAGCAGAATGACTCTGTGAGCCCCAGGAAATCCCGAGTGGCGGCCCAAAACTCAGCT 120

Qy         41 GluValValArgCysLeuAsnSerAlaLeuGlnValGlyCysGlyAlaPheAlaCysLeu 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GAAGTGGTTCGTTGCCTCAACAGTGCTCTACAGGTCGGCTGCGGGGCTTTTGCATGCCTG 180

Qy         61 GluAsnSerThrCysAspThrAspGlyMetTyrAspIleCysLysSerPheLeuTyrSer 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GAAAACTCCACCTGTGACACAGATGGGATGTATGACATCTGTAAATCCTTCTTGTACAGC 240

Qy         81 AlaAlaLysPheAspThrGlnGlyLysAlaPheValLysGluSerLeuLysCysIleAla 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GCTGCTAAATTTGACACTCAGGGAAAAGCATTCGTCAAAGAGAGCTTAAAATGCATCGCC 300

Qy        101 AsnGlyValThrSerLysValPheLeuAlaIleArgArgCysSerThrPheGlnArgMet 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 AACGGGGTCACCTCCAAGGTCTTCCTCGCCATTCGGAGGTGCTCCACTTTCCAAAGGATG 360

Qy        121 IleAlaGluValGlnGluGluCysTyrSerLysLeuAsnValCysSerIleAlaLysArg 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 ATTGCTGAGGTGCAGGAAGAGTGCTACAGCAAGCTGAATGTGTGCAGCATCGCCAAGCGG 420

Qy        141 AsnProGluAlaIleThrGluValValGlnLeuProAsnHisPheSerAsnArgTyrTyr 160
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Db        421 AACCCTGAAGCCATCACTGAGGTCGTCCAGCTGCCCAATCACTTCTCCAACAGATACTAT 480

Qy        161 AsnArgLeuValArgSerLeuLeuGluCysAspGluAspThrValSerThrIleArgAsp 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 AACAGACTTGTCCGAAGCCTGCTGGAATGTGATGAAGACACAGTCAGCACAATCAGAGAC 540

Qy        181 SerLeuMetGluLysIleGlyProAsnMetAlaSerLeuPheHisIleLeuGlnThrAsp 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 AGCCTGATGGAGAAAATTGGGCCTAACATGGCCAGCCTCTTCCACATCCTGCAGACAGAC 600

Qy        201 HisCysAlaGlnThrHisProArgAlaAspPheAsnArgArgArgThrAsnGluProGln 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CACTGTGCCCAAACACACCCACGAGCTGACTTCAACAGGAGACGCACCAATGAGCCGCAG 660

Qy        221 LysLeuLysValLeuLeuArgAsnLeuArgGlyGluGluAspSerProSerHisIleLys 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 AAGCTGAAAGTCCTCCTCAGGAACCTCCGAGGTGAGGAGGACTCTCCCTCCCACATCAAA 720

Qy        241 ArgThrSerHisGluSerAla 247
              |||||||||||||||||||||
Db        721 CGCACATCCCATGAGAGTGCA 741

RESULT 3
AR055558
LOCUS       AR055558                 771 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 1 from patent US 5837498.
ACCESSION   AR055558
VERSION     AR055558.1  GI:5981135
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 771)
  AUTHORS   Olsen,H.S. and Adams,M.D.
  TITLE     Corpuscles of stannius protein, stanniocalcin
  JOURNAL   Patent: US 5837498-A 1 17-NOV-1998;
FEATURES             Location/Qualifiers
     source          1. .771
                     /organism="unknown"
BASE COUNT      212 a    214 c    192 g    153 t
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ORIGIN

Alignment Scores:
Pred. No.:                2.69e-274       Length:          771
Score:                    247.00          Matches:         247
Percent Similarity:       100.00%         Conservative:    0
Best Local Similarity:    100.00%         Mismatches:      0
Query Match:              100.00%         Indels:          0
DB:                       6               Gaps:            0

US-09-705-500A-3 (1-247) x AR055558 (1-771)

Qy          1 MetLeuGlnAsnSerAlaValLeuLeuValLeuValIleSerAlaSerAlaThrHisGlu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         16 ATGCTCCAAAACTCAGCAGTGCTTCTGGTGCTGGTGATCAGTGCTTCTGCAACCCATGAG 75

Qy         21 AlaGluGlnAsnAspSerValSerProArgLysSerArgValAlaAlaGlnAsnSerAla 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         76 GCGGAGCAGAATGACTCTGTGAGCCCCAGGAAATCCCGAGTGGCGGCCCAAAACTCAGCT 135

Qy         41 GluValValArgCysLeuAsnSerAlaLeuGlnValGlyCysGlyAlaPheAlaCysLeu 60
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Db        136 GAAGTGGTTCGTTGCCTCAACAGTGCTCTACAGGTCGGCTGCGGGGCTTTTGCATGCCTG 195

Qy         61 GluAsnSerThrCysAspThrAspGlyMetTyrAspIleCysLysSerPheLeuTyrSer 80
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Db        196 GAAAACTCCACCTGTGACACAGATGGGATGTATGACATCTGTAAATCCTTCTTGTACAGC 255

Qy         81 AlaAlaLysPheAspThrGlnGlyLysAlaPheValLysGluSerLeuLysCysIleAla 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        256 GCTGCTAAATTTGACACTCAGGGAAAAGCATTCGTCAAAGAGAGCTTAAAATGCATCGCC 315

Qy        101 AsnGlyValThrSerLysValPheLeuAlaIleArgArgCysSerThrPheGlnArgMet 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        316 AACGGGGTCACCTCCAAGGTCTTCCTCGCCATTCGGAGGTGCTCCACTTTCCAAAGGATG 375

Qy        121 IleAlaGluValGlnGluGluCysTyrSerLysLeuAsnValCysSerIleAlaLysArg 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        376 ATTGCTGAGGTGCAGGAAGAGTGCTACAGCAAGCTGAATGTGTGCAGCATCGCCAAGCGG 435

Qy        141 AsnProGluAlaIleThrGluValValGlnLeuProAsnHisPheSerAsnArgTyrTyr 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        436 AACCCTGAAGCCATCACTGAGGTCGTCCAGCTGCCCAATCACTTCTCCAACAGATACTAT 495

Qy        161 AsnArgLeuValArgSerLeuLeuGluCysAspGluAspThrValSerThrIleArgAsp 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        496 AACAGACTTGTCCGAAGCCTGCTGGAATGTGATGAAGACACAGTCAGCACAATCAGAGAC 555

Qy        181 SerLeuMetGluLysIleGlyProAsnMetAlaSerLeuPheHisIleLeuGlnThrAsp 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        556 AGCCTGATGGAGAAAATTGGGCCTAACATGGCCAGCCTCTTCCACATCCTGCAGACAGAC 615

Qy        201 HisCysAlaGlnThrHisProArgAlaAspPheAsnArgArgArgThrAsnGluProGln 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        616 CACTGTGCCCAAACACACCCACGAGCTGACTTCAACAGGAGACGCACCAATGAGCCGCAG 675

Qy        221 LysLeuLysValLeuLeuArgAsnLeuArgGlyGluGluAspSerProSerHisIleLys 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        676 AAGCTGAAAGTCCTCCTCAGGAACCTCCGAGGTGAGGAGGACTCTCCCTCCCACATCAAA 735

Qy        241 ArgThrSerHisGluSerAla 247
              |||||||||||||||||||
Db        736 CGCACATCCCATGAGAGTGCA 756

RESULT 4
AR091578
LOCUS       AR091578                 771 bp    DNA     linear   PAT 07-SEP-2000
DEFINITION  Sequence 1 from patent US 5994301.
ACCESSION   AR091578
VERSION     AR091578.1  GI:10018333
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 771)
  AUTHORS   Olsen,H.S. and Adams,M.D.
  TITLE     Corpuscles of stannius protein, stanniocalcin
  JOURNAL   Patent: US 5994301-A 1 30-NOV-1999;
FEATURES             Location/Qualifiers
     source          1..771
                     /organism="unknown"
BASE COUNT      212 a    214 c    192 g    153 t
ORIGIN

Alignment Scores:
Pred. No.:                2.69e-274       Length:          771
Score:                    247.00          Matches:         247
Percent Similarity:       100.00%         Conservative:    0
Best Local Similarity:    100.00%         Mismatches:      0
Query Match:              100.00%         Indels:          0
DB:                       6               Gaps:            0

US-09-705-500A-3 (1-247) x AR091578 (1-771)

Qy          1 MetLeuGlnAsnSerAlaValLeuLeuValLeuValIleSerAlaSerAlaThrHisGlu 20
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Db         16 ATGCTCCAAAACTCAGCAGTGCTTCTGGTGCTGGTGATCAGTGCTTCTGCAACCCATGAG 75

Qy         21 AlaGluGlnAsnAspSerValSerProArgLysSerArgValAlaAlaGlnAsnSerAla 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         76 GCGGAGCAGAATGACTCTGTGAGCCCCAGGAAATCCCGAGTGGCGGCCCAAAACTCAGCT 135

Qy         41 GluValValArgCysLeuAsnSerAlaLeuGlnValGlyCysGlyAlaPheAlaCysLeu 60
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Db        136 GAAGTGGTTCGTTGCCTCAACAGTGCTCTACAGGTCGGCTGCGGGGCTTTTGCATGCCTG 195

Qy         61 GluAsnSerThrCysAspThrAspGlyMetTyrAspIleCysLysSerPheLeuTyrSer 80
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Db        196 GAAAACTCCACCTGTGACACAGATGGGATGTATGACATCTGTAAATCCTTCTTGTACAGC 255

Qy         81 AlaAlaLysPheAspThrGlnGlyLysAlaPheValLysGluSerLeuLysCysIleAla 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        256 GCTGCTAAATTTGACACTCAGGGAAAAGCATTCGTCAAAGAGAGCTTAAAATGCATCGCC 315

Qy        101 AsnGlyValThrSerLysValPheLeuAlaIleArgArgCysSerThrPheGlnArgMet 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        316 AACGGGGTCACCTCCAAGGTCTTCCTCGCCATTCGGAGGTGCTCCACTTTCCAAAGGATG 375

Qy        121 IleAlaGluValGlnGluGluCysTyrSerLysLeuAsnValCysSerIleAlaLysArg 140
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Db        376 ATTGCTGAGGTGCAGGAAGAGTGCTACAGCAAGCTGAATGTGTGCAGCATCGCCAAGCGG 435

Qy        141 AsnProGluAlaIleThrGluValValGlnLeuProAsnHisPheSerAsnArgTyrTyr 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        436 AACCCTGAAGCCATCACTGAGGTCGTCCAGCTGCCCAATCACTTCTCCAACAGATACTAT 495

Qy        161 AsnArgLeuValArgSerLeuLeuGluCysAspGluAspThrValSerThrIleArgAsp 180
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Db        496 AACAGACTTGTCCGAAGCCTGCTGGAATGTGATGAAGACACAGTCAGCACAATCAGAGAC 555

Qy        181 SerLeuMetGluLysIleGlyProAsnMetAlaSerLeuPheHisIleLeuGlnThrAsp 200
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Db        556 AGCCTGATGGAGAAAATTGGGCCTAACATGGCCAGCCTCTTCCACATCCTGCAGACAGAC 615

Qy        201 HisCysAlaGlnThrHisProArgAlaAspPheAsnArgArgArgThrAsnGluProGln 220
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Db        616 CACTGTGCCCAAACACACCCACGAGCTGACTTCAACAGGAGACGCACCAATGAGCCGCAG 675

Qy        221 LysLeuLysValLeuLeuArgAsnLeuArgGlyGluGluAspSerProSerHisIleLys 240
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Db        676 AAGCTGAAAGTCCTCCTCAGGAACCTCCGAGGTGAGGAGGACTCTCCCTCCCACATCAAA 735

Qy        241 ArgThrSerHisGluSerAla 247
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Db        736 CGCACATCCCATGAGAGTGCA 756
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RESULT 5
HSU46768
LOCUS       HSU46768                840 bp    mRNA    linear   PRI 22-FEB-1996
DEFINITION  Human stanniocalcin mRNA, complete cds.
ACCESSION   U46768
VERSION     U46768.1  GI:1199619
KEYWORDS    .
SOURCE      Homo sapiens.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 840)
  AUTHORS   Olsen,H.S., Cepeda,M.A., Zhang,Q.-Q., Rosen,C.A., Vozzolo,B.L. and
            Wagner,G.F.
  TITLE     Human stanniocalcin: a hormonal regulator of mineral metabolism
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. (1996) In press
REFERENCE   2  (bases 1 to 840)
  AUTHORS   Olsen,H.S.
  TITLE     Direct Submission
  JOURNAL   Submitted (22-JAN-1996) Henrik S. Olsen, Human Genome Sciences,
            9410 Key West Avenue, Rockville, MD 20850, USA
FEATURES             Location/Qualifiers
     source          1. .840
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
     CDS             35. .778
                     /codon_start=1
                     /product="stanniocalcin"
                     /protein_id="AAA88903.1"
                     /db_xref="GI:1199620"
                     /translation="MLQNSAVLLVLVISASATHEAEQNDSVSPRKSRVAAQNSAEVVR
                     CLNSALQVGCGAFACLENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANG
                     VTSKVFLAIRRCSTFQRMIAEVQEECYSKLNVCSIAKRNPEAITEVVQLPNHFSNRYY
                     NRLVRSLLECDEDTVSTIRDSLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRRTNE
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BASE COUNT      237 a    233 c    201 g    169 t
ORIGIN

Alignment Scores:
Pred. No.:              2.94e-274       Length:         840
Score:                  247.00          Matches:        247
Percent Similarity:     100.00%         Conservative:   0
Best Local Similarity:  100.00%         Mismatches:     0
Query Match:            100.00%         Indels:         0
DB:                     9               Gaps:           0

US-09-705-500A-3 (1-247) x HSU46768 (1-840)

Qy          1 MetLeuGlnAsnSerAlaValLeuLeuValLeuValIleSerAlaSerAlaThrHisGlu 20
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Db         35 ATGCTCCAAAACTCAGCAGTGCTTCTGGTGCTGGTGATCAGTGCTTCTGCAACCCATGAG 94

Qy         21 AlaGluGlnAsnAspSerValSerProArgLysSerArgValAlaAlaGlnAsnSerAla 40
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         95 GCGGAGCAGAATGACTCTGTGAGCCCCAGGAAATCCCGAGTGGCGGCCCAAAACTCAGCT 154

Qy         41 GluValValArgCysLeuAsnSerAlaLeuGlnValGlyCysGlyAlaPheAlaCysLeu 60
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        155 GAAGTGGTTCGTTGCCTCAACAGTGCTCTACAGGTCGGCTGCGGGGCTTTTGCATGCCTG 214

Qy         61 GluAsnSerThrCysAspThrAspGlyMetTyrAspIleCysLysSerPheLeuTyrSer 80
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        215 GAAAACTCCACCTGTGACACAGATGGGATGTATGACATCTGTAAATCCTTCTTGTACAGC 274

Qy         81 AlaAlaLysPheAspThrGlnGlyLysAlaPheValLysGluSerLeuLysCysIleAla 100
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Db        275 GCTGCTAAATTTGACACTCAGGGAAAAGCATTCGTCAAAGAGAGCTTAAAATGCATCGCC 334

Qy        101 AsnGlyValThrSerLysValPheLeuAlaIleArgArgCysSerThrPheGlnArgMet 120
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        335 AACGGGGTCACCTCCAAGGTCTTCCTCGCCATTCGGAGGTGCTCCACTTTCCAAAGGATG 394

Qy        121 IleAlaGluValGlnGluGluCysTyrSerLysLeuAsnValCysSerIleAlaLysArg 140
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        395 ATTGCTGAGGTGCAGGAAGAGTGCTACAGCAAGCTGAATGTGTGCAGCATCGCCAAGCGG 454

Qy        141 AsnProGluAlaIleThrGluValValGlnLeuProAsnHisPheSerAsnArgTyrTyr 160
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        455 AACCCTGAAGCCATCACTGAGGTCGTCCAGCTGCCCAATCACTTCTCCAACAGATACTAT 514

Qy        161 AsnArgLeuValArgSerLeuLeuGluCysAspGluAspThrValSerThrIleArgAsp 180
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        515 AACAGACTTGTCCGAAGCCTGCTGGAATGTGATGAAGACACAGTCAGCACAATCAGAGAC 574

Qy        181 SerLeuMetGluLysIleGlyProAsnMetAlaSerLeuPheHisIleLeuGlnThrAsp 200
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        575 AGCCTGATGGAGAAAATTGGGCCTAACATGGCCAGCCTCTTCCACATCCTGCAGACAGAC 634

Qy        201 HisCysAlaGlnThrHisProArgAlaAspPheAsnArgArgArgThrAsnGluProGln 220
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        635 CACTGTGCCCAAACACACCCACGAGCTGACTTCAACAGGAGACGCACCAATGAGCCGCAG 694

Qy        221 LysLeuLysValLeuLeuArgAsnLeuArgGlyGluGluAspSerProSerHisIleLys 240
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        695 AAGCTGAAAGTCCTCCTCAGGAACCTCCGAGGTGAGGAGGACTCTCCCTCCCACATCAAA 754

Qy        241 ArgThrSerHisGluSerAla 247
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Db        755 CGCACATCCCATGAGAGTGCA 775

RESULT 6
BC029044
LOCUS       BC029044                2481 bp    mRNA    linear   PRI 16-MAY-2002
DEFINITION  Homo sapiens, stanniocalcin 1, clone MGC:34539 IMAGE:5191420, mRNA,
            complete cds.
ACCESSION   BC029044
VERSION     BC029044.1  GI:20810067
KEYWORDS    MGC.
SOURCE      Homo sapiens.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 2481)
  AUTHORS   Strausberg,R.
  TITLE     Direct Submission
  JOURNAL   Submitted (01-MAY-2002) National Institutes of Health, Mammalian
            Gene Collection (MGC), Cancer Genomics Office, National Cancer
            Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
            USA
  REMARK    NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT     Contact: MGC help desk
            Email:cgapbs-r@mail.nih.gov
            Tissue Procurement: Life Technologies, Inc.
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Baylor College of Medicine Human Genome
            Sequencing Center
            Center code: BCM-HGSC
            Web site: http://www.hgsc.bcm.tmc.edu/cdna/
            Contact: amg@bcm.tmc.edu
            Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Hale, S.M.,
            Yoon, V.S., Kowis, C.R., Lawrence, S., Martin, R.G., Muzny, D.M.,
            Richards, S., Gibbs, R.A.

            Clone distribution: MGC clone distribution information can be found
            through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
            Series: IRAK Plate: 50 Row: k Column: 5
            This clone was selected for full length sequencing because it
            passed the following selection criteria: matched mRNA gi: 4507264.
FEATURES             Location/Qualifiers
     source          1. .2481
                     /organism="Homo sapiens"
                     /db_xref="LocusID:6781"
                     /db_xref="taxon:9606"
                     /clone="MGC:34539 IMAGE:5191420"
                     /tissue_type="Colon, Kidney, Stomach, adult, whole pooled"
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                     /clone_lib="NIH_MGC_116"
                     /lab_host="DH10B"
                     /note="Vector: pCMV-SPORT6"
     CDS             263. .1006
                     /codon_start=1
                     /product="stanniocalcin 1"
                     /protein_id="AAH29044.1"
                     /db_xref="GI:20810068"
                     /translation="MLQNSAVLLVLVISASATHEAEQNDSVSPRKSRVAAQNSAEVVR
                     CLNSALQVGCGAFACLENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANG
                     VTSKVFLAIRRCSTFQRMIAEVQEECYSKLNVCSIAKRNPEAITEVVQLPNHFSNRYY
                     NRLVRSLLECDEDTVSTIRDSLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRRTNE
                     PQKLKVLLRNLRGEEDSPSHIKRTSHESA"
BASE COUNT      745 a    599 c    520 g    617 t
ORIGIN

Alignment Scores:
Pred. No.:              9.01e-274      Length:         2481
Score:                  247.00         Matches:        247
Percent Similarity:     100.00%        Conservative:   0
Best Local Similarity:  100.00%        Mismatches:     0
Query Match:            100.00%        Indels:         0
DB:                     9              Gaps:           0

US-09-705-500A-3 (1-247) x BC029044 (1-2481)

Qy          1 MetLeuGlnAsnSerAlaValLeuLeuValLeuValIleSerAlaSerAlaThrHisGlu 20
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Db        263 ATGCTCCAAAACTCAGCAGTGCTTCTGGTGCTGGTGATCAGTGCTTCTGCAACCCATGAG 322

Qy         21 AlaGluGlnAsnAspSerValSerProArgLysSerArgValAlaAlaGlnAsnSerAla 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        323 GCGGAGCAGAATGACTCTGTGAGCCCCAGGAAATCCCGAGTGGCGGCTCAAAACTCAGCT 382

Qy         41 GluValValArgCysLeuAsnSerAlaLeuGlnValGlyCysGlyAlaPheAlaCysLeu 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        383 GAAGTGGTTCGTTGCCTCAACAGTGCTCTACAGGTCGGCTGCGGGGCTTTTGCATGCCTG 442

Qy         61 GluAsnSerThrCysAspThrAspGlyMetTyrAspIleCysLysSerPheLeuTyrSer 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        443 GAAAACTCCACCTGTGACACAGATGGGATGTATGACATCTGTAAATCCTTCTTGTACAGC 502

Qy         81 AlaAlaLysPheAspThrGlnGlyLysAlaPheValLysGluSerLeuLysCysIleAla 100
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Db        503 GCTGCTAAATTTGACACTCAGGGAAAAGCATTCGTCAAAGAGAGCTTAAAATGCATCGCC 562

Qy        101 AsnGlyValThrSerLysValPheLeuAlaIleArgArgCysSerThrPheGlnArgMet 120
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Db        563 AACGGGGTCACCTCCAAGGTCTTCCTCGCCATTCGGAGGTGCTCCACTTTCCAAAGGATG 622

Qy        121 IleAlaGluValGlnGluGluCysTyrSerLysLeuAsnValCysSerIleAlaLysArg 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        623 ATTGCTGAGGTGCAGGAAGAGTGCTACAGCAAGCTGAATGTGTGCAGCATCGCCAAGCGG 682

Qy        141 AsnProGluAlaIleThrGluValValGlnLeuProAsnHisPheSerAsnArgTyrTyr 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        683 AACCCTGAAGCCATCACTGAGGTCGTCCAGCTGCCCAATCACTTCTCCAACAGATACTAT 742

Qy        161 AsnArgLeuValArgSerLeuLeuGluCysAspGluAspThrValSerThrIleArgAsp 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        743 AACAGACTTGTCCGAAGCCTGCTGGAATGTGATGAAGACACAGTCAGCACAATCAGAGAC 802

Qy        181 SerLeuMetGluLysIleGlyProAsnMetAlaSerLeuPheHisIleLeuGlnThrAsp 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        803 AGCCTGATGGAGAAAATTGGGCCTAACATGGCCAGCCTCTTCCACATCCTGCAGACAGAC 862

Qy        201 HisCysAlaGlnThrHisProArgAlaAspPheAsnArgArgArgThrAsnGluProGln 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        863 CACTGTGCCCAAACACACCCACGAGCTGACTTCAACAGGAGACGCACCAATGAGCCGCAG 922

Qy        221 LysLeuLysValLeuLeuArgAsnLeuArgGlyGluGluAspSerProSerHisIleLys 240
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Db        923 AAGCTGAAAGTCCTCCTCAGGAACCTCCGAGGTGAGGAGGACTCTCCCTCCCACATCAAA 982

Qy        241 ArgThrSerHisGluSerAla 247
              ||||||||||||||||||||
Db        983 CGCACATCCCATGAGAGTGCA 1003

RESULT 7
HSU25997
LOCUS       HSU25997                3901 bp    mRNA    linear   PRI 02-APR-1998
DEFINITION  Homo sapiens stanniocalcin precursor (STC) mRNA, complete cds.
ACCESSION   U25997
VERSION     U25997.1  GI:3006202
KEYWORDS    .
SOURCE      Homo sapiens.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 3901)
  AUTHORS   Chang,A.C., Janosi,J., Hulsbeek,M., de Jong,D., Jeffrey,K.J.,
            Noble,J.R. and Reddel,R.R.
  TITLE     A novel human cDNA highly homologous to the fish hormone
            stanniocalcin
  JOURNAL   Mol. Cell. Endocrinol. 112 (2), 241-247 (1995)
  MEDLINE   96077825
   PUBMED   7489828
REFERENCE   2  (bases 1 to 3901)
  AUTHORS   Chang,A.C., Jeffrey,K.J., Tokutake,Y., Shimamoto,A., Neumann,A.A.,
            Dunham,M.A., Cha,J., Sugawara,M., Furuichi,Y. and Reddel,R.R.
  TITLE     Human stanniocalcin (STC): genomic structure, chromosomal
            localization, and the presence of CAG trinucleotide repeats
  JOURNAL   Genomics 47 (3), 393-398 (1998)
  MEDLINE   98149987
   PUBMED   9480753
REFERENCE   3  (bases 1 to 3901)
  AUTHORS   Chang,A.C.-M.
  TITLE     Direct Submission
  JOURNAL   Submitted (02-MAY-1995) Childrens Medical Research Institute, 214
            Hawkesbury Road, Westmead, NSW 2145, Australia
REFERENCE   4  (bases 1 to 3901)
  AUTHORS   Chang,A.C.-M.
  TITLE     Direct Submission
  JOURNAL   Submitted (02-APR-1998) Childrens Medical Research Institute, 214
            Hawkesbury Road, Westmead, NSW 2145, Australia
  REMARK    Sequence update by submitter
COMMENT     On Apr 2, 1998 this sequence version replaced gi:975297.
FEATURES             Location/Qualifiers
     source          1. .3901
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /cell_line="HT1080"
                     /cell_type="fibroblast"
                     /note="similar to the nucleotide sequence in GenBank
                     Accession Number S50179"
     gene            1. .3901
                     /gene="STC"
     repeat_region   30. .125
                     /rpt_type=tandem
                     /rpt_unit=cag
     CDS             285. .1028
                     /gene="STC"
                     /function="putative calcium responsive hormone"
                     /note="similar to SwissProt Accession Number Q08264"
                     /codon_start=1
                     /product="stanniocalcin precursor"
                     /protein_id="AAC09472.1"
                     /db_xref="GI:975298"
                     /translation="MLQNSAVLLVLVISASATHEAEQNDSVSPRKSRVAAQNSAEVVR
                     CLNSALQVGCGAFACLENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANG
                     VTSKVFLAIRRCSTFQRMIAEVQEECYSKLNVCSIAKRNPEAITEVVQLPNHFSNRYY
                     NRLVRSLLECDEDTVSTIRDSLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRRTNE
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     sig_peptide     285. .383
                     /gene="STC"
                     /note="pre-pro-peptide"
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     mat_peptide     384. .1025
                     /gene="STC"
                     /product="stanniocalcin"
                     /function="putative calcium responsive hormone"
     polyA_site      3882
                     /gene="STC"
                     /note="19 A nucleotides"
BASE COUNT     1152 a    910 c    784 g   1055 t
ORIGIN

Alignment Scores:
Pred. No.:              1.44e-273      Length:         3901
Score:                  247.00         Matches:        247
Percent Similarity:     100.00%        Conservative:   0
Best Local Similarity:  100.00%        Mismatches:     0
Query Match:            100.00%        Indels:         0
DB:                     9              Gaps:           0

US-09-705-500A-3 (1-247) x HSU25997 (1-3901)

Qy          1 MetLeuGlnAsnSerAlaValLeuLeuValLeuValIleSerAlaSerAlaThrHisGlu 20
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        285 ATGCTCCAAAACTCAGCAGTGCTTCTGGTGCTGGTGATCAGTGCTTCTGCAACCCATGAG 344

Qy         21 AlaGluGlnAsnAspSerValSerProArgLysSerArgValAlaAlaGlnAsnSerAla 40
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        345 GCGGAGCAGAATGACTCTGTGAGCCCCAGGAAATCCCGAGTGGCGGCTCAAAACTCAGCT 404

Qy         41 GluValValArgCysLeuAsnSerAlaLeuGlnValGlyCysGlyAlaPheAlaCysLeu 60
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        405 GAAGTGGTTCGTTGCCTCAACAGTGCTCTACAGGTCGGCTGCGGGGCTTTTGCATGCCTG 464

Qy         61 GluAsnSerThrCysAspThrAspGlyMetTyrAspIleCysLysSerPheLeuTyrSer 80
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        465 GAAAACTCCACCTGTGACACAGATGGGATGTATGACATCTGTAAATCCTTCTTGTACAGC 524

Qy         81 AlaAlaLysPheAspThrGlnGlyLysAlaPheValLysGluSerLeuLysCysIleAla 100
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        525 GCTGCTAAATTTGACACTCAGGGAAAAGCATTCGTCAAAGAGAGCTTAAAATGCATCGCC 584

Qy        101 AsnGlyValThrSerLysValPheLeuAlaIleArgArgCysSerThrPheGlnArgMet 120
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        585 AACGGGGTCACCTCCAAGGTCTTCCTCGCCATTCGGAGGTGCTCCACTTTCCAAAGGATG 644

Qy        121 IleAlaGluValGlnGluGluCysTyrSerLysLeuAsnValCysSerIleAlaLysArg 140
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        645 ATTGCTGAGGTGCAGGAAGAGTGCTACAGCAAGCTGAATGTGTGCAGCATCGCCAAGCGG 704

Qy        141 AsnProGluAlaIleThrGluValValGlnLeuProAsnHisPheSerAsnArgTyrTyr 160
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Db        705 AACCCTGAAGCCATCACTGAGGTCGTCCAGCTGCCCAATCACTTCTCCAACAGATACTAT 764

Qy        161 AsnArgLeuValArgSerLeuLeuGluCysAspGluAspThrValSerThrIleArgAsp 180
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Db        765 AACAGACTTGTCCGAAGCCTGCTGGAATGTGATGAAGACACAGTCAGCACAATCAGAGAC 824

Qy        181 SerLeuMetGluLysIleGlyProAsnMetAlaSerLeuPheHisIleLeuGlnThrAsp 200
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Db        825 AGCCTGATGGAGAAAATTGGGCCTAACATGGCCAGCCTCTTCCACATCCTGCAGACAGAC 884

Qy        201 HisCysAlaGlnThrHisProArgAlaAspPheAsnArgArgArgThrAsnGluProGln 220
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        885 CACTGTGCCCAAACACACCCACGAGCTGACTTCAACAGGAGACGCACCAATGAGCCGCAG 944

Qy        221 LysLeuLysValLeuLeuArgAsnLeuArgGlyGluGluAspSerProSerHisIleLys 240
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        945 AAGCTGAAAGTCCTCCTCAGGAACCTCCGAGGTGAGGAGGACTCTCCCTCCCACATCAAA 1004

Qy        241 ArgThrSerHisGluSerAla 247
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Db       1005 CGCACATCCCATGAGAGTGCA 1025

RESULT 8
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AX156292
LOCUS       AX156292                585 bp    DNA     linear   PAT 22-JUN-2001
DEFINITION  Sequence 149 from Patent WO0140269.
ACCESSION   AX156292
VERSION     AX156292.1  GI:14537293
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 585)
  AUTHORS   Dillon,D.C., Day,C.H., Jiang,Y., Houghton,R.L., Mitcham,J.L. and
            Wang,A.
  TITLE     Compositions and methods for therapy and diagnosis of breast cancer
  JOURNAL   Patent: WO 0140269-A 149 07-JUN-2001;
            CORIXA CORPORATION (US)
FEATURES             Location/Qualifiers
     source          1. .585
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
BASE COUNT      171 a    163 c    136 g    110 t      5 others
ORIGIN

Alignment Scores:
Pred. No.:              2.79e-174      Length:         585
Score:                  160.00         Matches:        160
Percent Similarity:     100.00%        Conservative:   0
Best Local Similarity:  100.00%        Mismatches:     0
Query Match:            64.78%         Indels:         0
DB:                     6              Gaps:           0

US-09-705-500A-3 (1-247) x AX156292 (1-585)

Qy         88 GlyLysAlaPheValLysGluSerLeuLysCysIleAlaAsnGlyValThrSerLysVal 107
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Db         33 GGAAAAGCATTCGTCAAAGAGAGCTTAAAATGCATCGCCAACGGGGTCACCTCCAAGGTC 92

Qy        108 PheLeuAlaIleArgArgCysSerThrPheGlnArgMetIleAlaGluValGlnGluGlu 127
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         93 TTCCTCGCCATTCGGAGGTGCTCCACTTTCCAAAGGATGATTGCTGAGGTGCAGGAAGAG 152

Qy        128 CysTyrSerLysLeuAsnValCysSerIleAlaLysArgAsnProGluAlaIleThrGlu 147
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        153 TGCTACAGCAAGCTGAATGTGTGCAGCATCGCCAAGCGGAACCCTGAAGCCATCACTGAG 212

Qy        148 ValValGlnLeuProAsnHisPheSerAsnArgTyrTyrAsnArgLeuValArgSerLeu 167
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        213 GTCGTCCAGCTGCCCAATCACTTCTCCAACAGATACTATAACAGACTTGTCCGAAGCCTG 272

Qy        168 LeuGluCysAspGluAspThrValSerThrIleArgAspSerLeuMetGluLysIleGly 187
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        273 CTGGAATGTGATGAAGACACAGTCAGCACAATCAGAGACAGCCTGATGGAGAAAATTGGG 332

Qy        188 ProAsnMetAlaSerLeuPheHisIleLeuGlnThrAspHisCysAlaGlnThrHisPro 207
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Db        333 CCTAACATGGCCAGCCTCTTCCACATCCTGCAGACAGACCACTGTGCCCAAACACACCCA 392

Qy        208 ArgAlaAspPheAsnArgArgArgThrAsnGluProGlnLysLeuLysValLeuLeuArg 227
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        393 CGAGCTGACTTCAACAGGAGACGCACCAATGAGCCGCAGAAGCTGAAAGTCCTCCTCAGG 452

Qy        228 AsnLeuArgGlyGluGluAspSerProSerHisIleLysArgThrSerHisGluSerAla 247
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        453 AACCTCCGAGGTGAGGAGGACTCTCCCTCCCACATCAAACGCACATCCCATGAGAGTGCA 512

RESULT 9
AF242179
LOCUS       AF242179               18216 bp    DNA     linear   PRI 21-FEB-2002
DEFINITION  Homo sapiens stanniocalcin 1 (STC1) gene, exons 1 through 4 and
            complete cds.
ACCESSION   AF242179
VERSION     AF242179.1  GI:18845002
KEYWORDS    .
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SOURCE      Homo sapiens.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 18216)
  AUTHORS   Jeffrey,K.J. and Reddel,R.R.
  TITLE     Characterization of the human stanniocalcin 1 gene
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 18216)
  AUTHORS   Jeffrey,K.J. and Reddel,R.R.
  TITLE     Direct Submission
  JOURNAL   Submitted (05-MAR-2000) Cancer Research Group, Children's Medical
            Research Institute, 214 Hawkesbury Road, Westmead, NSW 2145,
            Australia
FEATURES             Location/Qualifiers
     source          1. .18216
                     /organism="Homo sapiens"
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                     /chromosome="8"
                     /map="8p21-p11.2"
     gene            2003. .14892
                     /gene="STC1"
     mRNA            join(2003. .2408,4430. .4572,5283. .5494,11774. .14892)
                     /gene="STC1"
                     /product="stanniocalcin 1"
     exon            2003. .2408
                     /gene="STC1"
                     /number=1
     CDS             join(2291. .2408,4430. .4572,5283. .5494,11774. .12044)
                     /gene="STC1"
                     /codon_start=1
                     /product="stanniocalcin 1"
                     /protein_id="AAL79522.1"
                     /db_xref="GI:18845003"
                     /translation="MLQNSAVLLVLVISASATHEAEQNDSVSPRKSRVAAQNSAEVVR
                     CLNSALQVGCGAFACLENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANG
                     VTSKVFLAIRRCSTFQRMIAEVQEECYSKLNVCSIAKRNPEAITEVVQLPNHFSNRYY
                     NRLVRSLLECDEDTVSTIRDSLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRRTNE
                     PQKLKVLLRNLRGEEDSPSHIKRTSHESA"
     exon            4430. .4572
                     /gene="STC1"
                     /number=2
     exon            5283. .5494
                     /gene="STC1"
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     exon            11774. .14892
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                     /number=4
BASE COUNT     5230 a   4224 c   3566 g   5196 t
ORIGIN

Alignment Scores:
Pred. No.:              3.63e-92        Length:         18216
Score:                  90.00           Matches:        90
Percent Similarity:     100.00%         Conservative:   0
Best Local Similarity:  100.00%         Mismatches:     0
Query Match:            36.44%          Indels:         0
DB:                     9               Gaps:           0

US-09-705-500A-3 (1-247) x AF242179 (1-18216)

Qy        158 ArgTyrTyrAsnArgLeuValArgSerLeuLeuGluCysAspGluAspThrValSerThr 177
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Db      11772 AGATACTATAACAGACTTGTCCGAAGCCTGCTGGAATGTGATGAAGACACAGTCAGCACA 11831

Qy        178 IleArgAspSerLeuMetGluLysIleGlyProAsnMetAlaSerLeuPheHisIleLeu 197
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Db      11832 ATCAGAGACAGCCTGATGGAGAAAATTGGGCCTAACATGGCCAGCCTCTTCCACATCCTG 11891

Qy        198 GlnThrAspHisCysAlaGlnThrHisProArgAlaAspPheAsnArgArgArgThrAsn 217
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Db      11892 CAGACAGACCACTGTGCCCAAACACACCCACGAGCTGACTTCAACAGGAGACGCACCAAT 11951

Qy        218 GluProGlnLysLeuLysValLeuLeuArgAsnLeuArgGlyGluGluAspSerProSer 237
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Db      11952 GAGCCGCAGAAGCTGAAAGTCCTCCTCAGGAACCTCCGAGGTGAGGAGGACTCTCCCTCC 12011

Qy        238 HisIleLysArgThrSerHisGluSerAla 247
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Db      12012 CACATCAAACGCACATCCCATGAGAGTGCA 12041

RESULT 10
AC012119
LOCUS       AC012119              154898 bp    DNA     linear   PRI 27-MAR-2002
DEFINITION  Homo sapiens chromosome 15, clone RP11-175E9, complete sequence.
ACCESSION   AC012119
VERSION     AC012119.7  GI:19745088
KEYWORDS    HTG.
SOURCE      Homo sapiens.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 154898)
  AUTHORS   Birren,B., Linton,L., Nusbaum,C. and Lander,E.
  TITLE     Homo sapiens chromosome 15, clone RP11-175E9
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 154898)
  AUTHORS   Birren,B., Linton,L., Nusbaum,C., Lander,E., Allen,N., Anderson,M.,
            Baldwin,J., Barna,N., Beckerly,R., Boguslavkiy,L., Boukhgalter,B.,
            Brown,A., Castle,A., Colangelo,M., Collins,S., Collymore,A.,
            Cooke,P., DeArellano,K., Dewar,K., Domino,M., Donelan,L., Doyle,M.,
            Ferreira,P., FitzHugh,W., Forrest,C., Funke,R., Gage,D.,
            Galagan,J., Gardyna,S., Grant,G., Hagos,B., Heaford,A., Horton,L.,
            Howland,J.C., Johnson,R., Jones,C., Kann,L., Karatas,A., Klein,J.,
            Lehoczky,J., Lieu,C., Locke,K., Macdonald,P., Marquis,N.,
            McEwan,P., McGurk,A., McKernan,K., McLaughlin,J., Meldrim,J.,
            Morrow,J., Naylor,J., Norman,C.H., O'Connor,T., O'Donnell,P.,
            Peterson,K., Pollara,V., Riley,R., Roy,A., Santos,R., Severy,P.,
            Stange-Thomann,N., Stojanovic,N., Subramanian,A., Talamas,J.,
            Tesfaye,S., Tirrell,A., Vassiliev,H., Vo,A., Wheeler,J., Wu,X.,
            Wyman,D., Ye,W.J., Zimmer,A. and Zody,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (20-OCT-1999) Whitehead Institute/MIT Center for Genome
            Research, 320 Charles Street, Cambridge, MA 02141, USA
REFERENCE   3  (bases 1 to 154898)
  AUTHORS   Birren,B., Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N.,
            Anderson,S., Barna,N., Bastien,V., Boguslavkiy,L., Boukhgalter,B.,
            Brown,A., Camarata,J., Campopiano,A., Chang,J., Chazaro,B.,
            Choepel,Y., Colangelo,M., Collins,S., Collymore,A., Cook,A.,
            Cooke,P., DeArellano,K., Dewar,K., Diaz,J.S., Dodge,S., Faro,S.,
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            Ginde,S., Gord,S., Goyette,M., Graham,L., Grand-Pierre,N.,
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            Lamazares,R., Landers,T., Lehoczky,J., Levine,R., Liu,G.,
            MacLean,C., Macdonald,P., Major,J., Marquis,N., Matthews,C.,
            McCarthy,M., McEwan,P., McKernan,K., McPheeters,R., Meldrim,J.,
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            Norbu,C., Norman,C.H., O'Connor,T., O'Donnell,P., O'Neil,D.,
            Oliver,J., Peterson,K., Phunkhang,P., Pierre,N., Pollara,V.,
            Raymond,C., Retta,R., Rieback,M., Riley,R., Rise,C., Rogov,P.,
            Roman,J., Rosetti,M., Roy,A., Santos,R., Schauer,S., Schupback,R.,
            Seaman,S., Severy,P., Spencer,B., Stange-Thomann,N., Stojanovic,N.,
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            Topham,K., Travers,M., Travis,N., Trigilio,J., Vassiliev,H.,
            Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G.,
            Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (27-MAR-2002) Whitehead Institute/MIT Center for Genome
            Research, 320 Charles Street, Cambridge, MA 02141, USA
COMMENT     On Mar 27, 2002 this sequence version replaced gi:16041438.
            All repeats were identified using RepeatMasker:
            Smit, A.F.A. & Green, P. (1996-1997)
            http://ftp.genome.washington.edu/RM/RepeatMasker.html
            -------------- Genome Center
                Center: Whitehead Institute/ MIT Center for Genome Research
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            Center code: WIBR
            Web site: http://www-seq.wi.mit.edu
            Contact: sequence_submissions@genome.wi.mit.edu
          ------------- Project Information
            Center project name: L2190
            Center clone name: 175_E_9
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FEATURES             Location/Qualifiers
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                     /db_xref="taxon:9606"
                     /chromosome="15"
                     /map="15"
                     /clone="RP11-175E9"
                     /clone_lib="RPCI-11 Human Male BAC"
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     repeat_region   470. .526
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                     /rpt_family="(TTTTTG)n"
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                     /rpt_family="MIR3"
     repeat_region   complement(2064. .2205)
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     repeat_region   2738. .2895
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     repeat_region   complement(2999. .3591)
                     /rpt_family="L2"
     repeat_region   3708. .4365
                     /rpt_family="L1PA13"
     repeat_region   4406. .4434
                     /rpt_family="AT_rich"
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                     /rpt_family="AT_rich"
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     repeat_region   8133. .8319
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     repeat_region   11250. .11388
                     /rpt_family="(TA)n"
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     repeat_region   complement(12927. .13063)
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     repeat_region   13331. .13402
                     /rpt_family="L2"
     repeat_region   complement(13751. .14062)
                     /rpt_family="L2"
     repeat_region   14737. .14839
                     /rpt_family="Ricksha"
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                     /rpt_family="Ricksha"
     repeat_region   complement(16610. .17033)
                     /rpt_family="MLT2D"
     repeat_region   17153. .17437
                     /rpt_family="AluSx"
     repeat_region   17446. .17472
                     /rpt_family="(GAAA)n"
     repeat_region   18421. .18845
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                     /note="probably C; possibly CC"
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     repeat_region   20519. .20736
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                     /rpt_family="AT_rich"
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     repeat_region   25976. .26045
                     /rpt_family="L1MC/D"
     repeat_region   26046. .26369
                     /rpt_family="AluY"
     repeat_region   26370. .26767
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                     /rpt_family="AluSx"
     unsure          27050. .27054
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     unsure          27098. .27102
                     /note="<30 qual SNGL region"
     repeat_region   27821. .28040
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     repeat_region   28046. .28360
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                     /rpt_family="L1ME1"
     repeat_region   complement(28916. .29093)
                     /rpt_family="AluSx"

Alignment Scores:
Pred. No.:              3.32e-91        Length:         154898
Score:                  90.00           Matches:        90
Percent Similarity:     100.00%         Conservative:   0
Best Local Similarity:  100.00%         Mismatches:     0
Query Match:            36.44%          Indels:         0
DB:                     9               Gaps:           0
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US-09-705-500A-3 (1-247) x AC012119 (1-154898)

Qy        158 ArgTyrTyrAsnArgLeuValArgSerLeuLeuGluCysAspGluAspThrValSerThr 177
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Db      54210 AGATACTATAACAGACTTGTCCGAAGCCTGCTGGAATGTGATGAAGACACAGTCAGCACA 54269

Qy        178 IleArgAspSerLeuMetGluLysIleGlyProAsnMetAlaSerLeuPheHisIleLeu 197
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      54270 ATCAGAGACAGCCTGATGGAGAAAATTGGGCCTAACATGGCCAGCCTCTTCCACATCCTG 54329

Qy        198 GlnThrAspHisCysAlaGlnThrHisProArgAlaAspPheAsnArgArgArgThrAsn 217
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Db      54330 CAGACAGACCACTGTGCCCAAACACACCCACGAGCTGACTTCAACAGGAGACGCACCAAT 54389

Qy        218 GluProGlnLysLeuLysValLeuLeuArgAsnLeuArgGlyGluGluAspSerProSer 237
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Db      54390 GAGCCGCAGAAGCTGAAAGTCCTCCTCAGGAACCTCCGAGGTGAGGAGGACTCTCCCTCC 54449

Qy        238 HisIleLysArgThrSerHisGluSerAla 247
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Db      54450 CACATCAAACGCACATCCCATGAGAGTGCA 54479

RESULT 11
AF257506
LOCUS       AF257506                834 bp    mRNA    linear   MAM 09-MAY-2000
DEFINITION  Bos taurus stanniocalcin mRNA, complete cds.
ACCESSION   AF257506
VERSION     AF257506.1  GI:7739750
KEYWORDS    .
SOURCE      Bos taurus.
  ORGANISM  Bos taurus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
            Bovidae; Bovinae; Bos.
REFERENCE   1  (bases 1 to 834)
  AUTHORS   DiMattia,G.E.
  TITLE     bovine stanniocalcin cDNA sequence
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 834)
  AUTHORS   DiMattia,G.E.
  TITLE     Direct Submission
  JOURNAL   Submitted (18-APR-2000) Oncology, London Regional Cancer centre,
            790 Commissioners Rd., London, ON N6A 4L6, Canada
FEATURES             Location/Qualifiers
     source          1. .834
                     /organism="Bos taurus"
                     /db_xref="taxon:9913"
                     /tissue_type="ovary"
     CDS             1. .744
                     /codon_start=1
                     /product="stanniocalcin"
                     /protein_id="AAF68996.1"
                     /db_xref="GI:7739751"
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                     CLNSALQVGCGAFACLENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANG
                     VTSKVFLAIRRCSTFQRMIAEVQEECYTKLNVCSVAKRNPEAITEVVQLPNHFSNRYY
                     NRLVRSLLDCDEDTVSTIRDSLMEKIGPNMASLFHILQTDHCAHTQQRADFNRRRANE
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     3'UTR           745. .834
BASE COUNT      218 a    227 c    215 g    174 t
ORIGIN

Alignment Scores:
Pred. No.:              6.03e-89        Length:         834
Score:                  86.00           Matches:        86
Percent Similarity:     100.00%         Conservative:   0
Best Local Similarity:  100.00%         Mismatches:     0
Query Match:            34.82%          Indels:         0
DB:                     4               Gaps:           0

US-09-705-500A-3 (1-247) x AF257506 (1-834)

Qy         44 ArgCysLeuAsnSerAlaLeuGlnValGlyCysGlyAlaPheAlaCysLeuGluAsnSer 63
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Db        130 CGCTGCCTCAACAGCGCGCTGCAGGTTGGCTGTGGAGCTTTTGCATGCCTGGAGAACTCC 189

Qy         64 ThrCysAspThrAspGlyMetTyrAspIleCysLysSerPheLeuTyrSerAlaAlaLys 83
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Db        190 ACCTGTGACACAGATGGGATGTACGACATCTGTAAATCCTTCTTGTACAGCGCTGCTAAA 249

Qy         84 PheAspThrGlnGlyLysAlaPheValLysGluSerLeuLysCysIleAlaAsnGlyVal 103
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Db        250 TTTGACACTCAGGGAAAAGCATTTGTCAAAGAGAGCTTAAAGTGCATCGCCAACGGGGTC 309

Qy        104 ThrSerLysValPheLeuAlaIleArgArgCysSerThrPheGlnArgMetIleAlaGlu 123
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Db        310 ACCTCCAAGGTCTTCCTGGCCATTCGGAGGTGCTCTACTTTTCAGAGGATGATTGCCGAA 369

Qy        124 ValGlnGluGluCysTyr 129
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Db        370 GTCCAGGAGGAGTGCTAC 387

RESULT 12
RNU62667
LOCUS       RNU62667                1004 bp    mRNA    linear   ROD 02-JAN-1997
DEFINITION  Rattus norvegicus stanniocalcin (rSTC) mRNA, complete cds.
ACCESSION   U62667
VERSION     U62667.1  GI:1762530
KEYWORDS    .
SOURCE      Rattus norvegicus.
  ORGANISM  Rattus norvegicus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
            Rattus.
REFERENCE   1  (bases 1 to 1004)
  AUTHORS   Abe,T., Tanemoto,M., Hall,A.E., Brown,E.M. and Hebert,S.C.
  TITLE     Molecular cloning and characterization of rat stanniocalcin peptide
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 1004)
  AUTHORS   Abe,T., Tanemoto,M., Hall,A.E., Brown,E.M. and Hebert,S.C.
  TITLE     Direct Submission
  JOURNAL   Submitted (01-JUL-1996) Renal Division, Brigham and Women's
            Hospital, 75 Francis Street, Boston, MA 02115, USA
FEATURES             Location/Qualifiers
     source          1. .1004
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                     /strain="Sprague-Dawley"
                     /db_xref="taxon:10116"
                     /tissue_type="kidney"
     gene            1. .1004
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     CDS             110. .853
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                     ITSKVFLAIRRCSTFQRMIAEVQEDCYSKLNVCSIAKRNPEAITEVIQLPNHFSNRYY
                     NRLVRSLLECDEDTVSTIRDSLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRRTNE
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BASE COUNT      288 a    253 c    241 g    222 t
ORIGIN

Alignment Scores:
Pred. No.:              1.47e-86        Length:         1004
Score:                  84.00           Matches:        211
Percent Similarity:     97.24%          Conservative:   0
Best Local Similarity:  97.24%          Mismatches:     3
Query Match:            34.01%          Indels:         6
DB:                     10              Gaps:           0

US-09-705-500A-3 (1-247) x RNU62667 (1-1004)

Qy         19 HisGluAlaGluGlnAsnAspSerValSerProArgLysSerArgValAlaAlaGlnAsn 38
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Qy         39 SerAlaGluValValArgCysLeuAsnSerAlaLeuGlnValGlyCysGlyAlaPheAla 58
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Db        224 TCAGCTGAAGTGGTCCGCTGCCTCAACAGTGCCCTACAGGTTGGCTGTGGGGCTTTTGCA 283

Qy         59 CysLeuGluAsnSerThrCysAspThrAspGlyMetTyrAspIleCysLysSerPheLeu 78
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Db        284 TGCCTGGAAAACTCCACATGTGACACAGATGGGATGTACGACATTTGTAAATCCTTCTTG 343

Qy         79 TyrSerAlaAlaLysPheAspThrGlnGlyLysAlaPheValLysGluSerLeuLysCys 98
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Db        344 TACAGTGCTGCTAAATTTGACACTCAGGGAAAAGCATTTGTCAAAGAGAGCTTAAAGTGC 403

Qy         99 IleAlaAsn-GlyValThrSerLysValPheLeuAlaIleArgArgCysSerThrPheGl 118
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Db        404 ATCGCCAATGGGATC-ACCTCCAAGGTCTTCCTTGCCATTCGGAGGTGTTCTACTTTCCA 462

Qy        118 nArgMetIleAlaGluValGlnGluGlu-CysTyrSerLysLeuAsnValCysSerIleA 138
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Db        463 GAGGATGATCGCCGAGGTGCAGGAGGA-CTGCTACAGCAAGCTCAATGTTTGCAGCATTG 521

Qy        138 laLysArgAsnProGluAlaIleThrGluValVal-GlnLeuProAsnHisPheSerAsn 157
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Db        522 CCAAGCGCAACCCGGAAGCCATCACTGAAGTCAT-ACAGCTGCCCAATCACTTCTCCAAC 580

Qy        158 ArgTyrTyrAsnArgLeuValArgSerLeuLeuGluCysAspGluAspThrValSerThr 177
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Db        581 AGATACTACAACAGACTTGTCCGAAGCCTTCTGGAATGTGATGAAGATACGGTCAGCACA 640

Qy        178 IleArgAspSerLeuMetGluLysIleGlyProAsnMetAlaSerLeuPheHisIleLeu 197
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Db        641 ATCAGAGACAGCCTGATGGAGAAGATCGGGCCCAACATGGCCAGCCTCTTCCATATCCTG 700

Qy        198 GlnThrAspHisCysAlaGlnThrHisProArgAlaAspPheAsnArgArgArgThrAsn 217
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Db        701 CAGACAGACCACTGTGCCCAGACACATCCCAGAGCTGACTTCAATAGGAGGCGCACAAAT 760

Qy        218 GluProGlnLysLeuLysValLeuLeuArgAsnLeuArgGlyGlu 232
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Db        761 GAGCCACAGAAGCTGAAAGTCCTCCTCAGGAACCTCCGAGGTGAG 805

RESULT 13
MMU47815
LOCUS       MMU47815                1232 bp    DNA     linear   ROD 03-FEB-1998
DEFINITION  Mus musculus stanniocalcin gene, complete cds.
ACCESSION   U47815
VERSION     U47815.1  GI:2828524
KEYWORDS    .
SOURCE      house mouse strain=BALB/c.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 1232)
  AUTHORS   Chang,A.C., Dunham,M.A., Jeffrey,K.J. and Reddel,R.R.
  TITLE     Molecular cloning and characterization of mouse stanniocalcin cDNA
  JOURNAL   Mol. Cell. Endocrinol. 124 (1-2), 185-187 (1996)
  MEDLINE   97179050
   PUBMED   9027337
REFERENCE   2  (bases 1 to 1232)
  AUTHORS   Chang,A.C.M. and Reddel,R.R.
  TITLE     Direct Submission
  JOURNAL   Submitted (30-JAN-1996) Andy C.M. Chang, Cancer Research Group,
            Children's Medical Research Institute, 214 Hawkesbury Road,
            Westmead, Sydney, NSW 2145, Australia
FEATURES             Location/Qualifiers
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                     /protein_id="AAC00050.1"
                     /db_xref="GI:2828525"
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                     NRLVRSLLECDEDTVSTIRDSLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRRTNE
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BASE COUNT      356 a    338 c    274 g    264 t
ORIGIN

Alignment Scores:
Pred. No.:                1.81e-86        Length:          1232
Score:                    84.00           Matches:         211
Percent Similarity:       97.24%          Conservative:    0
Best Local Similarity:    97.24%          Mismatches:      3
Query Match:              34.01%          Indels:          6
DB:                       10              Gaps:            0

US-09-705-500A-3 (1-247) x MMU47815 (1-1232)

Qy         19 HisGluAlaGluGlnAsnAspSerValSerProArgLysSerArgValAlaAlaGlnAsn 38
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        282 CACGAGGCGGAACAAAATGATTCTGTGAGCCCCAGAAAATCCCGGGTGGCGGCTCAAAAT 341

Qy         39 SerAlaGluValValArgCysLeuAsnSerAlaLeuGlnValGlyCysGlyAlaPheAla 58
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        342 TCAGCTGAAGTGGTTCGCTGCCTCAACAGTGCCCTGCAGGTTGGCTGCGGGGCTTTTGCA 401

Qy         59 CysLeuGluAsnSerThrCysAspThrAspGlyMetTyrAspIleCysLysSerPheLeu 78
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        402 TGCCTGGAAAACTCCACATGTGACACAGATGGGATGTACGACATTTGTAAATCCTTCTTG 461

Qy         79 TyrSerAlaAlaLysPheAspThrGlnGlyLysAlaPheValLysGluSerLeuLysCys 98
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        462 TACAGTGCTGCTAAATTTGACACTCAGGGAAAAGCATTTGTCAAAGAGAGCTTAAAGTGC 521

Qy         99 IleAlaAsn-GlyValThrSerLysValPheLeuAlaIleArgArgCysSerThrPheGl 118
                  |||||||| |||   ||||||||||||||||||||||||||||||||||||||||||||||||
Db        522 ATCGCCAATGGGATC-ACCTCCAAGGTGTTCCTTGCCATTCGGAGGTGTTCGACTTTCCA 580

Qy        118 nArgMetIleAlaGluValGlnGluGlu-CysTyrSerLysLeuAsnValCysSerIleA 138
                  |||||||||||||||||||||||    ||||||||||||||||||||||||||||||||
Db        581 GAGGATGATCGCCGAGGTGCAGGAGGA-CTGCTACAGCAAGCTTAACGTTTGCAGCATCG 639

Qy        138 laLysArgAsnProGluAlaIleThrGluValVal-GlnLeuProAsnHisPheSerAsn 157
                  |||||||||||||||||||||||||||||    ||||||||||||||||||||||||
Db        640 CCAAGCGCAACCCGGAAGCCATCACTGAAGTCAT-ACAGCTGCCCAATCACTTCTCCAAC 698

Qy        158 ArgTyrTyrAsnArgLeuValArgSerLeuLeuGluCysAspGluAspThrValSerThr 177
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        699 AGATACTACAACAGACTTGTCCGAAGCCTTCTGGAATGTGATGAAGACACGGTCAGTACA 758

Qy        178 IleArgAspSerLeuMetGluLysIleGlyProAsnMetAlaSerLeuPheHisIleLeu 197
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        759 ATCAGAGACAGCCTGATGGAGAAGATCGGGCCCAACATGGCCAGCCTCTTCCACATCCTG 818

Qy        198 GlnThrAspHisCysAlaGlnThrHisProArgAlaAspPheAsnArgArgArgThrAsn 217
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        819 CAGACAGACCACTGTGCCCAGACACACCCCAGAGCTGACTTCAATAGGAGGCGCACAAAT 878

Qy        218 GluProGlnLysLeuLysValLeuLeuArgAsnLeuArgGlyGlu 232
                  ||||||||||||||||||||||||||||||||||||||||||||
Db        879 GAGCCACAGAAGCTGAAAGTCCTCCTCAGGAACCTCCGAGGTGAG 923

RESULT 14
BC021425
LOCUS       BC021425                2341 bp    mRNA    linear   ROD 07-AUG-2002
DEFINITION  Mus musculus, stanniocalcin, clone MGC:29066 IMAGE:5010981, mRNA,
            complete cds.
ACCESSION   BC021425
VERSION     BC021425.1  GI:18203894
KEYWORDS    MGC.
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SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 2341)
  AUTHORS   Strausberg,R.
  TITLE     Direct Submission
  JOURNAL   Submitted (14-JAN-2002) National Institutes of Health, Mammalian
            Gene Collection (MGC), Cancer Genomics Office, National Cancer
            Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
            USA
  REMARK    NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT     Contact: MGC help desk
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Gilbert Smith, Ph.D.
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: National Institutes of Health Intramural
            Sequencing Center (NISC),
            Gaithersburg, Maryland;
            Web site: http://www.nisc.nih.gov/
            Contact: nisc_mgc@nhgri.nih.gov
            Akhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
            Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,
            Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P.,
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            McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W.,
            Tsurgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L.,
            Young,A., Zhang,L.-H. and Green,E.D.

            Clone distribution: MGC clone distribution information can be found
            through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
            Series: IRAK Plate: 39 Row: f Column: 22.
FEATURES              Location/Qualifiers
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                      old mouse. Taken by biopsy."
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     CDS              123. .866
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BASE COUNT      694 a    559 c    478 g    610 t
ORIGIN

Alignment Scores:
Pred. No.:              3.51e-86        Length:         2341
Score:                  84.00           Matches:        211
Percent Similarity:     97.24%          Conservative:   0
Best Local Similarity:  97.24%          Mismatches:     3
Query Match:            34.01%          Indels:         6
DB:                     10              Gaps:           0

US-09-705-500A-3 (1-247) x BC021425 (1-2341)

Qy         19 HisGluAlaGluGlnAsnAspSerValSerProArgLysSerArgValAlaAlaGlnAsn 38
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Db        177 CACGAGGCGGAACAAAATGATTCTGTGAGCCCCAGAAAATCCCGGGTGGCGGCTCAAAAT 236

Qy         39 SerAlaGluValValArgCysLeuAsnSerAlaLeuGlnValGlyCysGlyAlaPheAla 58
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        237 TCAGCTGAAGTGGTTCGCTGCCTCAACAGTGCCCTGCAGGTTGGCTGCGGGGCTTTTGCA 296

Qy         59 CysLeuGluAsnSerThrCysAspThrAspGlyMetTyrAspIleCysLysSerPheLeu 78
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Db        297 TGCCTGGAAAACTCCACATGTGACACAGATGGGATGTACGACATTTGTAAATCCTTCTTG 356

Qy         79 TyrSerAlaAlaLysPheAspThrGlnGlyLysAlaPheValLysGluSerLeuLysCys 98
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Qy         99 IleAlaAsn-GlyValThrSerLysValPheLeuAlaIleArgArgCysSerThrPheGl 118
              |||||||| ||| |||||||||||||||||||||||||||||||||||||||||||||||
Db        417 ATCGCCAATGGGATC-ACCTCCAAGGTATTCCTTGCCATTCGGAGGTGTTCGACTTTCCA 475

Qy        118 nArgMetIleAlaGluValGlnGluGlu-CysTyrSerLysLeuAsnValCysSerIleA 138
              |||||||||||||||||||||||||    ||||||||||||||||||||||||||||||
Db        476 GAGGATGATCGCCGAGGTGCAGGAGGA-CTGCTACAGCAAGCTTAACGTTTGCAGCATCG 534

Qy        138 laLysArgAsnProGluAlaIleThrGluValVal-GlnLeuProAsnHisPheSerAsn 157
              |||||||||||||||||||||||||||||||    |||||||||||||||||||||||
Db        535 CCAAGCGCAACCCGGAAGCCATCACTGAAGTCAT-ACAGCTGCCCAATCACTTCTCCAAC 593

Qy        158 ArgTyrTyrAsnArgLeuValArgSerLeuLeuGluCysAspGluAspThrValSerThr 177
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Qy        178 IleArgAspSerLeuMetGluLysIleGlyProAsnMetAlaSerLeuPheHisIleLeu 197
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Qy        198 GlnThrAspHisCysAlaGlnThrHisProArgAlaAspPheAsnArgArgArgThrAsn 217
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Db        714 CAGACAGACCACTGTGCCCAGACACACCCCAGAGCTGACTTCAATAGGAGGCGCACAAAT 773

Qy        218 GluProGlnLysLeuLysValLeuLeuArgAsnLeuArgGlyGlu 232
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Db        774 GAGCCACAGAAGCTGAAAGTCCTCCTCAGGAACCTCCGAGGTGAG 818

RESULT 15
AF099098
LOCUS       AF099098               4183 bp    mRNA    linear   ROD 10-NOV-1998
DEFINITION  Mus musculus stanniocalcin precursor, mRNA, complete cds.
ACCESSION   AF099098
VERSION     AF099098.1  GI:3851659
KEYWORDS    .
SOURCE      Mus musculus.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 4183)
  AUTHORS   Varghese,R., Wong,C.K.C., Doel,H., Wagner,G.F. and DiMattia,G.E.
  TITLE     Comparative Analysis of Mammalian Stanniocalcin Genes
  JOURNAL   Endocrinology 139, 4717-4725 (1998)
REFERENCE   2  (bases 1 to 4183)
  AUTHORS   DiMattia,G.E., Varghese,R. and Wagner,G.F.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-OCT-1998) Oncology, London Regional Cancer Centre,
            790 Commissioners Rd., London, ONT N6C 4L6, Canada
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3'UTR 898. .4183
BASE COUNT 1215 a 979 c 798 g 1191 t
ORIGIN

Alignment Scores:

Pred. No.:	6.4e-86	Length:	4183
Score:	84.00	Matches:	210
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Best Local Similarity:	96.33%	Mismatches:	4
Query Match:	34.01%	Indels:	8
DB:	10	Gaps:	0

US-09-705-500A-3 (1-247) x AF099098 (1-4183)

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Qy         19 HisGluAlaGluGlnAsnAspSerValSerProArgLysSerArgValAlaAlaGlnAsn 38
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Db        208 CACGAGGCGGAACAAAATGATTCTGTGAGCCCCAGAAAATCCCGGGTGGCGGCTCAAAAT 267

Qy         39 SerAlaGluValValArgCysLeuAsnSerAlaLeuGlnValGlyCysGlyAlaPheAla 58
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        268 TCAGCTGAAGTGGTTCGCTGCCTCAACAGTGCCCTGCAGGTTGGCTGCGGGGCTTTTGCA 327

Qy         59 CysLeuGluAsnSerThrCysAspThrAspGlyMetTyrAspIleCysLysSerPheLeu 78
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        328 TGCCTGGAAAACTCCACATGTGACACAGATGGGATGTACGACATTTGTAAATCCTTCTTG 387

Qy         79 TyrSerAlaAlaLysPheAspThrGlnGlyLysAlaPheValLysGluSerLeuLysCys 98
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        388 TACAGTGCTGCTAAATTTGACACTCAGGGAAAAGCATTTGTCAAAGAGAGCTTAAAGTGC 447

Qy         99 IleAlaAsn-GlyValThrSerLysValPheLeuAlaIleArgArgCysSerThrPheGl 118
              ||||||||| |||   ||||||||||||||||||||||||||||||||||||||||||||
Db        448 ATCGCCAATGGGATC-ACCTCCAAGGTATTCCTTGCCATTCGGAGGTGTTCGACTTTCCA 506

Qy        118 nArgMetIleAlaGluValGlnGluGlu-CysTyrSerLysLeuAsnValCysSerIleA 138
              |||||||||||||||||||||||    ||||||||||||||||||||||||||||||||
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Qy        138 laLysArgAsnProGluAlaIleThrGluValVal-GlnLeu-ProAsnHisPheSerAs 157
              |||||||||||||||||||||||||||||||    |||    ||||||||||||||||
Db        566 CCAAGCGCAACCCGGAAGCCATCACTGAAGTCAT-ACAGCA-GCCCAATCACTTCTCCAA 623

Qy        157 nArgTyrTyrAsnArgLeuValArgSerLeuLeuGluCysAspGluAspThrValSerTh 177
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Db        624 CAGATACTACAACAGACTTGTCCGAAGCCTTCTGGAATGTGATGAAGACACGGTCAGCAC 683

Qy        177 rIleArgAspSerLeuMetGluLysIleGlyProAsnMetAlaSerLeuPheHisIleLe 197
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        684 AATCAGAGACAGCCTGATGGAGAAGATCGGGCCCAACATGGCCAGCCTCTTCCACATCCT 743

Qy        197 uGlnThrAspHisCysAlaGlnThrHisProArgAlaAspPheAsnArgArgArgThrAs 217
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        744 GCAGACAGACCACTGTGCCCAGACACACCCCAGAGCTGACTTCAATAGGAGGCGTACAAA 803

Qy        217 nGluProGlnLysLeuLysValLeuLeuArgAsnLeuArgGlyGlu 232
              |||||||||||||||||||||||||||||||||||||||||||||
Db        804 TGAGCCACAGAAGCTGAAAGTCCTCCTCAGGAACCTCCGAGGTGAG 849
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Search completed: June 12, 2003, 22:44:17
Job time : 2093 secs

GenCore version 5.1.6

OM protein - nucleic search, using frame_plus_p2n model

Run on: June 12, 2003, 21:14:10 ; Search time 223 Seconds
(without alignments)
2494.366 Million cell updates/sec

Title: US-09-705-500A-3
Perfect score: 247
Sequence: 1 MLQNSAVLLVLVISASATHE.....NLRGEEDSPSHIKRTSHESA 247

Scoring table: OLIGO
Xgapop 60.0 , Xgapext 60.0
Ygapop 60.0 , Ygapext 60.0
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2185239 seqs, 1125999159 residues

Word size: 1

Total number of hits satisfying chosen parameters: 4368725

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Command line parameters:
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-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=oligo -TRANS=human40.cdi
-LIST=1000 -DOCALIGN=200 -THR_SCORE=quality -THR_MIN=1 -ALIGN=15 -MODE=LOCAL
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	247	100.0	741	21	AAA97594	Human stanniocalci
	2	247	100.0	741	21	AAA11145	Human stanniocalci
	3	247	100.0	744	24	ABL40225	Human staniocalcin
	4	247	100.0	771	16	AAT02438	cDNA encoding stan
	5	247	100.0	771	21	AAZ39520	Human corpuscles o
	6	247	100.0	1283	22	AAF83297	Human stanniocalci
	7	247	100.0	3762	22	AAF83823	DNA encoding Lng10
	8	184	74.5	2572	21	AAF16051	Human prostate can
	9	160	64.8	585	22	AAH55624	Human breast tumou
c	10	72	29.1	219	22	ABA51055	Human breast cell
c	11	72	29.1	219	22	ABA69045	Human foetal liver
c	12	72	29.1	219	22	ABA35989	Probe #14455 for g
c	13	72	29.1	219	22	AAK17358	Human brain expres
c	14	72	29.1	219	22	AAK43155	Human bone marrow
c	15	72	29.1	219	22	AAI23927	Probe #13860 for g
c	16	72	29.1	219	22	AAI49233	Probe #17919 used
c	17	72	29.1	219	22	AAI09526	Probe #9517 used t
c	18	72	29.1	219	24	ABS17231	Human genome-deriv
	19	66	26.7	198	17	AAT28165	Senescence-related
c	20	41	16.6	362	22	ABA45937	Human breast cell
c	21	41	16.6	362	22	ABA56464	Human foetal liver
c	22	41	16.6	362	22	ABA26097	Probe #4563 for ge
c	23	41	16.6	362	22	AAK04623	Human brain expres
c	24	41	16.6	362	22	AAK30134	Human bone marrow
c	25	41	16.6	362	22	AAI14733	Probe #4666 for ge
c	26	41	16.6	362	22	AAI36098	Probe #4784 used t
c	27	41	16.6	362	22	AAI04536	Probe #4527 used t
c	28	41	16.6	362	24	ABS04715	Human genome-deriv
	29	40	16.2	420	22	AAH55616	Human breast tumou
	30	12	4.9	2191	9	AAN80655	Sequence encoding
	31	9	3.6	436	24	ABN76096	Human RNA polymera
	32	9	3.6	1360	23	AAS59785	Propionibacterium
	33	9	3.6	4188	20	AAX55767	Drosophila Robo 1
	34	9	3.6	4188	20	AAX57250	Drosophila sp. ROB
	35	9	3.6	4355	23	ABL22881	Drosophila melanog
c	36	9	3.6	8410	23	ABL22880	Drosophila melanog
	37	9	3.6	11470	23	ABL21296	Drosophila melanog
	38	9	3.6	53178	23	AAS59543	Propionibacterium
	39	9	3.6	96583	21	AAF22297	BAC containing rep
	40	8	3.2	26	22	AAH22262	Stanniocalcin prec
	41	8	3.2	77	22	AAF73631	HGF nucleic acid l
	42	8	3.2	162	24	ABN70013	Streptococcus poly
	43	8	3.2	324	22	AAS06373	Streptococcus pyog
	44	8	3.2	416	23	AAD23428	Human lung tumour-
	45	8	3.2	433	22	ABA08525	Human neuropilin-2
	46	8	3.2	938	24	ABQ13648	Oligonucleotide fo
c	47	8	3.2	938	24	ABQ13649	Oligonucleotide fo
c	48	8	3.2	1000	22	AAS30815	Human cDNA encodin
c	49	8	3.2	3006	24	ABQ69272	Listeria innocua D
c	50	8	3.2	3024	24	ABQ67866	Listeria innocua D
	51	8	3.2	3153	20	AAX77530	Human secreted pro
	52	8	3.2	3153	21	AAZ59472	Human secreted pro
	53	8	3.2	3568	21	AAZ99491	DNA encoding a mai
	54	8	3.2	3776	21	AAZ58263	Corn cellulose syn
	55	8	3.2	6707	22	AAK52417	Human polynucleoti
	56	8	3.2	6848	22	AAK52418	Human polynucleoti
c	57	8	3.2	7479	23	ABL14528	Drosophila melanog
	58	8	3.2	7525	22	AAS01192	Fertilisation-inde
	59	8	3.2	7545	22	ABA09525	Human secreted pro
	60	8	3.2	7545	22	AAK53401	Human polynucleoti
	61	8	3.2	7545	22	AAK53402	Human polynucleoti
	62	8	3.2	8911	22	ABA06809	Human genomic DNA
	63	8	3.2	8911	22	AAS41748	Genomic sequence #
c	64	8	3.2	10302	24	ABK81961	cDNA encoding huma
c	65	8	3.2	10386	23	AAS76114	DNA encoding novel
c	66	8	3.2	14286	20	AAX13099	Enterococcus faeca
	67	8	3.2	32768	20	AAX13336	Enterococcus faeca

	68	8	3.2	44377	18	AAT78508	Platenolide syntha
	69	8	3.2	44377	18	AAT80414	Platenolide syntha
c	70	8	3.2	81905	24	ABQ69244	Listeria innocua D
c	71	8	3.2	82689	24	ABQ67198	Listeria innocua p
c	72	8	3.2	1830121	17	AAT42063	Haemophilus influe
c	73	7	2.8	27	15	AAQ65538	Partial PSM Ag cDN
	74	7	2.8	27	16	AAT02439	Primer for stannio
	75	7	2.8	27	21	AAZ39521	Human corpuscles o
	76	7	2.8	27	22	AAF83299	Corpuscles of Stan
	77	7	2.8	28	21	AAA64276	PCR primer used to
	78	7	2.8	28	24	ABL53606	PCR primer N.top f
	79	7	2.8	28	24	ABL53608	PCR primer SsssN.t
c	80	7	2.8	31	21	AAZ39522	Human corpuscles o
c	81	7	2.8	31	22	AAF83300	Corpuscles of Stan
	82	7	2.8	37	21	AAZ39523	Human corpuscles o
	83	7	2.8	37	21	AAZ39525	Human corpuscles o
	84	7	2.8	37	22	AAF83301	Human stanniocalci
	85	7	2.8	37	22	AAF83303	Corpuscles of Stan
c	86	7	2.8	65	24	ABN54586	Mouse spliced tran
c	87	7	2.8	100	17	AAT30875	Primer 5 for 95 kD
	88	7	2.8	106	22	ABA69942	Human foetal liver
	89	7	2.8	106	22	AAK18151	Human brain expres
	90	7	2.8	106	22	AAK44042	Human bone marrow
	91	7	2.8	106	22	AAI50052	Probe #18738 used
	92	7	2.8	106	24	ABS18275	Human genome-deriv
c	93	7	2.8	107	21	AAA35572	Microsatellite nuc
c	94	7	2.8	113	21	AAA35570	Microsatellite nuc
c	95	7	2.8	132	24	ABK94678	G protein-coupled
c	96	7	2.8	132	24	ABK94679	G protein-coupled
	97	7	2.8	144	21	AAA27619	Endoplasmic reticu
	98	7	2.8	154	19	AAV17073	Oligonucleotide 1
c	99	7	2.8	154	22	ABA73099	Human foetal liver
c	100	7	2.8	154	22	ABA38583	Probe #17049 for g
c	101	7	2.8	154	22	AAK21534	Human brain expres
c	102	7	2.8	154	22	AAK47696	Human bone marrow
c	103	7	2.8	154	22	AAI26015	Probe #15948 for g
c	104	7	2.8	154	22	AAI53528	Probe #22214 used
c	105	7	2.8	154	24	ABS21739	Human genome-deriv
c	106	7	2.8	167	24	ABN23702	Human ORFX polynuc
	107	7	2.8	174	20	AAV90459	EST clone DT446.
c	108	7	2.8	182	23	AAS50413	Staphylococcus aur
c	109	7	2.8	182	23	AAS50778	Staphylococcus aur
	110	7	2.8	186	14	AAQ48582	Rice cDNA homologo
	111	7	2.8	186	22	AAF27529	Scorpion neurotoxi
c	112	7	2.8	201	24	ABK94675	G protein-coupled
c	113	7	2.8	201	24	ABK94676	G protein-coupled
	114	7	2.8	249	24	ABQ67279	Listeria innocua D
c	115	7	2.8	262	21	AAC09687	Human secreted pro
c	116	7	2.8	263	21	AAC24079	Human secreted pro
	117	7	2.8	277	24	ABL85600	Human ovarian canc
c	118	7	2.8	293	24	ABL84013	Human ovarian canc
c	119	7	2.8	294	24	ABK80208	Bacillus clausii g
c	120	7	2.8	297	24	ABQ67356	Listeria innocua D
c	121	7	2.8	300	20	AAZ14105	Human gene express
	122	7	2.8	339	21	AAA87248	Rat hepatocyte car
c	123	7	2.8	342	21	AAC74638	Human ORFX ORF193
c	124	7	2.8	342	24	ABN17088	Human ORFX polynuc
	125	7	2.8	344	22	ABA17907	Human nervous syst
	126	7	2.8	345	23	AAS55467	Streptococcus pneu
c	127	7	2.8	347	22	AAK72458	Human immune/haema
c	128	7	2.8	347	22	AAK72459	Human immune/haema
c	129	7	2.8	347	22	AAK72460	Human immune/haema
	130	7	2.8	347	24	ABN20125	Human ORFX polynuc
c	131	7	2.8	350	22	AAK58317	Human immune/haema
c	132	7	2.8	357	24	ABK94681	G protein-coupled
c	133	7	2.8	357	24	ABK94682	G protein-coupled
	134	7	2.8	359	22	AAK84437	Human immune/haema
c	135	7	2.8	361	19	AAV59571	Human secreted pro
c	136	7	2.8	378	22	AAK71926	Human immune/haema
	137	7	2.8	381	22	AAH66492	C glutamicum codin
	138	7	2.8	385	22	AAI83993	Human polynucleoti
	139	7	2.8	396	23	ABV13298	Human prostate exp
c	140	7	2.8	402	23	ABV07882	Human prostate exp
c	141	7	2.8	403	22	ABA44980	Human breast cell
c	142	7	2.8	403	22	ABA55456	Human foetal liver
c	143	7	2.8	403	22	ABA25174	Probe #3640 for ge
c	144	7	2.8	403	22	AAK03695	Human brain expres
c	145	7	2.8	403	22	AAK29155	Human bone marrow
c	146	7	2.8	403	22	AAI13743	Probe #3676 for ge
c	147	7	2.8	403	22	AAI35103	Probe #3789 used t
c	148	7	2.8	403	22	AAI03624	Probe #3615 used t
c	149	7	2.8	403	24	ABS03704	Human genome-deriv
	150	7	2.8	405	22	AAH31730	Human olfactory re
	151	7	2.8	408	22	AAI89693	Human polynucleoti
	152	7	2.8	413	24	ABL78655	Human ovarian canc
c	153	7	2.8	427	23	ABV13814	Human prostate exp
	154	7	2.8	428	23	ABV34416	Human prostate exp
	155	7	2.8	428	24	ABN15922	Human ORFX polynuc
c	156	7	2.8	430	21	AAA35315	Myrtaceae microsat
c	157	7	2.8	433	23	ABV04645	Human prostate exp
c	158	7	2.8	437	21	AAF15301	Trichoderma reesei
	159	7	2.8	441	21	AAC69761	Human breast tumou
	160	7	2.8	442	23	ABV00564	Human prostate exp
	161	7	2.8	447	24	ABL94002	Arabidopsis thalia
	162	7	2.8	450	22	AAS27369	cDNA encoding nove
	163	7	2.8	450	22	AAS34891	cDNA encoding nove
	164	7	2.8	450	22	AAS35014	cDNA encoding nove
c	165	7	2.8	457	24	ABK71922	Human cDNA encodin
c	166	7	2.8	459	24	ABN66777	Streptococcus poly
	167	7	2.8	463	22	ABA57939	Human foetal liver
	168	7	2.8	463	22	ABA27242	Probe #5708 for ge
	169	7	2.8	463	22	AAK06012	Human brain expres
	170	7	2.8	463	22	AAK31656	Human bone marrow
	171	7	2.8	463	22	AAI15773	Probe #5706 for ge
	172	7	2.8	463	22	AAI37533	Probe #6219 used t
	173	7	2.8	463	24	ABS06411	Human genome-deriv
	174	7	2.8	466	22	AAK63056	Human immune/haema
c	175	7	2.8	466	24	ABK09560	Human ovarian tumo
c	176	7	2.8	467	22	ABA57438	Human foetal liver
c	177	7	2.8	467	22	ABA58324	Human foetal liver
c	178	7	2.8	467	22	ABA26943	Probe #5409 for ge
c	179	7	2.8	467	22	ABA27452	Probe #5918 for ge
c	180	7	2.8	467	22	AAK05476	Human brain expres
c	181	7	2.8	467	22	AAK06421	Human brain expres
c	182	7	2.8	467	22	AAK31077	Human bone marrow
c	183	7	2.8	467	22	AAK32097	Human bone marrow
c	184	7	2.8	467	22	AAI15536	Probe #5469 for ge
c	185	7	2.8	467	22	AAI15944	Probe #5877 for ge
c	186	7	2.8	467	22	AAI36986	Probe #5672 used t
c	187	7	2.8	467	22	AAI37948	Probe #6634 used t
c	188	7	2.8	467	24	ABS05828	Human genome-deriv
c	189	7	2.8	467	24	ABS06864	Human genome-deriv
c	190	7	2.8	471	22	AAF88291	H. tuberculata HtH
c	191	7	2.8	471	23	ABV34926	Human prostate exp
c	192	7	2.8	471	23	ABV37806	Human prostate exp
c	193	7	2.8	471	23	ABV43775	Human prostate exp
c	194	7	2.8	475	22	ABA51905	Human foetal liver
c	195	7	2.8	475	22	ABA21723	Probe #189 for gen
c	196	7	2.8	475	22	AAK00200	Human brain expres
c	197	7	2.8	475	22	AAI10268	Probe #201 for gen
c	198	7	2.8	475	22	AAI31515	Probe #201 used to
c	199	7	2.8	475	22	AAI00205	Probe #196 used to
c	200	7	2.8	475	24	ABS00211	Human genome-deriv
	201	7	2.8	476	22	ABA57313	Human foetal liver
	202	7	2.8	476	22	AAK05348	Human brain expres
	203	7	2.8	476	22	AAK30942	Human bone marrow
	204	7	2.8	476	22	AAI36855	Probe #5541 used t
	205	7	2.8	476	24	ABS05690	Human genome-deriv
	206	7	2.8	485	22	AAL05330	Human reproductive
	207	7	2.8	485	23	ABL98199	Human testicular a
c	208	7	2.8	486	24	ABL69649	Prostate cancer re
	209	7	2.8	492	23	AAS54483	Staphylococcus aur
	210	7	2.8	492	24	ABN92528	Staphylococcus epi
	211	7	2.8	510	21	AAA35325	Myrtaceae microsat
c	212	7	2.8	511	24	ABQ37258	Oligonucleotide fo
	213	7	2.8	511	24	ABQ37259	Oligonucleotide fo

c 214	7	2.8	512	22	AAL16491	Human breast cance
c 215	7	2.8	512	22	AAK63297	Human immune/haema
c 216	7	2.8	523	24	ABL82662	Human ovarian canc
c 217	7	2.8	526	22	AAH29173	Drosophila melanog
218	7	2.8	530	22	AAF44755	Nucellin-like aspa
219	7	2.8	535	22	AAK92418	Human cDNA 3'-end
220	7	2.8	537	23	AAS51897	Staphylococcus aur
221	7	2.8	540	22	ABA70548	Human foetal liver
222	7	2.8	540	22	ABA37150	Probe #15616 for g
223	7	2.8	540	22	AAK18793	Human brain expres
224	7	2.8	540	22	AAK44730	Human bone marrow
225	7	2.8	540	22	AAI24992	Probe #14925 for g
226	7	2.8	540	22	AAI50708	Probe #19394 used
227	7	2.8	540	24	ABS18968	Human genome-deriv
c 228	7	2.8	546	23	ABV60194	Human prostate exp
229	7	2.8	547	24	ABQ18604	Oligonucleotide fo
c 230	7	2.8	547	24	ABQ18605	Oligonucleotide fo
231	7	2.8	549	21	AAC95282	Cat flea head and
232	7	2.8	549	21	AAC95296	Cat flea head and
c 233	7	2.8	552	22	AAH94228	Human foetal cDNA,
c 234	7	2.8	553	22	AAK10523	Human brain expres
c 235	7	2.8	553	22	AAI42156	Probe #10842 used
c 236	7	2.8	553	22	AAH33244	Human colon cancer
c 237	7	2.8	553	24	ABS10438	Human genome-deriv
c 238	7	2.8	558	20	AAX21087	Polynucleotide seq
239	7	2.8	558	24	ABN90996	Staphylococcus epi
c 240	7	2.8	565	22	ABA07470	Human ovarian and
c 241	7	2.8	565	22	AAL00107	Human reproductive
c 242	7	2.8	569	22	ABA61221	Human foetal liver
c 243	7	2.8	569	22	ABA29076	Probe #7542 for ge
c 244	7	2.8	569	22	AAK09517	Human brain expres
c 245	7	2.8	569	22	AAK35410	Human bone marrow
c 246	7	2.8	569	22	AAI17034	Probe #6967 for ge
c 247	7	2.8	569	22	AAI41122	Probe #9808 used t
c 248	7	2.8	569	24	ABS09780	Human genome-deriv
c 249	7	2.8	570	21	AAZ80460	Human colon cancer
250	7	2.8	574	24	ABQ23120	Oligonucleotide fo
c 251	7	2.8	574	24	ABQ23121	Oligonucleotide fo
c 252	7	2.8	576	21	AAC39247	Zea mays DNA fragm
c 253	7	2.8	576	24	ABQ46996	Oligonucleotide fo
254	7	2.8	576	24	ABQ46997	Oligonucleotide fo
255	7	2.8	578	24	ABL78472	Human ovarian canc
256	7	2.8	589	22	AAS26048	Human cDNA encodin
257	7	2.8	593	24	ABN73077	Bovine embryonic g
c 258	7	2.8	600	22	ABA60560	Human foetal liver
c 259	7	2.8	600	22	ABA28706	Probe #7172 for ge
c 260	7	2.8	600	22	AAK08842	Human brain expres
c 261	7	2.8	600	22	AAK34730	Human bone marrow
c 262	7	2.8	600	22	AAI16820	Probe #6753 for ge
c 263	7	2.8	600	22	AAI40449	Probe #9135 used t
264	7	2.8	600	23	ABV51336	Human prostate exp
c 265	7	2.8	600	24	ABS09307	Human genome-deriv
c 266	7	2.8	605	24	AAS61749	Lung small cell ca
c 267	7	2.8	613	24	ABQ46578	Oligonucleotide fo
268	7	2.8	613	24	ABQ46579	Oligonucleotide fo
c 269	7	2.8	614	21	AAZ80312	Human colon cancer
c 270	7	2.8	634	24	ABQ21524	Oligonucleotide fo
271	7	2.8	634	24	ABQ21525	Oligonucleotide fo
c 272	7	2.8	636	24	ABQ27142	Oligonucleotide fo
273	7	2.8	636	24	ABQ27143	Oligonucleotide fo
274	7	2.8	638	24	ABQ35550	Oligonucleotide fo
c 275	7	2.8	638	24	ABQ35551	Oligonucleotide fo
c 276	7	2.8	648	24	ABK48055	cDNA encoding BAG
277	7	2.8	661	18	AAT58734	LsrDNA sequence fr
278	7	2.8	661	21	AAF12581	Aspergillus oryzae
c 279	7	2.8	663	21	AAZ80317	Human colon cancer
280	7	2.8	669	21	AAF15194	Trichoderma reesei
c 281	7	2.8	671	24	ABQ70141	Listeria monocytog
282	7	2.8	676	18	AAT58731	LsrDNA sequence fr
283	7	2.8	676	18	AAT58732	LsrDNA sequence fr
284	7	2.8	676	18	AAT58733	LsrDNA sequence fr
285	7	2.8	706	24	ABQ21244	Oligonucleotide fo
c 286	7	2.8	706	24	ABQ21245	Oligonucleotide fo
c 287	7	2.8	707	23	AAS79803	DNA encoding novel
288	7	2.8	708	22	AAS26477	Human cDNA encodin
c 289	7	2.8	720	24	ABK77916	Bacillus clausii g
290	7	2.8	742	22	AAH04108	Human cDNA clone (
c 291	7	2.8	746	20	AAZ15502	Human gene express
c 292	7	2.8	746	24	ABQ49670	Oligonucleotide fo
293	7	2.8	746	24	ABQ49671	Oligonucleotide fo
294	7	2.8	751	19	AAZ96466	S. pneumoniae deri
c 295	7	2.8	753	18	AAT83841	DNA encoding a NAD
296	7	2.8	754	22	AAH04575	Human cDNA clone (
c 297	7	2.8	758	24	ABK24347	DNA encoding human
c 298	7	2.8	760	22	AAK93609	Human cDNA clone r
299	7	2.8	766	21	AAC70734	Single nucleotide
300	7	2.8	766	21	AAC70743	Single nucleotide
301	7	2.8	766	21	AAC70746	Single nucleotide
302	7	2.8	766	21	AAC70749	Single nucleotide
303	7	2.8	766	21	AAC70758	Single nucleotide
304	7	2.8	766	21	AAC70761	Single nucleotide
305	7	2.8	767	21	AAC70755	Single nucleotide
c 306	7	2.8	772	22	AAH05393	Human cDNA clone (
307	7	2.8	782	21	AAZ54149	Neisseria meningit
308	7	2.8	783	24	ABK82087	Novel floral meris
309	7	2.8	783	24	ABK82088	Novel floral meris
310	7	2.8	789	24	ABK82085	DNA encoding novel
c 311	7	2.8	803	22	AAH08514	Human cDNA clone (
312	7	2.8	804	24	ABQ22330	Oligonucleotide fo
c 313	7	2.8	804	24	ABQ22331	Oligonucleotide fo
c 314	7	2.8	827	22	AAH00278	Clostridium innocu
c 315	7	2.8	828	24	ABQ14816	Oligonucleotide fo
316	7	2.8	828	24	ABQ14817	Oligonucleotide fo
c 317	7	2.8	829	22	AAK92060	Human cDNA 5'-end
c 318	7	2.8	829	22	AAK94003	Human cDNA clone r
c 319	7	2.8	840	22	AAK91841	Human cDNA 5'-end
c 320	7	2.8	840	22	AAK93244	Human cDNA clone r
321	7	2.8	842	23	AAS64811	DNA encoding novel
c 322	7	2.8	850	22	AAK91630	Human cDNA 5'-end
c 323	7	2.8	850	22	AAK93967	Human cDNA clone r
324	7	2.8	871	22	AAK53371	Human polynucleoti
325	7	2.8	876	20	AAX57461	Rat U3 gene trap d
326	7	2.8	876	22	AAH53635	S. epidermidis ope
327	7	2.8	876	24	ABQ86200	Lactobacillus rham
c 328	7	2.8	877	23	AAS78219	DNA encoding novel
329	7	2.8	888	21	AAA53944	ORF3 sequence enco
330	7	2.8	888	24	AAL43622	Rhodococcus picric
331	7	2.8	888	24	ABK51840	R. erythropolis HL
332	7	2.8	888	24	AAD27243	Rhodococcus erythr
333	7	2.8	894	24	ABN93305	Staphylococcus epi
c 334	7	2.8	903	23	AAS49515	Staphylococcus aur
335	7	2.8	904	18	AAV06139	Viral infection ge
c 336	7	2.8	907	22	AAI97804	Human neuroblastom
c 337	7	2.8	918	21	AAA96346	cDNA encoding a no
c 338	7	2.8	918	22	AAS46162	Human DNA encoding
c 339	7	2.8	918	22	AAC87039	Nucleotide sequenc
c 340	7	2.8	918	24	ABL95707	Human angiogenesis
c 341	7	2.8	918	24	ABL88218	Human PRO4356 cDNA
342	7	2.8	924	23	AAS51669	Staphylococcus aur
343	7	2.8	925	24	ABQ28174	Oligonucleotide fo
c 344	7	2.8	925	24	ABQ28175	Oligonucleotide fo
345	7	2.8	927	23	AAS54897	Staphylococcus aur
c 346	7	2.8	932	22	AAI85849	Human polynucleoti
c 347	7	2.8	938	20	AAX97972	Human secreted pro
348	7	2.8	939	22	AAH31729	Human olfactory re
349	7	2.8	942	24	ABQ49750	Oligonucleotide fo
c 350	7	2.8	942	24	ABQ49751	Oligonucleotide fo
351	7	2.8	975	24	ABQ88048	Human GPCRX cDNA #
352	7	2.8	994	24	ABQ68324	Listeria monocytog
353	7	2.8	1002	20	AAX57454	Rat U3 gene trap d
c 354	7	2.8	1003	21	AAC51274	Arabidopsis thalia
c 355	7	2.8	1020	21	AAC34514	Arabidopsis thalia
356	7	2.8	1022	24	ABK75075	Bacillus lichenifo
357	7	2.8	1031	20	AAX57455	Rat U3 gene trap d
c 358	7	2.8	1031	24	ABL63688	Breast cancer rela
359	7	2.8	1038	23	ABL19931	Drosophila melanog

360	7	2.8	1050	20	AAX61596	B. burgdorferi ant
c 361	7	2.8	1084	24	ABQ27874	Oligonucleotide fo
362	7	2.8	1084	24	ABQ27875	Oligonucleotide fo
c 363	7	2.8	1087	21	AAC48569	Arabidopsis thalia
c 364	7	2.8	1092	21	AAC32957	Arabidopsis thalia
365	7	2.8	1098	24	ABK68585	Human DNA for olfa
c 366	7	2.8	1109	21	AAZ95380	Human colon specif
c 367	7	2.8	1112	24	ABK35314	Human cDNA encodin
c 368	7	2.8	1117	21	AAC53267	Arabidopsis thalia
c 369	7	2.8	1127	22	AAH98845	Human EST-derived
c 370	7	2.8	1132	23	AAS81120	DNA encoding novel
371	7	2.8	1149	22	AAH67166	C glutamicum codin
372	7	2.8	1152	20	AAX61595	B. burgdorferi ant
373	7	2.8	1155	22	AAS42252	Human cDNA encodin
374	7	2.8	1155	24	ABK37538	DNA encoding G-cou
c 375	7	2.8	1164	21	AAZ65061	Membrane-bound pro
c 376	7	2.8	1164	22	AAS46035	Human DNA encoding
c 377	7	2.8	1164	22	AAF44207	Human PRO511 (UNQ5
378	7	2.8	1179	24	AAD25931	Micromonospora car
c 379	7	2.8	1182	18	AAV75110	Staphylococcus aur
c 380	7	2.8	1200	24	ABK80414	Bacillus clausii g
c 381	7	2.8	1200	24	ABQ39212	Oligonucleotide fo
382	7	2.8	1200	24	ABQ39213	Oligonucleotide fo
383	7	2.8	1206	24	ABK73614	Bacillus lichenifo
c 384	7	2.8	1224	15	AAQ74693	Early Ripening Tom
385	7	2.8	1227	24	ABK79498	Bacillus clausii g
386	7	2.8	1229	21	AAC47295	Arabidopsis thalia
387	7	2.8	1231	21	AAC33652	Arabidopsis thalia
388	7	2.8	1235	21	AAC99128	Human pancreatic c
389	7	2.8	1248	21	AAC45822	Arabidopsis thalia
390	7	2.8	1252	23	AAS82036	DNA encoding novel
391	7	2.8	1259	21	AAC35954	Arabidopsis thalia
c 392	7	2.8	1269	23	AAS54825	Staphylococcus aur
c 393	7	2.8	1269	23	AAS55224	Staphylococcus aur
c 394	7	2.8	1269	23	AAS55394	Staphylococcus aur
395	7	2.8	1277	22	AAH43308	O. sativa aldehyde
396	7	2.8	1292	23	ABV29093	Human prostate exp
397	7	2.8	1297	22	AAF76856	Human secreted pro
c 398	7	2.8	1302	22	AAC81967	Human cytomegalovi
c 399	7	2.8	1320	24	ABQ68719	Listeria monocytog
c 400	7	2.8	1336	23	AAS59735	Propionibacterium
401	7	2.8	1344	22	AAL05558	Human reproductive
402	7	2.8	1344	22	AAL05559	Human reproductive
403	7	2.8	1347	23	ABL24049	Drosophila melanog
c 404	7	2.8	1372	22	AAF23908	Human secreted pro
405	7	2.8	1372	23	AAS68774	DNA encoding novel
406	7	2.8	1374	21	AAF22354	Human secreted pro
c 407	7	2.8	1378	23	ABL08505	Drosophila melanog
c 408	7	2.8	1386	24	AAD31758	Soybean HMG-CoA ly
c 409	7	2.8	1439	22	AAD05201	Human secreted pro
410	7	2.8	1452	23	ABL22309	Drosophila melanog
c 411	7	2.8	1469	23	ABL15297	Drosophila melanog
412	7	2.8	1471	22	AAS01535	Human secretory mo
413	7	2.8	1488	23	ABL12287	Drosophila melanog
c 414	7	2.8	1534	24	ABK24348	DNA encoding human
415	7	2.8	1540	22	ABA13110	Human nervous syst
416	7	2.8	1548	21	AAC43772	Zea mays DNA fragm
c 417	7	2.8	1548	22	AAK94131	Human full-length
c 418	7	2.8	1559	21	AAF21409	Human low adenosin
c 419	7	2.8	1559	21	AAA35287	Human adenosine re
c 420	7	2.8	1563	22	AAH17993	Human cDNA sequenc
421	7	2.8	1574	21	AAC47799	Arabidopsis thalia
c 422	7	2.8	1594	22	AAS63183	Human purified sec
423	7	2.8	1630	22	AAH17209	Human cDNA sequenc
424	7	2.8	1632	23	AAS86184	DNA encoding novel
425	7	2.8	1635	21	AAC42737	Arabidopsis thalia
426	7	2.8	1637	22	AAF61182	Human beta1-adreno
427	7	2.8	1637	22	AAF61183	Human beta1-adreno
428	7	2.8	1637	22	AAF61184	Human beta1-adreno
429	7	2.8	1637	22	AAF61185	Human beta1-adreno
430	7	2.8	1637	22	AAF61186	Human beta1-adreno
431	7	2.8	1637	22	AAF61187	Human beta1-adreno
432	7	2.8	1637	22	AAF61188	Human beta1-adreno
433	7	2.8	1637	22	AAF61189	Human beta1-adreno
434	7	2.8	1651	21	AAC48337	Arabidopsis thalia
c 435	7	2.8	1657	24	ABK35099	Human cDNA encodin
c 436	7	2.8	1674	22	AAI60766	Human polynucleoti
437	7	2.8	1689	14	AAQ43964	Human dopamine D1
c 438	7	2.8	1689	18	AAV74490	Staphylococcus aur
439	7	2.8	1697	22	AAL26442	Human breast cance
440	7	2.8	1697	22	AAS44958	cDNA encoding nove
c 441	7	2.8	1714	22	AAK53171	Human polynucleoti
442	7	2.8	1721	22	AAS45146	cDNA encoding nove
443	7	2.8	1723	21	AAA38338	Human beta-adrener
444	7	2.8	1723	21	AAZ98399	Human beta1-adreno
445	7	2.8	1723	24	ABK92208	Prostate cancer-as
446	7	2.8	1723	24	ABK40731	Human beta1-adreno
447	7	2.8	1739	21	AAC46456	Arabidopsis thalia
448	7	2.8	1742	22	AAL26679	Human breast cance
c 449	7	2.8	1765	22	AAH57384	Human skeletal mus
450	7	2.8	1767	24	AAL38373	Chimeric sequence
451	7	2.8	1767	24	AAL38388	Chimeric sequence
452	7	2.8	1773	23	AAS69907	DNA encoding novel
453	7	2.8	1780	21	AAC46905	Arabidopsis thalia
454	7	2.8	1784	24	ABA94657	Theobroma cacoa as
455	7	2.8	1804	21	AAC37770	Arabidopsis thalia
c 456	7	2.8	1833	22	AAS27322	cDNA encoding nove
457	7	2.8	1838	23	ABL18713	Drosophila melanog
458	7	2.8	1839	23	ABL29475	Drosophila melanog
459	7	2.8	1875	21	AAC44954	Arabidopsis thalia
460	7	2.8	1877	22	AAK94681	Human full-length
c 461	7	2.8	1878	23	AAS82037	DNA encoding novel
462	7	2.8	1885	21	AAC44283	Arabidopsis thalia
463	7	2.8	1904	21	AAC39032	Arabidopsis thalia
464	7	2.8	1908	21	AAF13098	Aspergillus oryzae
c 465	7	2.8	1910	21	AAC49576	Arabidopsis thalia
c 466	7	2.8	1912	21	AAC36318	Arabidopsis thalia
c 467	7	2.8	1922	23	ABL18577	Drosophila melanog
468	7	2.8	1932	21	AAA64472	cDNA encoding an a
469	7	2.8	1959	21	AAA07582	Marigold beta-cycl
470	7	2.8	1984	24	ABL70613	Chemically treated
471	7	2.8	1984	24	ABL34634	Human metastasis a
472	7	2.8	2031	21	AAC78066	Human cancer assoc
473	7	2.8	2031	22	AAH34419	Human colon cancer
c 474	7	2.8	2072	24	AAS17156	Mouse lymphoid spe
c 475	7	2.8	2081	22	AAK94152	Human full-length
c 476	7	2.8	2084	24	ABK54274	Mouse 7 transmembr
c 477	7	2.8	2085	21	AAA91745	7TM receptor DNA s
c 478	7	2.8	2113	22	AAS29811	Human cytoskeletal
479	7	2.8	2119	21	AAC77599	Human ORFX ORF3154
480	7	2.8	2129	20	AAX89290	Human regulatory p
c 481	7	2.8	2186	23	ABL04877	Drosophila melanog
c 482	7	2.8	2192	22	AAH14845	Human cDNA sequenc
c 483	7	2.8	2265	24	ABA05630	Human phosphoester
c 484	7	2.8	2274	23	ABL05917	Drosophila melanog
c 485	7	2.8	2288	22	AAS40806	cDNA encoding nove
c 486	7	2.8	2288	23	ABK43535	DNA encoding novel
c 487	7	2.8	2291	22	AAH14087	Human cDNA sequenc
488	7	2.8	2291	23	ABL10669	Drosophila melanog
c 489	7	2.8	2325	22	AAH16042	Human cDNA sequenc
490	7	2.8	2342	12	AAQ14955	Rat dopamine D1 re
c 491	7	2.8	2392	23	ABL15536	Drosophila melanog
c 492	7	2.8	2397	23	AAS72734	DNA encoding novel
493	7	2.8	2418	22	AAH17392	Human cDNA sequenc
c 494	7	2.8	2427	23	ABL27848	Drosophila melanog
495	7	2.8	2431	23	ABL22460	Drosophila melanog
c 496	7	2.8	2433	21	AAC49572	Arabidopsis thalia
c 497	7	2.8	2471	22	AAI58190	Human polynucleoti
498	7	2.8	2492	22	AAS26830	Human cDNA encodin
c 499	7	2.8	2507	23	ABL05567	Drosophila melanog
c 500	7	2.8	2510	21	AAF21410	Human low adenosin
c 501	7	2.8	2510	21	AAA35288	Human adenosine re
502	7	2.8	2513	23	ABL14845	Drosophila melanog
c 503	7	2.8	2541	23	AAS84523	DNA encoding novel
c 504	7	2.8	2567	23	ABL27850	Drosophila melanog
505	7	2.8	2624	24	ABK12639	DNA encoding Physc

506	7	2.8	2636	23	ABL04197	Drosophila melanog
c 507	7	2.8	2641	23	ABL27796	Drosophila melanog
c 508	7	2.8	2651	19	AAV52349	Streptococcus pneu
c 509	7	2.8	2652	16	AAT05619	Mouse liver acute
510	7	2.8	2656	24	ABQ70740	Listeria monocytog
c 511	7	2.8	2680	22	AAH55013	S. epidermidis gen
c 512	7	2.8	2681	17	AAT30870	Engineered 95 kD p
513	7	2.8	2739	24	ABQ91574	M. capsulatus gene
514	7	2.8	2826	23	ABL25640	Drosophila melanog
515	7	2.8	2853	23	ABL14121	Drosophila melanog
c 516	7	2.8	2869	16	AAQ89340	Mouse Stat3 (19sf6
c 517	7	2.8	2869	17	AAT31280	Mouse STAT4 cDNA c
c 518	7	2.8	2869	21	AAC93231	Mouse STAT3 nucleo
c 519	7	2.8	2869	24	AAS96848	Mouse STAT3 cDNA.
520	7	2.8	2888	22	AAI60318	Human polynucleoti
c 521	7	2.8	2906	23	ABK43478	DNA encoding novel
c 522	7	2.8	2924	24	ABI99454	Mouse ischaemic co
c 523	7	2.8	2928	22	AAS27107	cDNA encoding nove
c 524	7	2.8	2945	22	AAH15778	Human cDNA sequenc
c 525	7	2.8	2962	22	AAK52187	Human polynucleoti
526	7	2.8	2964	24	ABK84590	Human cDNA differe
527	7	2.8	2964	24	ABL69596	Prostate cancer re
c 528	7	2.8	2966	20	AAX83493	Human farnesylated
c 529	7	2.8	2968	20	AAV83752	cDNA encoding huma
c 530	7	2.8	3013	23	ABL29601	Drosophila melanog
531	7	2.8	3014	12	AAQ14954	Human dopamine D1
c 532	7	2.8	3016	22	AAK94251	Human full-length
c 533	7	2.8	3033	21	AAZ29720	Modified T. cruzi
c 534	7	2.8	3033	22	AAK94389	Human full-length
535	7	2.8	3093	23	ABL06507	Drosophila melanog
c 536	7	2.8	3093	23	ABL15330	Drosophila melanog
c 537	7	2.8	3126	22	AAH55007	S. epidermidis gen
c 538	7	2.8	3128	23	ABL16879	Drosophila melanog
c 539	7	2.8	3130	24	ABN99365	Human secreted pro
c 540	7	2.8	3207	19	AAV08372	Cellulose synthase
c 541	7	2.8	3241	23	ABL02985	Drosophila melanog
c 542	7	2.8	3253	21	AAZ29719	T. cruzi complemen
c 543	7	2.8	3261	23	ABL19839	Drosophila melanog
c 544	7	2.8	3268	22	AAH54810	S. epidermidis gen
c 545	7	2.8	3294	23	ABV24728	Human prostate exp
c 546	7	2.8	3294	23	ABV25290	Human prostate exp
c 547	7	2.8	3342	19	AAV37494	Human hepatocyte n
548	7	2.8	3347	23	ABL24048	Drosophila melanog
549	7	2.8	3349	23	ABL21784	Drosophila melanog
c 550	7	2.8	3363	22	AAS23404	Candida albicans e
c 551	7	2.8	3365	24	ABK84203	Human cDNA differe
c 552	7	2.8	3389	16	AAT01031	Human leucine zipp
c 553	7	2.8	3389	18	AAT89349	Human leucine-zipp
c 554	7	2.8	3431	19	AAV35791	Human trident tran
555	7	2.8	3459	22	AAH15747	Human cDNA sequenc
c 556	7	2.8	3492	24	ABL64768	Lung cancer relate
c 557	7	2.8	3492	24	ABL65402	Lung cancer relate
c 558	7	2.8	3492	24	ABL66510	Lung cancer relate
559	7	2.8	3546	21	AAA39454	Yeast UPF1 gene.
560	7	2.8	3622	23	ABL17330	Drosophila melanog
c 561	7	2.8	3639	23	ABL18971	Drosophila melanog
c 562	7	2.8	3690	23	ABL29839	Drosophila melanog
563	7	2.8	3730	23	ABL13240	Drosophila melanog
564	7	2.8	3792	23	ABL26158	Drosophila melanog
565	7	2.8	3842	23	ABL15059	Drosophila melanog
c 566	7	2.8	3843	23	ABL22308	Drosophila melanog
c 567	7	2.8	3879	23	ABL13243	Drosophila melanog
c 568	7	2.8	3934	24	ABK15171	Human REPTR 3 cDNA
c 569	7	2.8	3940	23	ABL15296	Drosophila melanog
570	7	2.8	3981	23	ABL18576	Drosophila melanog
c 571	7	2.8	4010	24	ABI99508	Mouse ischaemic co
572	7	2.8	4054	23	ABL23578	Drosophila melanog
c 573	7	2.8	4082	21	AAC76412	Human ORFX ORF1967
c 574	7	2.8	4165	23	ABL23366	Drosophila melanog
c 575	7	2.8	4174	23	AAS89195	DNA encoding novel
c 576	7	2.8	4221	23	ABL16299	Drosophila melanog
577	7	2.8	4235	22	ABA08948	Human semaphorin d
578	7	2.8	4235	22	AAH99661	Human protein enco
579	7	2.8	4241	23	ABL29474	Drosophila melanog
c 580	7	2.8	4354	23	ABL07437	Drosophila melanog
581	7	2.8	4376	21	AAA14818	DNA encoding a C1
582	7	2.8	4376	23	ABA92720	Chrysosporium C1 s
583	7	2.8	4388	22	AAS08694	Micromonospora DNA
c 584	7	2.8	4448	20	AAX20564	Polynucleotide seq
585	7	2.8	4453	23	ABL10668	Drosophila melanog
c 586	7	2.8	4472	23	ABL30304	Drosophila melanog
587	7	2.8	4540	23	ABL03172	Drosophila melanog
588	7	2.8	4588	22	AAI60826	Human polynucleoti
c 589	7	2.8	4647	23	ABL15923	Drosophila melanog
c 590	7	2.8	4736	24	AAS62248	cDNA sequence #35
591	7	2.8	4737	21	AAZ51566	Staphylococcus aur
592	7	2.8	4748	23	ABL14844	Drosophila melanog
c 593	7	2.8	4793	23	ABL18712	Drosophila melanog
c 594	7	2.8	4827	24	AAD27213	Human 61166 EST co
595	7	2.8	4970	23	ABL07992	Drosophila melanog
596	7	2.8	5021	24	ABN81530	Human HVE-CAD-2 pr
597	7	2.8	5055	21	AAC76108	Human ORFX ORF1663
c 598	7	2.8	5058	23	ABL30358	Drosophila melanog
599	7	2.8	5082	23	ABL29600	Drosophila melanog
600	7	2.8	5150	23	AAS59565	Propionibacterium
c 601	7	2.8	5224	24	ABK63469	Rat sequence diffe
c 602	7	2.8	5273	24	ABK94959	Human novel polynu
603	7	2.8	5293	23	ABL14120	Drosophila melanog
604	7	2.8	5312	24	ABK39997	Human chemically p
605	7	2.8	5312	24	ABL32842	Human immune syste
606	7	2.8	5364	24	ABK40005	Human chemically p
c 607	7	2.8	5390	23	ABL30087	Drosophila melanog
c 608	7	2.8	5453	22	AAS29791	Human cytoskeletal
c 609	7	2.8	5502	23	ABL16878	Drosophila melanog
610	7	2.8	5539	22	AAI61239	Human polynucleoti
c 611	7	2.8	5539	22	AAI61239	Human polynucleoti
c 612	7	2.8	5740	23	ABL05916	Drosophila melanog
613	7	2.8	5768	22	AAL05331	Human reproductive
614	7	2.8	5768	23	ABL98200	Human testicular a
615	7	2.8	5802	22	AAI59453	Human polynucleoti
c 616	7	2.8	5802	22	AAI59453	Human polynucleoti
617	7	2.8	5821	18	AAT58686	DNA encoding S. fr
c 618	7	2.8	5859	24	ABQ70983	Listeria monocytog
c 619	7	2.8	5872	23	ABL06506	Drosophila melanog
620	7	2.8	5886	20	AAX87388	Human PFIC1-BRIC-1
c 621	7	2.8	5918	20	AAX13045	Enterococcus faeca
622	7	2.8	6072	24	ABK83452	Human cDNA differe
623	7	2.8	6113	24	ABL33822	Human immune syste
624	7	2.8	6157	24	ABQ70939	Listeria monocytog
c 625	7	2.8	6161	22	AAH14365	Human cDNA sequenc
626	7	2.8	6169	23	ABL29838	Drosophila melanog
c 627	7	2.8	6197	23	ABL04070	Drosophila melanog
c 628	7	2.8	6200	24	ABL34215	Human immune syste
629	7	2.8	6236	23	ABL07156	Drosophila melanog
630	7	2.8	6302	23	ABL02889	Drosophila melanog
c 631	7	2.8	6310	24	ABL70321	Chemically treated
c 632	7	2.8	6310	24	AAS61268	Human gene regulat
c 633	7	2.8	6310	24	ABK31364	Signal transductio
634	7	2.8	6351	24	ABL70299	Chemically treated
635	7	2.8	6351	24	ABL33446	Human immune syste
636	7	2.8	6351	24	AAS61231	Human gene regulat
637	7	2.8	6351	24	ABK31336	Signal transductio
638	7	2.8	6426	20	AAX20538	Polynucleotide seq
639	7	2.8	6452	17	AAT30193	Peripheral nervous
c 640	7	2.8	6554	22	ABA18544	Human nervous syst
c 641	7	2.8	6554	22	ABA18924	Human nervous syst
642	7	2.8	6559	23	ABL04876	Drosophila melanog
c 643	7	2.8	6567	22	ABA18923	Human nervous syst
c 644	7	2.8	6607	23	ABL18970	Drosophila melanog
645	7	2.8	6712	23	ABL18545	Drosophila melanog
646	7	2.8	6863	23	ABL11213	Drosophila melanog
c 647	7	2.8	6880	22	AAK72785	Human immune/haema
648	7	2.8	6880	22	AAK79613	Human immune/haema
c 649	7	2.8	6910	23	ABL17928	Drosophila melanog
650	7	2.8	6953	23	ABL07436	Drosophila melanog
651	7	2.8	6985	23	ABL13148	Drosophila melanog

c 652	7	2.8	7207	20	AAX23032	Swine HEV ORF 1 ge
c 653	7	2.8	7231	23	ABL13394	Drosophila melanog
c 654	7	2.8	7302	23	AAS52198	Staphylococcus aur
c 655	7	2.8	7309	22	AAS46567	Tumour suppressor
c 656	7	2.8	7309	24	ABK34010	Human DNA for stag
c 657	7	2.8	7309	24	ABL33816	Human immune syste
658	7	2.8	7330	23	ABL04196	Drosophila melanog
659	7	2.8	7402	23	ABL12286	Drosophila melanog
660	7	2.8	7584	23	ABL12310	Drosophila melanog
c 661	7	2.8	7703	23	ABL19576	Drosophila melanog
c 662	7	2.8	7746	21	AAA07836	Human homologue of
663	7	2.8	7822	23	ABL22414	Drosophila melanog
c 664	7	2.8	7959	21	AAA81510	N. meningitidis pa
665	7	2.8	7965	18	AAV74632	Staphylococcus aur
666	7	2.8	7978	23	ABL13574	Drosophila melanog
667	7	2.8	8011	24	ABL32079	Human immune syste
668	7	2.8	8011	24	AAD28369	Human chemically t
669	7	2.8	8339	18	AAV74486	Staphylococcus aur
670	7	2.8	8418	23	ABL15922	Drosophila melanog
c 671	7	2.8	8461	23	ABL10100	Drosophila melanog
c 672	7	2.8	8691	23	ABL19838	Drosophila melanog
c 673	7	2.8	8746	23	ABL02984	Drosophila melanog
674	7	2.8	8998	24	ABL33706	Human immune syste
675	7	2.8	9024	21	AAC86431	Wheat SSII gene SE
676	7	2.8	9114	23	ABL02888	Drosophila melanog
c 677	7	2.8	9122	22	AAL36088	Human musculoskele
678	7	2.8	9147	23	ABL09222	Drosophila melanog
679	7	2.8	9209	24	ABL34427	Human immune syste
680	7	2.8	9219	22	AAS46808	Tumour suppressor
681	7	2.8	9710	23	ABL30086	Drosophila melanog
682	7	2.8	9796	24	ABK69846	Human secreted pro
683	7	2.8	9941	21	AAA81461	N. meningitidis pa
c 684	7	2.8	10060	22	AAK85905	Human immune/haema
c 685	7	2.8	10172	22	AAD21290	Human phospholipas
c 686	7	2.8	10262	23	ABL18544	Drosophila melanog
c 687	7	2.8	10284	23	ABL11212	Drosophila melanog
688	7	2.8	10873	23	ABL05566	Drosophila melanog
c 689	7	2.8	11136	23	ABL16298	Drosophila melanog
c 690	7	2.8	11145	23	ABL20336	Drosophila melanog
c 691	7	2.8	11520	23	ABL14118	Drosophila melanog
692	7	2.8	11715	9	AAN81564	Genomic sequence e
693	7	2.8	11724	8	AAN70102	Complete genomic s
694	7	2.8	11724	22	AAH57497	Human liver cell s
695	7	2.8	11725	17	AAT32796	Human protein C ge
696	7	2.8	11725	18	AAT79723	Human protein C ge
697	7	2.8	11725	20	AAZ32179	Human protein C nu
698	7	2.8	11725	22	AAF54051	Human protein C cD
699	7	2.8	11831	19	AAV52198	Streptococcus pneu
c 700	7	2.8	12028	23	ABL02788	Drosophila melanog
701	7	2.8	12029	23	ABL15508	Drosophila melanog
c 702	7	2.8	12039	23	ABL19574	Drosophila melanog
703	7	2.8	12508	21	AAA53941	12.5 kb picric aci
704	7	2.8	12508	24	AAD27240	Rhodococcus erythr
705	7	2.8	12523	24	AAL43619	Rhodococcus erythr
706	7	2.8	12523	24	ABK51837	Rhodococcus erythr
707	7	2.8	12905	21	AAZ99100	S. fradiae tylosin
c 708	7	2.8	12905	21	AAZ99101	S. fradiae tylosin
709	7	2.8	13161	22	AAF97867	Human neuroblastom
c 710	7	2.8	13169	23	ABL18727	Drosophila melanog
711	7	2.8	13767	23	ABL15058	Drosophila melanog
c 712	7	2.8	14417	22	AAK71816	Human immune/haema
713	7	2.8	14417	22	AAK73113	Human immune/haema
714	7	2.8	14417	22	AAK87584	Human immune/haema
c 715	7	2.8	14417	22	AAI62923	Human genomic DNA
c 716	7	2.8	14426	22	AAK71814	Human immune/haema
c 717	7	2.8	14426	22	AAK71817	Human immune/haema
718	7	2.8	14426	22	AAK73099	Human immune/haema
719	7	2.8	14426	22	AAK73115	Human immune/haema
c 720	7	2.8	14426	22	AAK85290	Human immune/haema
721	7	2.8	14426	22	AAK87568	Human immune/haema
722	7	2.8	14426	22	AAK87586	Human immune/haema
c 723	7	2.8	14426	22	AAI62921	Human genomic DNA
c 724	7	2.8	14426	22	AAI62924	Human genomic DNA
c 725	7	2.8	14448	22	AAK71815	Human immune/haema
726	7	2.8	14448	22	AAK73111	Human immune/haema
727	7	2.8	14448	22	AAK87580	Human immune/haema
c 728	7	2.8	14448	22	AAI62922	Human genomic DNA
c 729	7	2.8	14451	22	AAK71818	Human immune/haema
730	7	2.8	14451	22	AAK73116	Human immune/haema
731	7	2.8	14451	22	AAK87587	Human immune/haema
c 732	7	2.8	14451	22	AAI62925	Human genomic DNA
733	7	2.8	14825	23	ABL17382	Drosophila melanog
c 734	7	2.8	14897	23	ABL04980	Drosophila melanog
c 735	7	2.8	15500	22	AAS46508	Tumour suppressor
736	7	2.8	15987	23	ABL14198	Drosophila melanog
c 737	7	2.8	16122	22	AAS22908	DNA encoding novel
c 738	7	2.8	16341	22	AAS23002	DNA encoding novel
c 739	7	2.8	16397	18	AAV74516	Staphylococcus aur
c 740	7	2.8	16642	23	ABL20140	Drosophila melanog
741	7	2.8	16682	22	AAK70010	Human immune/haema
742	7	2.8	16682	22	AAK79798	Human immune/haema
743	7	2.8	17141	24	AAD26486	Bovine gamma globi
744	7	2.8	17286	22	AAL36869	Human musculoskele
745	7	2.8	17491	24	ABL34574	Human metastasis a
c 746	7	2.8	18467	23	ABL06976	Drosophila melanog
c 747	7	2.8	18846	23	AAS55261	Staphylococcus aur
748	7	2.8	18974	21	AAA81485	N. meningitidis pa
749	7	2.8	20245	22	AAK72318	Human immune/haema
750	7	2.8	20245	24	ABK69845	Human secreted pro
751	7	2.8	20383	21	AAZ93709	F-box protein Cdc4
c 752	7	2.8	20578	22	ABA16515	Human nervous syst
c 753	7	2.8	22188	23	ABL28616	Drosophila melanog
754	7	2.8	22494	22	AAD11724	Human asthma-assoc
c 755	7	2.8	23241	22	AAK84291	Human immune/haema
c 756	7	2.8	23241	22	AAK87225	Human immune/haema
757	7	2.8	23695	24	ABQ66981	Human angiogenesis
c 758	7	2.8	23996	22	ABA18618	Human nervous syst
759	7	2.8	24028	22	AAL05519	Human reproductive
760	7	2.8	24993	22	AAK65726	Human immune/haema
761	7	2.8	25656	23	ABL13242	Drosophila melanog
c 762	7	2.8	26995	22	AAS29963	Human lung antigen
763	7	2.8	27433	23	ABL20312	Drosophila melanog
c 764	7	2.8	28098	23	ABL14892	Drosophila melanog
c 765	7	2.8	29112	23	AAS59609	Propionibacterium
c 766	7	2.8	31718	22	AAS39915	Genomic sequence #
c 767	7	2.8	31718	22	AAS39916	Genomic sequence #
c 768	7	2.8	31718	22	AAL06415	Human reproductive
c 769	7	2.8	31718	22	AAL06416	Human reproductive
770	7	2.8	31718	22	AAK73104	Human immune/haema
771	7	2.8	31718	22	AAK73120	Human immune/haema
c 772	7	2.8	31718	22	AAK87442	Human immune/haema
c 773	7	2.8	31718	22	AAK87443	Human immune/haema
774	7	2.8	31718	22	AAK87573	Human immune/haema
775	7	2.8	31718	22	AAK87592	Human immune/haema
c 776	7	2.8	31718	22	AAK90359	Human digestive sy
c 777	7	2.8	31718	22	AAK90360	Human digestive sy
c 778	7	2.8	31741	22	ABA21231	Human nervous syst
c 779	7	2.8	32188	22	ABA18472	Human nervous syst
c 780	7	2.8	32195	22	AAS36517	Human cardiovascul
c 781	7	2.8	32219	22	AAS36516	Human cardiovascul
c 782	7	2.8	32768	20	AAX20515	Polynucleotide seq
c 783	7	2.8	35465	22	AAF54723	Nucleotide sequenc
c 784	7	2.8	35832	23	ABL18726	Drosophila melanog
c 785	7	2.8	38644	21	AAF21424	Human low adenosin
c 786	7	2.8	38644	21	AAA35302	Human adenosine re
787	7	2.8	40359	23	ABL30382	Drosophila melanog
788	7	2.8	42566	24	AAL47390	Murine brain circu
789	7	2.8	44001	22	AAK74850	Human immune/haema
790	7	2.8	44242	23	ABL19930	Drosophila melanog
791	7	2.8	52872	23	ABL04952	Drosophila melanog
c 792	7	2.8	67279	23	ABL07668	Drosophila melanog
c 793	7	2.8	99014	24	ABN96931	Gene #3429 used to
c 794	7	2.8	100848	22	AAF28552	Genomic fragment #
c 795	7	2.8	105184	24	ABK24122	Bacterial artifici
c 796	7	2.8	119198	24	ABK83565	Human cDNA differe
797	7	2.8	119211	22	AAF28553	Genomic fragment #

c 798	7	2.8	122186	22	AAC89560	Human histone deac
799	7	2.8	149480	24	ABL61947	Colon adenocarcino
800	7	2.8	149480	24	ABL61948	Colon adenocarcino
801	7	2.8	149480	24	ABL68365	Kidney cancer rela
802	7	2.8	198161	24	ABK83564	Human cDNA differe
c 803	7	2.8	249487	24	ABN85733	Mouse genomic regi
804	7	2.8	265118	22	AAH41227	Pyrococcus abyssi
805	7	2.8	349980	21	AAF21607	Neisseria meningit
c 806	7	2.8	349980	21	AAF21607	Neisseria meningit
807	7	2.8	349980	22	AAF86431	Pyrococcus abyssi
c 808	7	2.8	349980	22	AAH41226	Pyrococcus abyssi
809	7	2.8	349980	22	AAH68528	C glutamicum codin
c 810	7	2.8	349980	22	AAH68530	C glutamicum codin
c 811	7	2.8	349980	22	AAH68531	C glutamicum codin
c 812	7	2.8	349980	22	AAH68533	C glutamicum codin
813	7	2.8	495269	24	ABQ67195	Listeria innocua c
c 814	7	2.8	534720	19	AAV30458	Rhizobium species
c 815	7	2.8	536165	19	AAV30459	Rhizobium species
c 816	7	2.8	611590	21	AAF22303	Arabidopsis thalia
817	7	2.8	640681	24	ABA92787	Buchnera sp. genom
c 818	7	2.8	910715	20	AAX20248	Borrelia burgdorfe
c 819	7	2.8	1038602	20	AAZ01425	Complete genome se
820	7	2.8	1163020	24	ABQ67197	Listeria innocua c
c 821	7	2.8	1163020	24	ABQ67197	Listeria innocua c
822	7	2.8	1437668	21	AAA81490	N. meningitidis B
c 823	7	2.8	1437668	21	AAA81490	N. meningitidis B
c 824	7	2.8	1664976	19	AAV21209	Methanococcus jann
825	7	2.8	1830121	17	AAT42063	Haemophilus influe
826	7	2.8	2365589	24	ABA90521	Genomic sequence o
c 827	7	2.8	2365589	24	ABA90521	Genomic sequence o
828	7	2.8	2944528	24	ABA03041	Listeria monocytog
c 829	7	2.8	2944528	24	ABA03041	Listeria monocytog
830	7	2.8	3011208	24	ABQ69245	Listeria innocua D
c 831	7	2.8	3011208	24	ABQ69245	Listeria innocua D
832	7	2.8	4403765	22	AAI99683	Mycobacterium tube
c 833	7	2.8	4403765	22	AAI99683	Mycobacterium tube
834	7	2.8	4411529	22	AAI99682	Mycobacterium tube
c 835	7	2.8	4411529	22	AAI99682	Mycobacterium tube
836	6	2.4	19	19	AAV64174	Human cerebral pro
837	6	2.4	20	16	AAQ81020	Antisense oligomer
c 838	6	2.4	20	20	AAX38469	E. coli SecA antis
839	6	2.4	20	22	AAF99852	Immunostimulatory
840	6	2.4	20	22	AAF99853	Immunostimulatory
841	6	2.4	20	22	AAF54690	Human HLA Class I
842	6	2.4	20	24	ABI94933	Capture oligonucle
843	6	2.4	23	24	ABK61028	Human CLCA1 gene e
c 844	6	2.4	23	24	ABK61046	Human CLCA1 gene e
c 845	6	2.4	24	20	AAX86863	Apospory-specific
c 846	6	2.4	24	22	AAC93133	Avian endogenous r
847	6	2.4	24	24	ABI86436	Capture oligonucle
c 848	6	2.4	24	24	ABI86437	Capture oligonucle
849	6	2.4	25	21	AAC96489	HLA DQB1 gene PCR
c 850	6	2.4	25	21	AAA38608	Actinobacillus ple
851	6	2.4	26	17	AAT68977	Primer for univers
c 852	6	2.4	26	19	AAX10005	Human biallelic po
853	6	2.4	27	20	AAZ34520	Death activator de
c 854	6	2.4	27	20	AAX90603	Primer-1 for ampli
855	6	2.4	27	21	AAZ46939	Human saccharide-t
856	6	2.4	27	24	ABK50929	HUCEP-9 associated
c 857	6	2.4	30	11	AAQ03584	Preprochymosin lea
858	6	2.4	30	17	AAT12664	IL4.Y124D PCR prim
859	6	2.4	30	18	AAT89610	Hepatitis C virus
c 860	6	2.4	31	21	AAA97426	Pea pra2 gene prom
c 861	6	2.4	32	17	AAX35077	PCR primer used to
862	6	2.4	32	20	ABL41456	TNF fusion vector
c 863	6	2.4	33	22	AAH75483	Human ribosome pro
c 864	6	2.4	34	21	AAZ48090	Saccharomyces cere
865	6	2.4	37	21	AAA61446	Human glycine tran
866	6	2.4	38	21	AAA61432	Human glycine tran
c 867	6	2.4	38	21	AAA08974	Primer 2 for human
868	6	2.4	39	22	AAH20281	Go19 linker librar
869	6	2.4	40	17	AAT70708	Stenotic carotid a
c 870	6	2.4	41	22	AAH75485	Human ribosome pro
c 871	6	2.4	41	22	AAH75486	Human ribosome pro
872	6	2.4	42	16	AAQ97732	Toxoplasma gondii
873	6	2.4	42	20	AAV99889	S. cerevisiae UBC5
c 874	6	2.4	42	21	AAA97395	Pea pra2 light-rep
c 875	6	2.4	44	17	AAT39166	Primer for amplify
c 876	6	2.4	44	17	AAT17211	SRE-ZBP DNA bindin
c 877	6	2.4	45	20	AAX88586	Human chromosome 1
c 878	6	2.4	45	24	AAD38247	Human zsig33-epsil
c 879	6	2.4	45	24	AAD25768	Human zsig33-epsil
c 880	6	2.4	47	21	AAZ65709	Human map-related
881	6	2.4	47	21	AAZ65978	Human map-related
c 882	6	2.4	47	21	AAZ67392	Human map-related
883	6	2.4	47	21	AAZ67729	Human map-related
c 884	6	2.4	47	21	AAZ68208	Human map-related
885	6	2.4	47	21	AAZ68638	Human map-related
c 886	6	2.4	50	22	AAI74761	Human silent SNP c
887	6	2.4	51	20	AAZ12481	PCR primer used to
c 888	6	2.4	51	22	AAL32628	Human SNP oligonuc
889	6	2.4	51	22	AAL32969	Human SNP oligonuc
890	6	2.4	51	22	AAL33027	Human SNP oligonuc
c 891	6	2.4	51	22	AAI74760	Human silent SNP c
c 892	6	2.4	51	22	AAI76504	Human silent SNP c
c 893	6	2.4	51	22	AAI76505	Human silent SNP c
c 894	6	2.4	51	22	AAI79162	Human silent SNP c
c 895	6	2.4	51	22	AAH89442	Human coding sequ
c 896	6	2.4	51	22	AAH89443	Human coding sequ
897	6	2.4	51	22	AAH79823	Human DNA containi
c 898	6	2.4	54	18	AAV76546	Staphylococcus aur
899	6	2.4	55	20	AAX15977	PCR primer B1-3 us
c 900	6	2.4	56	21	AAA53493	Potential bsrFIR N
901	6	2.4	59	17	AAT42373	Clone X3,J2, J3, J
902	6	2.4	59	21	AAC25547	Human secreted pro
c 903	6	2.4	60	24	ABN33078	Human spliced tran
c 904	6	2.4	60	24	ABN35969	Human spliced tran
905	6	2.4	60	24	ABN36137	Human spliced tran
c 906	6	2.4	60	24	ABN43984	Human spliced tran
c 907	6	2.4	60	24	ABN50307	Human spliced tran
c 908	6	2.4	60	24	ABN59090	Human spliced tran
c 909	6	2.4	61	14	AAQ46667	Substrate-cleaving
c 910	6	2.4	62	18	AAV77154	Staphylococcus aur
c 911	6	2.4	63	24	AAS98512	Human protective D
912	6	2.4	65	22	AAD14210	Synthetic transcri
c 913	6	2.4	65	24	ABN28559	Rat spliced transc
c 914	6	2.4	65	24	ABN28662	Rat spliced transc
915	6	2.4	65	24	ABN30757	Rat spliced transc
916	6	2.4	65	24	ABN54790	Mouse spliced tran
c 917	6	2.4	65	24	ABN56070	Mouse spliced tran
918	6	2.4	65	24	ABN57947	Mouse spliced tran
919	6	2.4	65	24	ABN58046	Mouse spliced tran
920	6	2.4	66	20	AAV83789	Antimicrobial pept
921	6	2.4	66	22	AAS04729	Synthetic gene shP
c 922	6	2.4	70	21	AAC69958	TGF-beta-1-binding
923	6	2.4	71	18	AAV77697	Staphylococcus aur
924	6	2.4	72	20	AAX16057	DNA encoding lytic
925	6	2.4	72	20	AAX19277	Cytosol localised
c 926	6	2.4	75	22	AAD16088	IRES II amplifying
c 927	6	2.4	75	22	AAD16090	CITE element ampli
c 928	6	2.4	75	24	AAD38241	Human zsig33-beta
c 929	6	2.4	75	24	AAD25762	Human zsig33-beta
c 930	6	2.4	77	21	AAA57051	Human colon cancer
c 931	6	2.4	84	21	AAC55447	Entry vector pENTR
932	6	2.4	85	17	AAT17893	DNA encoding amphi
c 933	6	2.4	87	7	AAN60663	HIV virus gag regi
934	6	2.4	87	20	AAX85199	Motif I final clus
935	6	2.4	88	17	AAT17895	DNA encoding amphi
936	6	2.4	88	21	ABA97779	Peptide antibiotic
937	6	2.4	93	23	ABV34747	Human prostate exp
938	6	2.4	93	23	ABV43599	Human prostate exp
939	6	2.4	94	18	AAT76878	Parapox virus Hind
940	6	2.4	95	21	AAA35563	Microsatellite nuc
941	6	2.4	95	21	AAA35564	Microsatellite nuc
942	6	2.4	95	21	AAA35565	Microsatellite nuc
943	6	2.4	95	21	AAA35566	Microsatellite nuc

944	6	2.4	95	21	AAA35567	Microsatellite nuc
945	6	2.4	95	21	AAA35568	Microsatellite nuc
946	6	2.4	95	21	AAA35569	Microsatellite nuc
947	6	2.4	97	24	ABL59281	Nucleotide sequenc
948	6	2.4	97	24	AAD25614	MLL-AF4/98(+) chim
949	6	2.4	98	21	AAA35562	Microsatellite nuc
950	6	2.4	99	21	AAC16143	Human secreted pro
951	6	2.4	100	21	AAZ29367	Antimicrobial pept
c 952	6	2.4	102	22	ABA72223	Human foetal liver
c 953	6	2.4	102	22	AAK20645	Human brain expres
c 954	6	2.4	102	22	AAK46789	Human bone marrow
c 955	6	2.4	102	22	AAI52628	Probe #21314 used
956	6	2.4	103	21	AAZ29366	Antimicrobial pept
c 957	6	2.4	105	21	AAA35571	Microsatellite nuc
958	6	2.4	105	22	ABA48866	Human breast cell
959	6	2.4	105	22	AAI21704	Probe #11637 for g
960	6	2.4	105	22	AAF75432	Codon-optimised HP
961	6	2.4	113	23	ABV00929	Human prostate exp
962	6	2.4	114	13	AAQ23247	Nematode resistant
963	6	2.4	114	16	AAT21530	Human gene signatu
c 964	6	2.4	116	21	AAC21599	Human secreted pro
965	6	2.4	117	20	AAX16062	DNA encoding lytic
966	6	2.4	117	20	AAX19278	Extracellular loca
967	6	2.4	120	22	ABA74029	Human foetal liver
968	6	2.4	120	22	ABA39091	Probe #17557 for g
969	6	2.4	120	22	AAK22482	Human brain expres
970	6	2.4	120	22	AAK48650	Human bone marrow
971	6	2.4	120	22	AAH74363	Nucleotide sequenc
972	6	2.4	120	22	AAI26289	Probe #16222 for g
973	6	2.4	120	22	AAI54478	Probe #23164 used
974	6	2.4	120	24	ABS22396	Human genome-deriv
c 975	6	2.4	123	24	ABN69729	Streptococcus poly
c 976	6	2.4	124	18	AAV79086	Staphylococcus aur
977	6	2.4	125	20	AAH86956	Human single nucle
978	6	2.4	129	21	AAC29030	Human secreted pro
979	6	2.4	131	19	AAX12762	Human biallelic po
980	6	2.4	131	20	AAH86528	Human single nucle
981	6	2.4	131	22	AAS33505	Human cDNA encodin
c 982	6	2.4	131	22	AAS37743	Novel human diagno
c 983	6	2.4	133	21	AAA58232	D. immitis ankyrin
984	6	2.4	133	21	AAA58233	D. immitis ankyrin
c 985	6	2.4	133	22	ABA51094	Human breast cell
c 986	6	2.4	133	22	ABA69088	Human foetal liver
c 987	6	2.4	133	22	ABA36029	Probe #14495 for g
c 988	6	2.4	133	22	AAK17400	Human brain expres
c 989	6	2.4	133	22	AAK43197	Human bone marrow
c 990	6	2.4	133	22	AAI23974	Probe #13907 for g
c 991	6	2.4	133	22	AAI49274	Probe #17960 used
c 992	6	2.4	133	22	AAI09564	Probe #9555 used t
c 993	6	2.4	133	24	ABS17278	Human genome-deriv
c 994	6	2.4	133	24	AAL37918	Dirofilaria immiti
995	6	2.4	133	24	AAL37919	Complement strand
c 996	6	2.4	134	15	AAQ77387	Human genome fragm
997	6	2.4	136	19	AAV19191	Human XAG growth f
c 998	6	2.4	136	22	ABA51335	Human breast cell
c 999	6	2.4	136	22	ABA69346	Human foetal liver
c1000	6	2.4	136	22	ABA36276	Probe #14742 for g

ALIGNMENTS

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RESULT 1
AAA97594
ID   AAA97594 standard; cDNA; 741 BP.
XX
AC   AAA97594;
XX
DT   02-FEB-2001  (first entry)
XX
DE   Human stanniocalcin cDNA.
XX
KW   Human; stanniocalcin; STC; osteogenesis; bone disease; osteoporosis;
KW   mineral metabolism regulator; prophylaxis; therapy; ss.
XX
OS   Homo sapiens.
XX
PN   JP2000229880-A.
XX
PD   22-AUG-2000.
XX
PF   10-FEB-1999;   99JP-0033262.
XX
PR   10-FEB-1999;   99JP-0033262.
XX
PA   (SNOW ) SNOW BRAND MILK PROD CO LTD.
XX
DR   WPI; 2000-605236/58.
DR   P-PSDB; AAB23264.
XX
PT   An osteogenesis promoter useful in the prevention and/or treatment of
PT   bone diseases such as osteoporosis -
XX
PS   Example 1; Page 4-5; 6pp; Japanese.
XX
CC   The invention relates to a novel osteogenesis-promoting composition
CC   which contains stanniocalcin (STC) as the active component.
CC   Stanniocalcin is a possible regulator of mineral metabolism. The
CC   composition is useful as a prophylactic and/or therapeutic agent for
CC   bone diseases such as osteoporosis. The present sequence represents
CC   cDNA encoding human stanniocalcin which was used in an exemplification
CC   of the invention.
XX
SQ   Sequence 741 BP; 201 A; 209 C; 183 G; 148 T; 0 other;

Alignment Scores:
Pred. No.:                2.91e-246      Length:          741
Score:                    247.00         Matches:         247
Percent Similarity:       100.00%        Conservative:    0
Best Local Similarity:    100.00%        Mismatches:      0
Query Match:              100.00%        Indels:          0
DB:                       21             Gaps:            0

US-09-705-500A-3 (1-247) x AAA97594 (1-741)

Qy          1 MetLeuGlnAsnSerAlaValLeuLeuValLeuValIleSerAlaSerAlaThrHisGlu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGCTCCAAAACTCAGCAGTGCTTCTGGTGCTGGTGATCAGTGCTTCTGCAACCCATGAG 60

Qy         21 AlaGluGlnAsnAspSerValSerProArgLysSerArgValAlaAlaGlnAsnSerAla 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GCGGAGCAGAATGACTCTGTGAGCCCCAGGAAATCCCGAGTGGCGGCCCAAAACTCAGCT 120

Qy         41 GluValValArgCysLeuAsnSerAlaLeuGlnValGlyCysGlyAlaPheAlaCysLeu 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GAAGTGGTTCGTTGCCTCAACAGTGCTCTACAGGTCGGCTGCGGGGCTTTTGCATGCCTG 180

Qy         61 GluAsnSerThrCysAspThrAspGlyMetTyrAspIleCysLysSerPheLeuTyrSer 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GAAAACTCCACCTGTGACACAGATGGGATGTATGACATCTGTAAATCCTTCTTGTACAGC 240

Qy         81 AlaAlaLysPheAspThrGlnGlyLysAlaPheValLysGluSerLeuLysCysIleAla 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GCTGCTAAATTTGACACTCAGGGAAAAGCATTCGTCAAAGAGAGCTTAAAATGCATCGCC 300

Qy        101 AsnGlyValThrSerLysValPheLeuAlaIleArgArgCysSerThrPheGlnArgMet 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 AACGGGGTCACCTCCAAGGTCTTCCTCGCCATTCGGAGGTGCTCCACTTTCCAAAGGATG 360

Qy        121 IleAlaGluValGlnGluGluCysTyrSerLysLeuAsnValCysSerIleAlaLysArg 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 ATTGCTGAGGTGCAGGAAGAGTGCTACAGCAAGCTGAATGTGTGCAGCATCGCCAAGCGG 420

Qy        141 AsnProGluAlaIleThrGluValValGlnLeuProAsnHisPheSerAsnArgTyrTyr 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 AACCCTGAAGCCATCACTGAGGTCGTCCAGCTGCCCAATCACTTCTCCAACAGATACTAT 480
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Qy        161 AsnArgLeuValArgSerLeuLeuGluCysAspGluAspThrValSerThrIleArgAsp 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 AACAGACTTGTCCGAAGCCTGCTGGAATGTGATGAAGACACAGTCAGCACAATCAGAGAC 540

Qy        181 SerLeuMetGluLysIleGlyProAsnMetAlaSerLeuPheHisIleLeuGlnThrAsp 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 AGCCTGATGGAGAAAATTGGGCCTAACATGGCCAGCCTCTTCCACATCCTGCAGACAGAC 600

Qy        201 HisCysAlaGlnThrHisProArgAlaAspPheAsnArgArgArgThrAsnGluProGln 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CACTGTGCCCAAACACACCCACGAGCTGACTTCAACAGGAGACGCACCAATGAGCCGCAG 660

Qy        221 LysLeuLysValLeuLeuArgAsnLeuArgGlyGluGluAspSerProSerHisIleLys 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 AAGCTGAAAGTCCTCCTCAGGAACCTCCGAGGTGAGGAGGACTCTCCCTCCCACATCAAA 720

Qy        241 ArgThrSerHisGluSerAla 247
              ||||||||||||||||||||
Db        721 CGCACATCCCATGAGAGTGCA 741
```

RESULT 2
AAA11145
ID AAA11145 standard; cDNA; 741 BP.
XX
AC AAA11145;
XX
DT 26-SEP-2000 (first entry)
XX
DE Human stanniocalcin coding sequence.
XX
KW PCR primer; human; stanniocalcin; inhibitor; differentiation; maturation;
KW adipocyte; obesity; diabetes; hypertension; heart disease; ss.
XX
OS Homo sapiens.
XX
PN WO200016795-A1.
XX
PD 30-MAR-2000.
XX
PF 17-SEP-1999; 99WO-JP05080.
XX
PR 17-SEP-1998; 98JP-0263004.
XX
PA (SNOW) SNOW BRAND MILK PROD CO LTD.
XX
PI Goto M, Tomoyasu A, Yamaguchi K, Kinosaki M, Nakagawa N;
XX
DR WPI; 2000-283445/24.
DR P-PSDB; AAY92901.
XX
PT Treating or preventing obesity, which is a risk factor for diabetes,
PT hypertension and heart disease, comprises administering an agent
PT containing stanniocalcin -
XX
PS Example 1; Page 14-15; 19pp; Japanese.
XX
CC This sequence represents the coding sequence for the human stanniocalcin
CC protein. The stanniocalcin gene was isolated from IMR-90 cells.
CC Stanniocalcin is an inhibitor of the differentiation and maturation of
CC adipocytes. The protein is used for preventing and treating obesity which
CC is a risk factor for diabetes, hypertension, and heart disease.
XX
SQ Sequence 741 BP; 201 A; 209 C; 183 G; 148 T; 0 other;

Alignment Scores:

Pred. No.:	2.91e-246	Length:	741
Score:	247.00	Matches:	247
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	21	Gaps:	0

US-09-705-500A-3 (1-247) x AAA11145 (1-741)

```
Qy          1 MetLeuGlnAsnSerAlaValLeuLeuValLeuValIleSerAlaSerAlaThrHisGlu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGCTCCAAAACTCAGCAGTGCTTCTGGTGCTGGTGATCAGTGCTTCTGCAACCCATGAG 60

Qy         21 AlaGluGlnAsnAspSerValSerProArgLysSerArgValAlaAlaGlnAsnSerAla 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GCGGAGCAGAATGACTCTGTGAGCCCCAGGAAATCCCGAGTGGCGGCCCAAAACTCAGCT 120

Qy         41 GluValValArgCysLeuAsnSerAlaLeuGlnValGlyCysGlyAlaPheAlaCysLeu 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GAAGTGGTTCGTTGCCTCAACAGTGCTCTACAGGTCGGCTGCGGGGCTTTTGCATGCCTG 180

Qy         61 GluAsnSerThrCysAspThrAspGlyMetTyrAspIleCysLysSerPheLeuTyrSer 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GAAAACTCCACCTGTGACACAGATGGGATGTATGACATCTGTAAATCCTTCTTGTACAGC 240

Qy         81 AlaAlaLysPheAspThrGlnGlyLysAlaPheValLysGluSerLeuLysCysIleAla 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GCTGCTAAATTTGACACTCAGGGAAAAGCATTCGTCAAAGAGAGCTTAAAATGCATCGCC 300

Qy        101 AsnGlyValThrSerLysValPheLeuAlaIleArgArgCysSerThrPheGlnArgMet 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 AACGGGGTCACCTCCAAGGTCTTCCTCGCCATTCGGAGGTGCTCCACTTTCCAAAGGATG 360

Qy        121 IleAlaGluValGlnGluGluCysTyrSerLysLeuAsnValCysSerIleAlaLysArg 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 ATTGCTGAGGTGCAGGAAGAGTGCTACAGCAAGCTGAATGTGTGCAGCATCGCCAAGCGG 420

Qy        141 AsnProGluAlaIleThrGluValValGlnLeuProAsnHisPheSerAsnArgTyrTyr 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 AACCCTGAAGCCATCACTGAGGTCGTCCAGCTGCCCAATCACTTCTCCAACAGATACTAT 480

Qy        161 AsnArgLeuValArgSerLeuLeuGluCysAspGluAspThrValSerThrIleArgAsp 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 AACAGACTTGTCCGAAGCCTGCTGGAATGTGATGAAGACACAGTCAGCACAATCAGAGAC 540

Qy        181 SerLeuMetGluLysIleGlyProAsnMetAlaSerLeuPheHisIleLeuGlnThrAsp 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 AGCCTGATGGAGAAAATTGGGCCTAACATGGCCAGCCTCTTCCACATCCTGCAGACAGAC 600

Qy        201 HisCysAlaGlnThrHisProArgAlaAspPheAsnArgArgArgThrAsnGluProGln 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CACTGTGCCCAAACACACCCACGAGCTGACTTCAACAGGAGACGCACCAATGAGCCGCAG 660

Qy        221 LysLeuLysValLeuLeuArgAsnLeuArgGlyGluGluAspSerProSerHisIleLys 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 AAGCTGAAAGTCCTCCTCAGGAACCTCCGAGGTGAGGAGGACTCTCCCTCCCACATCAAA 720

Qy        241 ArgThrSerHisGluSerAla 247
              ||||||||||||||||||||
Db        721 CGCACATCCCATGAGAGTGCA 741
```

RESULT 3
ABL40225
ID ABL40225 standard; cDNA; 744 BP.
XX
AC ABL40225;
XX
DT 23-MAY-2002 (first entry)
XX
DE Human staniocalcin 1 encoding cDNA.
XX
KW Human; staniocalcin 1; osteopathic; osteogenesis failure; osteoporosis;
KW bone mass reduction; traumatic bone injury; osteomalacia; bone disease;
KW rheumatic bone disease; cancer associated bone disease; rachitis;
KW arthritis deformans; gene; ss.
XX
OS Homo sapiens.
XX
FH Key   Location/Qualifiers
FT CDS   1..744
FT   /*tag= a

```
FT                   /product= "staniocalcin 1"
XX
PN   WO200204013-A1.
XX
PD   17-JAN-2002.
XX
PF   10-JUL-2001; 2001WO-JP05962.
XX
PR   11-JUL-2000; 2000JP-0209926.
XX
PA   (BMLB-) BML INC.
XX
PI   Yoshiko Y,  Koide Y,  Igarashi A,  Takano S,  Maeda N,  Aubin JE;
XX
DR   WPI; 2002-164600/21.
DR   P-PSDB; ABB06259.
XX
PT   Agent used for treating bone diseases e.g. osteoporosis, traumatic bone
PT   injury, osteomalacia, rheumatic bone diseases, bone diseases associated
PT   with cancer and arthritis deformans containing staniocalcin I -
XX
PS   Claim 2; Fig 1; 24pp; Japanese.
XX
CC   The present invention describes an agent containing staniocalcin 1,
CC   particularly of human origin. Staniocalcin 1 has osteopathic activity.
CC   The agent can be used for treating diseases relating to osteogenesis
CC   failure or reduction in bone mass e.g. osteoporosis, traumatic bone
CC   injury, osteomalacia, rheumatic bone diseases, bone diseases associated
CC   with cancer, bone diseases due to phosphorus or calcium metabolic error,
CC   rachitis and arthritis deformans. The agent increases bone mass. The
CC   present sequence encodes human staniocalcin 1.
XX
SQ   Sequence 744 BP; 203 A; 209 C; 183 G; 149 T; 0 other;

Alignment Scores:
Pred. No.:                2.92e-246      Length:          744
Score:                    247.00         Matches:         247
Percent Similarity:       100.00%        Conservative:    0
Best Local Similarity:    100.00%        Mismatches:      0
Query Match:              100.00%        Indels:          0
DB:                       24             Gaps:            0

US-09-705-500A-3 (1-247) x ABL40225 (1-744)

Qy          1 MetLeuGlnAsnSerAlaValLeuLeuValLeuValIleSerAlaSerAlaThrHisGlu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGCTCCAAAACTCAGCAGTGCTTCTGGTGCTGGTGATCAGTGCTTCTGCAACCCATGAG 60

Qy         21 AlaGluGlnAsnAspSerValSerProArgLysSerArgValAlaAlaGlnAsnSerAla 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GCGGAGCAGAATGACTCTGTGAGCCCCAGGAAATCCCGAGTGGCGGCCCAAAACTCAGCT 120

Qy         41 GluValValArgCysLeuAsnSerAlaLeuGlnValGlyCysGlyAlaPheAlaCysLeu 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GAAGTGGTTCGTTGCCTCAACAGTGCTCTACAGGTCGGCTGCGGGGCTTTTGCATGCCTG 180

Qy         61 GluAsnSerThrCysAspThrAspGlyMetTyrAspIleCysLysSerPheLeuTyrSer 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GAAAACTCCACCTGTGACACAGATGGGATGTATGACATCTGTAAATCCTTCTTGTACAGC 240

Qy         81 AlaAlaLysPheAspThrGlnGlyLysAlaPheValLysGluSerLeuLysCysIleAla 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GCTGCTAAATTTGACACTCAGGGAAAAGCATTCGTCAAAGAGAGCTTAAAATGCATCGCC 300

Qy        101 AsnGlyValThrSerLysValPheLeuAlaIleArgArgCysSerThrPheGlnArgMet 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 AACGGGGTCACCTCCAAGGTCTTCCTCGCCATTCGGAGGTGCTCCACTTTCCAAAGGATG 360

Qy        121 IleAlaGluValGlnGluGluCysTyrSerLysLeuAsnValCysSerIleAlaLysArg 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 ATTGCTGAGGTGCAGGAAGAGTGCTACAGCAAGCTGAATGTGTGCAGCATCGCCAAGCGG 420

Qy        141 AsnProGluAlaIleThrGluValValGlnLeuProAsnHisPheSerAsnArgTyrTyr 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 AACCCTGAAGCCATCACTGAGGTCGTCCAGCTGCCCAATCACTTCTCCAACAGATACTAT 480

Qy        161 AsnArgLeuValArgSerLeuLeuGluCysAspGluAspThrValSerThrIleArgAsp 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 AACAGACTTGTCCGAAGCCTGCTGGAATGTGATGAAGACACAGTCAGCACAATCAGAGAC 540

Qy        181 SerLeuMetGluLysIleGlyProAsnMetAlaSerLeuPheHisIleLeuGlnThrAsp 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 AGCCTGATGGAGAAAATTGGGCCTAACATGGCCAGCCTCTTCCACATCCTGCAGACAGAC 600

Qy        201 HisCysAlaGlnThrHisProArgAlaAspPheAsnArgArgArgThrAsnGluProGln 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CACTGTGCCCAAACACACCCACGAGCTGACTTCAACAGGAGACGCACCAATGAGCCGCAG 660

Qy        221 LysLeuLysValLeuLeuArgAsnLeuArgGlyGluGluAspSerProSerHisIleLys 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 AAGCTGAAAGTCCTCCTCAGGAACCTCCGAGGTGAGGAGGACTCTCCCTCCCACATCAAA 720

Qy        241 ArgThrSerHisGluSerAla 247
              |||||||||||||||||||||
Db        721 CGCACATCCCATGAGAGTGCA 741

RESULT 4
AAT02438
ID   AAT02438 standard; cDNA; 771 BP.
XX
AC   AAT02438;
XX
DT   19-APR-1996  (first entry)
XX
DE   cDNA encoding stanniocalcin from Corpuscles of Stannius.
XX
KW   stanniocalcin; Corpuscles of Stannius; hypocalcaemia; hypercalcaemia;
KW   electrolyte disorder; osteoporosis; Paget's disease; treatment; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             16..759
FT                   /*tag=  a
FT                   /product= prepro-stanniocalcin
FT   mat_peptide     115..757
FT                   /*tag=  b
FT                   /product= mature stannicalcin
FT   misc_feature    16..114
FT                   /*tag=  c
FT                   /note= "encodes prepro region"
XX
PN   WO9524411-A1.
XX
PD   14-SEP-1995.
XX
PF   09-MAY-1994;   94WO-US05136.
XX
PR   08-MAR-1994;   94US-0208005.
XX
PA   (HUMA-) HUMAN GENOME SCI INC.
XX
PI   Adams MD,  Olsen H;
XX
DR   WPI; 1995-328227/42.
DR   P-PSDB; AAR84522.
XX
PT   Human corpuscles of Stannius polypeptide(s) - used to treat
PT   hypercalcaemia, hypocalcaemia and other electrolyte disorders
XX
PS   Claim 1; Fig 1; 41pp; English.
XX
CC   The cDNA encodes a stanniocalcin, a Corpuscles of Stannius polypeptide.
CC   Stanniocalcin functions as a hypocalcaemic agent, and can be used for
CC   the treatment of e.g. electrolyte disorders which lead to renal, bone
CC   and heart diseases, hypertension, hypercalcaemia and disorders due to
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CC   elevated bone resorption, e.g. osteoporosis and Paget's disease.
XX
SQ   Sequence 771 BP; 212 A; 214 C; 192 G; 153 T; 0 other;

Alignment Scores:
Pred. No.:              3.02e-246      Length:         771
Score:                  247.00         Matches:        247
Percent Similarity:     100.00%        Conservative:   0
Best Local Similarity:  100.00%        Mismatches:     0
Query Match:            100.00%        Indels:         0
DB:                     16             Gaps:           0

US-09-705-500A-3 (1-247) x AAT02438 (1-771)

Qy          1 MetLeuGlnAsnSerAlaValLeuLeuValLeuValIleSerAlaSerAlaThrHisGlu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         16 ATGCTCCAAAACTCAGCAGTGCTTCTGGTGCTGGTGATCAGTGCTTCTGCAACCCATGAG 75

Qy         21 AlaGluGlnAsnAspSerValSerProArgLysSerArgValAlaAlaGlnAsnSerAla 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         76 GCGGAGCAGAATGACTCTGTGAGCCCCAGGAAATCCCGAGTGGCGGCCCAAAACTCAGCT 135

Qy         41 GluValValArgCysLeuAsnSerAlaLeuGlnValGlyCysGlyAlaPheAlaCysLeu 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        136 GAAGTGGTTCGTTGCCTCAACAGTGCTCTACAGGTCGGCTGCGGGGCTTTTGCATGCCTG 195

Qy         61 GluAsnSerThrCysAspThrAspGlyMetTyrAspIleCysLysSerPheLeuTyrSer 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        196 GAAAACTCCACCTGTGACACAGATGGGATGTATGACATCTGTAAATCCTTCTTGTACAGC 255

Qy         81 AlaAlaLysPheAspThrGlnGlyLysAlaPheValLysGluSerLeuLysCysIleAla 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        256 GCTGCTAAATTTGACACTCAGGGAAAAGCATTCGTCAAAGAGAGCTTAAAATGCATCGCC 315

Qy        101 AsnGlyValThrSerLysValPheLeuAlaIleArgArgCysSerThrPheGlnArgMet 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        316 AACGGGGTCACCTCCAAGGTCTTCCTCGCCATTCGGAGGTGCTCCACTTTCCAAAGGATG 375

Qy        121 IleAlaGluValGlnGluGluCysTyrSerLysLeuAsnValCysSerIleAlaLysArg 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        376 ATTGCTGAGGTGCAGGAAGAGTGCTACAGCAAGCTGAATGTGTGCAGCATCGCCAAGCGG 435

Qy        141 AsnProGluAlaIleThrGluValValGlnLeuProAsnHisPheSerAsnArgTyrTyr 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        436 AACCCTGAAGCCATCACTGAGGTCGTCCAGCTGCCCAATCACTTCTCCAACAGATACTAT 495

Qy        161 AsnArgLeuValArgSerLeuLeuGluCysAspGluAspThrValSerThrIleArgAsp 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        496 AACAGACTTGTCCGAAGCCTGCTGGAATGTGATGAAGACACAGTCAGCACAATCAGAGAC 555

Qy        181 SerLeuMetGluLysIleGlyProAsnMetAlaSerLeuPheHisIleLeuGlnThrAsp 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        556 AGCCTGATGGAGAAAATTGGGCCTAACATGGCCAGCCTCTTCCACATCCTGCAGACAGAC 615

Qy        201 HisCysAlaGlnThrHisProArgAlaAspPheAsnArgArgArgThrAsnGluProGln 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        616 CACTGTGCCCAAACACACCCACGAGCTGACTTCAACAGGAGACGCACCAATGAGCCGCAG 675

Qy        221 LysLeuLysValLeuLeuArgAsnLeuArgGlyGluGluAspSerProSerHisIleLys 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        676 AAGCTGAAAGTCCTCCTCAGGAACCTCCGAGGTGAGGAGGACTCTCCCTCCCACATCAAA 735

Qy        241 ArgThrSerHisGluSerAla 247
              ||||||||||||||||||||
Db        736 CGCACATCCCATGAGAGTGCA 756

RESULT 5
AAZ39520
ID   AAZ39520 standard; cDNA; 771 BP.
XX
AC   AAZ39520;
XX
DT   11-FEB-2000  (first entry)
XX
DE   Human corpuscles of stanius polypeptide encoding cDNA.
XX
KW   Corpuscles of stanius polypeptide; calcium; inhibition; human; renal;
KW   therapeutic; bone; heart disease; hypocalcemia; osteoperosis; ss.
XX
OS   Homo sapiens.
XX
PN   US5994301-A.
XX
PD   30-NOV-1999.
XX
PF   28-APR-1995;   95US-0431117.
XX
PR   08-MAR-1994;   94US-0208005.
XX
PA   (HUMA-) HUMAN GENOME SCI INC.
XX
PI   Adams MD,  Olsen HS;
XX
DR   WPI; 2000-038269/03.
DR   P-PSDB; AAY57166.
XX
PT   Human corpuscles of stanius polypeptides used to inhibit calcium uptake
PT   -
XX
PS   Disclosure; Fig 1A-B; 23pp; English.
XX
CC   This cDNA encodes a human corpuscles of stanius polypeptide, having a
CC   calcium uptake inhibitory activity. The cDNA is deposited under the
CC   accession number ATCC Deposit No. 75652. The polypeptide can be used in a
CC   method for the treatment of a patient having need to inhibit uptake of
CC   calcium. The method is also used for the therapeutic treatment of renal,
CC   bone, and heart diseases, and the antagonist (may be an antibody) may be
CC   used for treating hypocalcemia., and osteoperosis.
XX
SQ   Sequence 771 BP; 212 A; 214 C; 192 G; 153 T; 0 other;

Alignment Scores:
Pred. No.:              3.02e-246      Length:         771
Score:                  247.00         Matches:        247
Percent Similarity:     100.00%        Conservative:   0
Best Local Similarity:  100.00%        Mismatches:     0
Query Match:            100.00%        Indels:         0
DB:                     21             Gaps:           0

US-09-705-500A-3 (1-247) x AAZ39520 (1-771)

Qy          1 MetLeuGlnAsnSerAlaValLeuLeuValLeuValIleSerAlaSerAlaThrHisGlu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         16 ATGCTCCAAAACTCAGCAGTGCTTCTGGTGCTGGTGATCAGTGCTTCTGCAACCCATGAG 75

Qy         21 AlaGluGlnAsnAspSerValSerProArgLysSerArgValAlaAlaGlnAsnSerAla 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         76 GCGGAGCAGAATGACTCTGTGAGCCCCAGGAAATCCCGAGTGGCGGCCCAAAACTCAGCT 135

Qy         41 GluValValArgCysLeuAsnSerAlaLeuGlnValGlyCysGlyAlaPheAlaCysLeu 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        136 GAAGTGGTTCGTTGCCTCAACAGTGCTCTACAGGTCGGCTGCGGGGCTTTTGCATGCCTG 195

Qy         61 GluAsnSerThrCysAspThrAspGlyMetTyrAspIleCysLysSerPheLeuTyrSer 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        196 GAAAACTCCACCTGTGACACAGATGGGATGTATGACATCTGTAAATCCTTCTTGTACAGC 255

Qy         81 AlaAlaLysPheAspThrGlnGlyLysAlaPheValLysGluSerLeuLysCysIleAla 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        256 GCTGCTAAATTTGACACTCAGGGAAAAGCATTCGTCAAAGAGAGCTTAAAATGCATCGCC 315

Qy        101 AsnGlyValThrSerLysValPheLeuAlaIleArgArgCysSerThrPheGlnArgMet 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        316 AACGGGGTCACCTCCAAGGTCTTCCTCGCCATTCGGAGGTGCTCCACTTTCCAAAGGATG 375

Qy        121 IleAlaGluValGlnGluGluCysTyrSerLysLeuAsnValCysSerIleAlaLysArg 140
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                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        376 ATTGCTGAGGTGCAGGAAGAGTGCTACAGCAAGCTGAATGTGTGCAGCATCGCCAAGCGG 435

Qy        141 AsnProGluAlaIleThrGluValValGlnLeuProAsnHisPheSerAsnArgTyrTyr 160
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        436 AACCCTGAAGCCATCACTGAGGTCGTCCAGCTGCCCAATCACTTCTCCAACAGATACTAT 495

Qy        161 AsnArgLeuValArgSerLeuLeuGluCysAspGluAspThrValSerThrIleArgAsp 180
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        496 AACAGACTTGTCCGAAGCCTGCTGGAATGTGATGAAGACACAGTCAGCACAATCAGAGAC 555

Qy        181 SerLeuMetGluLysIleGlyProAsnMetAlaSerLeuPheHisIleLeuGlnThrAsp 200
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        556 AGCCTGATGGAGAAAATTGGGCCTAACATGGCCAGCCTCTTCCACATCCTGCAGACAGAC 615

Qy        201 HisCysAlaGlnThrHisProArgAlaAspPheAsnArgArgArgThrAsnGluProGln 220
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        616 CACTGTGCCCAAACACACCCACGAGCTGACTTCAACAGGAGACGCACCAATGAGCCGCAG 675

Qy        221 LysLeuLysValLeuLeuArgAsnLeuArgGlyGluGluAspSerProSerHisIleLys 240
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        676 AAGCTGAAAGTCCTCCTCAGGAACCTCCGAGGTGAGGAGGACTCTCCCTCCCACATCAAA 735

Qy        241 ArgThrSerHisGluSerAla 247
                |||||||||||||||||||
Db        736 CGCACATCCCATGAGAGTGCA 756

RESULT 6
AAF83297
ID   AAF83297 standard; cDNA; 1283 BP.
XX
AC   AAF83297;
XX
DT   09-JUL-2001  (first entry)
XX
DE   Human stanniocalcin (STC) protein encoding cDNA.
XX
KW   Stanniocalcin; STC; neuroprotective; antiinflammatory; antianemic;
KW   antirheumatic; antiarthritic; dermatological; antiallergic; human;
KW   nephrotropic; antithyroid; immunosuppressive; antidiabetic; vulnerary;
KW   antiasthmatic; hemostatic; antiarrhythmic; vasotropic; antipsoriatic;
KW   antitumor; anti HIV; antiparkinsonian; nootropic; cell proliferation;
KW   hemostatic; thrombolytic; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             45..788
FT                   /*tag=  a
FT                   /product= "stanniocalcin"
XX
PN   WO200130969-A2.
XX
PD   03-MAY-2001.
XX
PF   20-OCT-2000; 2000WO-US29432.
XX
PR   27-OCT-1999;   99US-0161740.
XX
PA   (HUMA-) HUMAN GENOME SCI INC.
PA   (UYHE-) UNIV HELSINKI.
XX
PI   Olsen HS,  Zhang K,  Lindsberg P,  Tatlisumak T,  Kaste M;
PI   Andersson LC;
XX
DR   WPI; 2001-308626/32.
DR   P-PSDB; AAB62473.
XX
PT   Novel composition useful for treating or protecting neural cells, for
PT   treating Addison's disease, organ rejection, hyperproliferative
PT   disorder, cancer, AIDS, multiple sclerosis, comprises stanniocalcin
PT   polypeptide  -
XX
PS   Example 2; Fig 1A-C; 253pp; English.
XX
CC   The invention relates to a human stanniocalcin (STC) polypeptide. A
CC   pharmaceutical composition comprising the STC is useful for treating a
CC   patient in need of increased levels of STC activity. STC and its
CC   modulators are useful for treating disorders or abnormalities of nervous
CC   system, cerebrovascular diseases, dementia, encephalitis, central
CC   nervous system infections or neoplasms, demyelinating diseases,
CC   encephalomyelitis, spinal cord diseases, mental retardation such as
CC   Down's syndrome, Tay-Sachs disease, neuromuscular diseases such as
CC   muscular dystrophy, myasthenia gravis, deficiencies or disorders of
CC   immune system such as Addison's disease, hemolytic anemia, rheumatoid
CC   arthritis, dermatitis, glomerulonephritis, Goodpasture's Syndrome,
CC   Grave's disease, multiple sclerosis, autoimmune thyroiditis, systemic
CC   lupus erythematosus, insulin dependent diabetes mellitus, allergic
CC   reactions and conditions such as asthma, for treating and/or preventing
CC   organ rejection or graft-versus-host disease, hyperproliferative diseases
CC   such as purpura, Gaucher's disease, cardiovascular disorders such as
CC   arrhythmias, telangiectasia, vasculitis, and for treatment of disease or
CC   disorders with neovascularization. The composition can be used to treat
CC   hemangioma, psoriasis, angiofibroma, atherosclerotic plaques, delayed
CC   wound healing, granulations, Osler-Weber syndrome, solid tumors such as
CC   Kaposi's sarcoma, cancer, AIDS, neurodegenerative disorders such as
CC   Alzheimer's disease, Parkinson's disease, wound healing, and for treating
CC   or detecting infectious agents. The present sequence represents a cDNA
CC   encoding the human STC polypeptide.
XX
SQ   Sequence 1283 BP; 379 A; 327 C; 273 G; 301 T; 3 other;

Alignment Scores:
Pred. No.:              4.93e-246       Length:         1283
Score:                  247.00          Matches:        247
Percent Similarity:     100.00%         Conservative:   0
Best Local Similarity:  100.00%         Mismatches:     0
Query Match:            100.00%         Indels:         0
DB:                     22              Gaps:           0

US-09-705-500A-3 (1-247) x AAF83297 (1-1283)

Qy          1 MetLeuGlnAsnSerAlaValLeuLeuValLeuValIleSerAlaSerAlaThrHisGlu 20
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         45 ATGCTCCAAAACTCAGCAGTGCTTCTGGTGCTGGTGATCAGTGCTTCTGCAACCCATGAG 104

Qy         21 AlaGluGlnAsnAspSerValSerProArgLysSerArgValAlaAlaGlnAsnSerAla 40
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        105 GCGGAGCAGAATGACTCTGTGAGCCCCAGGAAATCCCGAGTGGCGGCCCAAAACTCAGCT 164

Qy         41 GluValValArgCysLeuAsnSerAlaLeuGlnValGlyCysGlyAlaPheAlaCysLeu 60
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        165 GAAGTGGTTCGTTGCCTCAACAGTGCTCTACAGGTCGGCTGCGGGGCTTTTGCATGCCTG 224

Qy         61 GluAsnSerThrCysAspThrAspGlyMetTyrAspIleCysLysSerPheLeuTyrSer 80
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        225 GAAAACTCCACCTGTGACACAGATGGGATGTATGACATCTGTAAATCCTTCTTGTACAGC 284

Qy         81 AlaAlaLysPheAspThrGlnGlyLysAlaPheValLysGluSerLeuLysCysIleAla 100
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        285 GCTGCTAAATTTGACACTCAGGGAAAAGCATTCGTCAAAGAGAGCTTAAAATGCATCGCC 344

Qy        101 AsnGlyValThrSerLysValPheLeuAlaIleArgArgCysSerThrPheGlnArgMet 120
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        345 AACGGGGTCACCTCCAAGGTCTTCCTCGCCATTCGGAGGTGCTCCACTTTCCAAAGGATG 404

Qy        121 IleAlaGluValGlnGluGluCysTyrSerLysLeuAsnValCysSerIleAlaLysArg 140
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        405 ATTGCTGAGGTGCAGGAAGAGTGCTACAGCAAGCTGAATGTGTGCAGCATCGCCAAGCGG 464

Qy        141 AsnProGluAlaIleThrGluValValGlnLeuProAsnHisPheSerAsnArgTyrTyr 160
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        465 AACCCTGAAGCCATCACTGAGGTCGTCCAGCTGCCCAATCACTTCTCCAACAGATACTAT 524

Qy        161 AsnArgLeuValArgSerLeuLeuGluCysAspGluAspThrValSerThrIleArgAsp 180
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        525 AACAGACTTGTCCGAAGCCTGCTGGAATGTGATGAAGACACAGTCAGCACAATCAGAGAC 584

Qy        181 SerLeuMetGluLysIleGlyProAsnMetAlaSerLeuPheHisIleLeuGlnThrAsp 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        585 AGCCTGATGGAGAAAATTGGGCCTAACATGGCCAGCCTCTTCCACATCCTGCAGACAGAC 644

Qy        201 HisCysAlaGlnThrHisProArgAlaAspPheAsnArgArgArgThrAsnGluProGln 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        645 CACTGTGCCCAAACACACCCACGAGCTGACTTCAACAGGAGACGCACCAATGAGCCGCAG 704

Qy        221 LysLeuLysValLeuLeuArgAsnLeuArgGlyGluGluAspSerProSerHisIleLys 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        705 AAGCTGAAAGTCCTCCTCAGGAACCTCCGAGGTGAGGAGGACTCTCCCTCCCACATCAAA 764

Qy        241 ArgThrSerHisGluSerAla 247
              |||||||||||||||||||
Db        765 CGCACATCCCATGAGAGTGCA 785

RESULT 7
AAF83823
ID   AAF83823 standard; DNA; 3762 BP.
XX
AC   AAF83823;
XX
DT   06-AUG-2001  (first entry)
XX
DE   DNA encoding Lng108, a diagnostic marker for cancer.
XX
KW   Lng108; cancer; diagnostic marker; cytotoxic; immune response;
KW   imaging; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             174..917
FT                   /*tag=  a
FT                   /product= "Lng108"
XX
PN   WO200132209-A1.
XX
PD   10-MAY-2001.
XX
PF   03-NOV-2000; 2000WO-US30482.
XX
PR   04-NOV-1999;   99US-0163444.
XX
PA   (DIAD-) DIADEXUS INC.
XX
PI   Recipon H,  Macina RA,  Chen S,  Sun Y;
XX
DR   WPI; 2001-316386/33.
DR   P-PSDB; AAB62690.
XX
PT   Novel assay for diagnosing and monitoring cancer, involves determining
PT   levels of Lng108 in cells, tissues or bodily fluids of the patient, and
PT   comparing with control -
XX
PS   Disclosure; Page 31-33; 36pp; English.
XX
CC   The invention relates to diagnosing the presence of cancer or diagnosing
CC   metastases of cancer in a patient that involves determining levels of
CC   Lng108 in a sample of cells, tissues or bodily fluids in a patient, and
CC   comparing the determined levels with levels of Lng108 a normal human
CC   control.  The method is useful for diagnosing the presence of cancer,
CC   diagnosing metastases of cancer, staging cancer, monitoring cancer, and
CC   monitoring a change in stage of the cancer, in a patient. A therapeutic
CC   agent which is an antibody labeled with paramagnetic ions or a
CC   radioisotope, and conjugated with a cytotoxic agent is useful for imaging
CC   cancer in a patient. A molecule which downregulates the expression or
CC   activity of Lng108, is useful for treating cancer in a patient. Lng108
CC   protein is useful for inducing an immune response against a target cell
CC   expressing Lng108. The present sequence represents a DNA encoding the
CC   Lng108 polypeptide.
XX
SQ   Sequence 3762 BP; 1063 A; 865 C; 725 G; 1038 T; 71 other;

Alignment Scores:
Pred. No.:              1.39e-245      Length:          3762
Score:                  247.00         Matches:         247
Percent Similarity:     100.00%        Conservative:    0
Best Local Similarity:  100.00%        Mismatches:      0
Query Match:            100.00%        Indels:          0
DB:                     22             Gaps:            0

US-09-705-500A-3 (1-247) x AAF83823 (1-3762)

Qy          1 MetLeuGlnAsnSerAlaValLeuLeuValLeuValIleSerAlaSerAlaThrHisGlu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        174 ATGCTCCAAAACTCAGCAGTGCTTCTGGTGCTGGTGATCAGTGCTTCTGCAACCCATGAG 233

Qy         21 AlaGluGlnAsnAspSerValSerProArgLysSerArgValAlaAlaGlnAsnSerAla 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        234 GCGGAGCAGAATGACTCTGTGAGCCCCAGGAAATCCCGAGTGGCGGCTCAAAACTCAGCT 293

Qy         41 GluValValArgCysLeuAsnSerAlaLeuGlnValGlyCysGlyAlaPheAlaCysLeu 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        294 GAAGTGGTTCGTTGCCTCAACAGTGCTCTACAGGTCGGCTGCGGGGCTTTTGCATGCCTG 353

Qy         61 GluAsnSerThrCysAspThrAspGlyMetTyrAspIleCysLysSerPheLeuTyrSer 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        354 GAAAACTCCACCTGTGACACAGATGGGATGTATGACATCTGTAAATCCTTCTTGTACAGC 413

Qy         81 AlaAlaLysPheAspThrGlnGlyLysAlaPheValLysGluSerLeuLysCysIleAla 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        414 GCTGCTAAATTTGACACTCAGGGAAAAGCATTCGTCAAAGAGAGCTTAAAATGCATCGCC 473

Qy        101 AsnGlyValThrSerLysValPheLeuAlaIleArgArgCysSerThrPheGlnArgMet 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        474 AACGGGGTCACCTCCAAGGTCTTCCTCGCCATTCGGAGGTGCTCCACTTTCCAAAGGATG 533

Qy        121 IleAlaGluValGlnGluGluCysTyrSerLysLeuAsnValCysSerIleAlaLysArg 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        534 ATTGCTGAGGTGCAGGAAGAGTGCTACAGCAAGCTGAATGTGTGCAGCATCGCCAAGCGG 593

Qy        141 AsnProGluAlaIleThrGluValValGlnLeuProAsnHisPheSerAsnArgTyrTyr 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        594 AACCCTGAAGCCATCACTGAGGTCGTCCAGCTGCCCAATCACTTCTCCAACAGATACTAT 653

Qy        161 AsnArgLeuValArgSerLeuLeuGluCysAspGluAspThrValSerThrIleArgAsp 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        654 AACAGACTTGTCCGAAGCCTGCTGGAATGTGATGAAGACACAGTCAGCACAATCAGAGAC 713

Qy        181 SerLeuMetGluLysIleGlyProAsnMetAlaSerLeuPheHisIleLeuGlnThrAsp 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        714 AGCCTGATGGAGAAAATTGGGCCTAACATGGCCAGCCTCTTCCACATCCTGCAGACAGAC 773

Qy        201 HisCysAlaGlnThrHisProArgAlaAspPheAsnArgArgArgThrAsnGluProGln 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        774 CACTGTGCCCAAACACACCCACGAGCTGACTTCAACAGGAGACGCACCAATGAGCCGCAG 833

Qy        221 LysLeuLysValLeuLeuArgAsnLeuArgGlyGluGluAspSerProSerHisIleLys 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        834 AAGCTGAAAGTCCTCCTCAGGAACCTCCGAGGTGAGGAGGACTCTCCCTCCCACATCAAA 893

Qy        241 ArgThrSerHisGluSerAla 247
              |||||||||||||||||||
Db        894 CGCACATCCCATGAGAGTGCA 914

RESULT 8
AAF16051
ID   AAF16051 standard; cDNA; 2572 BP.
XX
AC   AAF16051;
XX
DT   13-MAR-2001  (first entry)
XX
```

```
DE   Human prostate cancer antigen nucleotide sequence SEQ ID NO:486.
XX
KW   Human; prostate cancer; prostate cancer antigen; detection; diagnosis;
KW   neuroprotective; cytostatic; cardioactive; immunomodulatory; muscular;
KW   vulnerary; gastrointestinal; nephrotropic; antiinfective; gynaecological;
KW   antibacterial; gene therapy; neural; immune; reproductive; renal;
KW   gastrointestinal; pulmonary; cardiovascular; proliferative disorder;
KW   wound; infectious disease; ss.
XX
OS   Homo sapiens.
XX
PN   WO200055174-A1.
XX
PD   21-SEP-2000.
XX
PF   08-MAR-2000; 2000WO-US05988.
XX
PR   12-MAR-1999;   99US-0124270.
XX
PA   (HUMA-) HUMAN GENOME SCI INC.
PA   (ROSE/) ROSEN C A.
XX
PI   Rosen CA,  Ruben SM;
XX
DR   WPI; 2000-587513/55.
DR   P-PSDB; AAB56848.
XX
PT   Prostate cancer associated gene sequences, referred to as prostate
PT   cancer antigens, useful for treatment, prevention, and diagnosis of
PT   disorders such as prostate cancer -
XX
PS   Claim 1; Page 956-957; 2338pp; English.
XX
CC   AAF15566 to AAF16505 encode the human prostate cancer associated
CC   proteins, called prostate cancer antigens, given in AAB56363 to AAB57302.
CC   The prostate cancer antigens can have neuroprotective, cytostatic,
CC   cardioactive, immunomodulatory, muscular, vulnerary, gastrointestinal,
CC   nephrotropic, antiinfective, gynaecological and antibacterial activities,
CC   and can be used in gene therapy. The prostate cancer antigen
CC   polynucleotides may be used for detection of prostate cancer, chromosome
CC   identification, as chromosome markers, and for numerous other diagnostic
CC   or research purposes. The prostate cancer antigens may be used to treat
CC   disorders such as neural, immune, muscular, reproductive,
CC   gastrointestinal, pulmonary, cardiovascular, renal, and proliferative
CC   disorders, wounds, and infectious diseases. AAF16506 to AAF16514 to
CC   AAB57303 represent sequences used in the exemplification of the present
CC   invention.
XX
SQ   Sequence 2572 BP; 746 A; 636 C; 539 G; 646 T; 5 other;

Alignment Scores:
Pred. No.:              1.81e-180      Length:         2572
Score:                  184.00         Matches:        246
Percent Similarity:     98.80%         Conservative:   0
Best Local Similarity:  98.80%         Mismatches:     1
Query Match:            74.49%         Indels:         3
DB:                     21             Gaps:           0

US-09-705-500A-3 (1-247) x AAF16051 (1-2572)

Qy          1 MetLeuGlnAsnSerAlaValLeuLeuValLeuValIleSerAlaSerAlaThrHisGlu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        265 ATGCTCCAAAACTCAGCAGTGCTTCTGGTGCTGGTGATCAGTGCTTCTGCAACCCATGAG 324

Qy         21 AlaGluGlnAsnAspSerValSerProArgLysSerArgValAlaAlaGlnAsnSerAla 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        325 GCGGAGCAGAATGACTCTGTGAGCCCCAGGAAATCCCGAGTGGCGGCTCAAAACTCAGCT 384

Qy         41 GluValValArgCysLeuAsnSerAlaLeuGlnValGlyCysGlyAlaPheAlaCysLeu 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        385 GAAGTGGTTCGTTGCCTCAACAGTGCTCTACAGGTCGGCTGCGGGGCTTTTGCATGCCTG 444

Qy         61 GluAsnSerThrCysAspThrAspGlyMetTyrAspIleCysLysSerPheLeuTyrSer 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        445 GAAAACTCCACCTGTGACACAGATGGGATGTATGACATCTGTAAATCCTTCTTGTACAGC 504

Qy         81 AlaAlaLysPheAspThrGlnGlyLysAlaPheValLysGluSerLeuLysCysIleAla 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        505 GCTGCTAAATTTGACACTCAGGGAAAAGCATTCGTCAAAGAGAGCTTAAAATGCATCGCC 564

Qy        101 AsnGlyValThrSerLysValPheLeuAlaIleArgArgCysSerThrPheGlnArgMet 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        565 AACGGGGTCACCTCCAAGGTCTTCCTCGCCATTCGGAGGTGCTCCACTTTCCAAAGGATG 624

Qy        121 IleAlaGluValGlnGluGluCysTyrSerLysLeuAsnValCysSerIleAlaLysArg 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        625 ATTGCTGAGGTGCAGGAAGAGTGCTACAGCAAGCTGAATGTGTGCAGCATCGCCAAGCGG 684

Qy        141 AsnProGluAlaIleThrGluValValGlnLeuProAsnHisPheSerAsnArgTyrTyr 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        685 AACCCTGAAGCCATCACTGAGGTCGTCCAGCTGCCCAATCACTTCTCCAACAGATACTAT 744

Qy        161 AsnArgLeuValArgSerLeuLeuGluCysAspGluAspThrValSerThrIleArgAsp 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        745 AACAGACTTGTCCGAAGCCTGCTGGAATGTGATGAAGACACAGTCAGCACAATCAGAGAC 804

Qy        181 SerLeuMetGluLys-Ile-GlyProAsnMetAlaSerLeuPheHisIleLeuGlnThrA 200
              |||||||||||    ||| ||||||||||||||||||||||||||||||||||||||||||||
Db        805 AGCCTGATGGAGRA-AATTNGGGCCTAACATGGCCAGCCTCTTCCACATCCTGCAGACAG 863

Qy        200 spHisCysAlaGlnThrHisProArgAlaAspPheAsnArgArgArgThrAsnGluProG 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        864 ACCACTGTGCCCAAACACACCCACGAGCTGACTTCAACAGGAGACGCACCAATGAGCCGC 923

Qy        220 lnLysLeuLysValLeuLeuArgAsnLeuArgGlyGluGluAspSerProSerHisIleL 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        924 AGAAGCTGAAAGTCCTCCTCAGGAACCTCCGAGGTGAGGAGGACTCTCCCTCCCACATCA 983

Qy        240 ysArgThrSerHisGluSerAla 247
              ||||||||||||||||||||||||
Db        984 AACGCACATCCCATGAGAGTGCA 1006

RESULT 9
AAH55624
ID   AAH55624 standard; DNA; 585 BP.
XX
AC   AAH55624;
XX
DT   04-SEP-2001  (first entry)
XX
DE   Human breast tumour protein clone 48987 DNA sequence.
XX
KW   Cytostatic; vaccine; human; breast tumour protein; breast cancer;
KW   gene therapy; ds.
XX
OS   Homo sapiens.
XX
PN   WO200140269-A2.
XX
PD   07-JUN-2001.
XX
PF   29-NOV-2000; 2000WO-US32520.
XX
PR   30-NOV-1999;   99US-0451651.
PR   22-FEB-2000; 2000US-0510662.
PR   10-MAR-2000; 2000US-0523586.
PR   07-APR-2000; 2000US-0545068.
PR   15-MAY-2000; 2000US-0571025.
XX
PA   (CORI-) CORIXA CORP.
XX
PI   Dillon DC,  Day CH,  Jiang Y,  Houghton RL,  Mitcham JL,  Wang A;
XX
DR   WPI; 2001-356154/37.
XX
PT   Breast tumor polypeptides and the nucleic acids that encode them,
```

```
PT   useful for the prevention, diagnosis and treatment of breast cancer -
XX
PS   Claim 24; Page 168; 221pp; English.
XX
CC   The present sequence is a human breast tumour protein coding sequence.
CC   This sequence may be used in the prevention, diagnosis and treatment of
CC   diseases associated with inappropriate expression of the breast tumour
CC   protein e.g. breast cancer. For example, this sequence may be used to
CC   treat disorders associated with decreased expression by rectifying
CC   mutations or deletions in a patient's genome that affect the activity of
CC   breast tumour protein by expressing inactive proteins or to supplement
CC   the patients own production of the breast tumour protein. Additionally,
CC   the present sequence may be used to produce the breast tumour protein, by
CC   inserting the nucleic acids into a host cell and culturing the cell to
CC   express the protein. The present sequence and its complementary sequences
CC   may also be used as DNA probes in diagnostic assays to detect and
CC   quantitate the presence of similar nucleic acids in samples, and
CC   therefore which patients may be in need of restorative therapy.
XX
SQ   Sequence 585 BP; 171 A; 163 C; 136 G; 110 T; 5 other;

Alignment Scores:
Pred. No.:              3.2e-156        Length:         585
Score:                  160.00          Matches:        160
Percent Similarity:     100.00%         Conservative:   0
Best Local Similarity:  100.00%         Mismatches:     0
Query Match:            64.78%          Indels:         0
DB:                     22              Gaps:           0

US-09-705-500A-3 (1-247) x AAH55624 (1-585)

Qy         88 GlyLysAlaPheValLysGluSerLeuLysCysIleAlaAsnGlyValThrSerLysVal 107
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         33 GGAAAAGCATTCGTCAAAGAGAGCTTAAAATGCATCGCCAACGGGGTCACCTCCAAGGTC 92

Qy        108 PheLeuAlaIleArgArgCysSerThrPheGlnArgMetIleAlaGluValGlnGluGlu 127
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         93 TTCCTCGCCATTCGGAGGTGCTCCACTTTCCAAAGGATGATTGCTGAGGTGCAGGAAGAG 152

Qy        128 CysTyrSerLysLeuAsnValCysSerIleAlaLysArgAsnProGluAlaIleThrGlu 147
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        153 TGCTACAGCAAGCTGAATGTGTGCAGCATCGCCAAGCGGAACCCTGAAGCCATCACTGAG 212

Qy        148 ValValGlnLeuProAsnHisPheSerAsnArgTyrTyrAsnArgLeuValArgSerLeu 167
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        213 GTCGTCCAGCTGCCCAATCACTTCTCCAACAGATACTATAACAGACTTGTCCGAAGCCTG 272

Qy        168 LeuGluCysAspGluAspThrValSerThrIleArgAspSerLeuMetGluLysIleGly 187
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        273 CTGGAATGTGATGAAGACACAGTCAGCACAATCAGAGACAGCCTGATGGAGAAAATTGGG 332

Qy        188 ProAsnMetAlaSerLeuPheHisIleLeuGlnThrAspHisCysAlaGlnThrHisPro 207
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        333 CCTAACATGGCCAGCCTCTTCCACATCCTGCAGACAGACCACTGTGCCCAAACACACCCA 392

Qy        208 ArgAlaAspPheAsnArgArgArgThrAsnGluProGlnLysLeuLysValLeuLeuArg 227
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        393 CGAGCTGACTTCAACAGGAGACGCACCAATGAGCCGCAGAAGCTGAAAGTCCTCCTCAGG 452

Qy        228 AsnLeuArgGlyGluGluAspSerProSerHisIleLysArgThrSerHisGluSerAla 247
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        453 AACCTCCGAGGTGAGGAGGACTCTCCCTCCCACATCAAACGCACATCCCATGAGAGTGCA 512

RESULT 10
ABA51055/c
ID   ABA51055 standard; DNA; 219 BP.
XX
AC   ABA51055;
XX
DT   01-FEB-2002  (first entry)
XX
DE   Human breast cell single exon nucleic acid probe #9750.
XX
KW   Human; microarray; single exon probe; gene expression; breast;
KW   disease; cancer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200157271-A2.
XX
PD   09-AUG-2001.
XX
PF   30-JAN-2001; 2001WO-US00662.
XX
PR   04-FEB-2000; 2000US-0180312.
PR   26-MAY-2000; 2000US-0207456.
PR   30-JUN-2000; 2000US-0608408.
PR   03-AUG-2000; 2000US-0632366.
PR   21-SEP-2000; 2000US-0234687.
PR   27-SEP-2000; 2000US-0236359.
PR   04-OCT-2000; 2000GB-0024263.
XX
PA   (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI   Penn SG,  Hanzel DK,  Chen W,  Rank DR;
XX
DR   WPI; 2001-496933/54.
XX
PT   New spatially-addressable set of single exon nucleic acid probes,
PT   useful for measuring gene expression in sample derived from human
PT   breast, comprises number of single exon nucleic acid probes  -
XX
PS   Claim 4; SEQ ID NO 9750; 327pp + sequence listing; English.
XX
CC   The invention relates to a spatially-addressable set of single exon
CC   nucleic acid probes for measuring gene expression in a sample derived
CC   from human breast and BT 474 cells. The method involves contacting
CC   the probes with a collection of detectably labelled nucleic acids
CC   derived from mRNA of human breast, and then measuring the label
CC   bound to each probe of the microarray. The probes are useful for
CC   verifying the expression of regions of genomic DNA predicted to
CC   encode proteins. They are useful for gene discovery, and for
CC   determining predisposition and/or prognosing breast disease. Gene
CC   expression analysis is useful for assessing the toxicity of chemical
CC   agents on cells. The microarray of this invention presents a far greater
CC   diversity of probes for measuring gene expression, with far less bias
CC   than expressed sequence tag microarrays. The method is suitable for
CC   rapid production of functional information from genomic sequence. The
CC   present sequence is a single exon nucleic acid probe of the invention.
CC   Note: The sequence data for this patent did not form part of the
CC   printed specification, but was obtained in electronic format directly
CC   from WIPO at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence 219 BP; 43 A; 55 C; 60 G; 61 T; 0 other;

Alignment Scores:
Pred. No.:              1.86e-65        Length:         219
Score:                  72.00           Matches:        72
Percent Similarity:     100.00%         Conservative:   0
Best Local Similarity:  100.00%         Mismatches:     0
Query Match:            29.15%          Indels:         0
DB:                     22              Gaps:           0

US-09-705-500A-3 (1-247) x ABA51055 (1-219)

Qy         88 GlyLysAlaPheValLysGluSerLeuLysCysIleAlaAsnGlyValThrSerLysVal 107
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        219 GGAAAAGCATTCGTCAAAGAGAGCTTAAAATGCATCGCCAACGGGGTCACCTCCAAGGTC 160

Qy        108 PheLeuAlaIleArgArgCysSerThrPheGlnArgMetIleAlaGluValGlnGluGlu 127
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        159 TTCCTCGCCATTCGGAGGTGCTCCACTTTCCAAAGGATGATTGCTGAGGTGCAGGAAGAG 100

Qy        128 CysTyrSerLysLeuAsnValCysSerIleAlaLysArgAsnProGluAlaIleThrGlu 147
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         99 TGCTACAGCAAGCTGAATGTGTGCAGCATCGCCAAGCGGAACCCTGAAGCCATCACTGAG 40
```

```
Qy        148 ValValGlnLeuProAsnHisPheSerAsnArgTyr 159
              ||||||||||||||||||||||||||||||||||||
Db         39 GTCGTCCAGCTGCCCAATCACTTCTCCAACAGGTAC 4

RESULT 11
ABA69045/c
ID   ABA69045 standard; DNA; 219 BP.
XX
AC   ABA69045;
XX
DT   01-FEB-2002  (first entry)
XX
DE   Human foetal liver single exon nucleic acid probe #17350.
XX
KW   Human; foetal liver; gene expression; single exon nucleic acid probe; ss.
XX
OS   Homo sapiens.
XX
PN   WO200157277-A2.
XX
PD   09-AUG-2001.
XX
PF   30-JAN-2001; 2001WO-US00669.
XX
PR   04-FEB-2000; 2000US-0180312.
PR   26-MAY-2000; 2000US-0207456.
PR   30-JUN-2000; 2000US-0608408.
PR   03-AUG-2000; 2000US-0632366.
PR   21-SEP-2000; 2000US-0234687.
PR   27-SEP-2000; 2000US-0236359.
PR   04-OCT-2000; 2000GB-0024263.
XX
PA   (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI   Penn SG,  Hanzel DK,  Chen W,  Rank DR;
XX
DR   WPI; 2001-483447/52.
XX
PT   Human genome-derived single exon nucleic acid probes useful for
PT   analyzing gene expression in human fetal liver -
XX
PS   Claim 4; SEQ ID NO 17350; 639pp + sequence listing; English.
XX
CC   The invention relates to a single exon nucleic acid probe for
CC   measuring human gene expression in a sample derived from human foetal
CC   liver. The single exon nucleic acid probes may be used for predicting,
CC   measuring and displaying gene expression in samples derived from human
CC   fetal liver. The present sequence is a single exon nucleic acid
CC   probe of the invention.
CC   Note: The sequence data for this patent did not form part of the
CC   printed specification, but was obtained in electronic format directly
CC   from WIPO at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence 219 BP; 43 A; 55 C; 60 G; 61 T; 0 other;

Alignment Scores:
Pred. No.:              1.86e-65        Length:         219
Score:                  72.00           Matches:        72
Percent Similarity:     100.00%         Conservative:   0
Best Local Similarity:  100.00%         Mismatches:     0
Query Match:            29.15%          Indels:         0
DB:                     22              Gaps:           0

US-09-705-500A-3 (1-247) x ABA69045 (1-219)

Qy         88 GlyLysAlaPheValLysGluSerLeuLysCysIleAlaAsnGlyValThrSerLysVal 107
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        219 GGAAAAGCATTCGTCAAAGAGAGCTTAAAATGCATCGCCAACGGGGTCACCTCCAAGGTC 160

Qy        108 PheLeuAlaIleArgArgCysSerThrPheGlnArgMetIleAlaGluValGlnGluGlu 127
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        159 TTCCTCGCCATTCGGAGGTGCTCCACTTTCCAAAGGATGATTGCTGAGGTGCAGGAAGAG 100

Qy        128 CysTyrSerLysLeuAsnValCysSerIleAlaLysArgAsnProGluAlaIleThrGlu 147
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         99 TGCTACAGCAAGCTGAATGTGTGCAGCATCGCCAAGCGGAACCCTGAAGCCATCACTGAG 40

Qy        148 ValValGlnLeuProAsnHisPheSerAsnArgTyr 159
              ||||||||||||||||||||||||||||||||||||
Db         39 GTCGTCCAGCTGCCCAATCACTTCTCCAACAGGTAC 4

RESULT 12
ABA35989/c
ID   ABA35989 standard; DNA; 219 BP.
XX
AC   ABA35989;
XX
DT   23-JAN-2002  (first entry)
XX
DE   Probe #14455 for gene expression analysis in human heart cell sample.
XX
KW   Human; gene expression; heart; microarray; vascular system; probe;
KW   cardiovascular disease; hypertension; cardiac arrhythmia;
KW   congenital heart disease; ss.
XX
OS   Homo sapiens.
XX
PN   WO200157274-A2.
XX
PD   09-AUG-2001.
XX
PF   30-JAN-2001; 2001WO-US00666.
XX
PR   04-FEB-2000; 2000US-0180312.
PR   26-MAY-2000; 2000US-0207456.
PR   30-JUN-2000; 2000US-0608408.
PR   03-AUG-2000; 2000US-0632366.
PR   21-SEP-2000; 2000US-0234687.
PR   27-SEP-2000; 2000US-0236359.
PR   04-OCT-2000; 2000GB-0024263.
XX
PA   (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI   Penn SG,  Hanzel DK,  Chen W,  Rank DR;
XX
DR   WPI; 2001-488899/53.
XX
PT   Single exon nucleic acid probes for analyzing gene expression in human
PT   hearts -
XX
PS   Claim 4; SEQ ID No 14455; 530pp; English.
XX
CC   The present invention relates to single exon nucleic acid probes for
CC   measuring human gene expression in a sample derived from human heart. The
CC   present sequence is one such probe. The probes may be used for
CC   predicting, measuring and displaying gene expression in samples derived
CC   from the human heart via microarrays. By measuring gene expression, the
CC   probes are useful for predicting, diagnosing, grading, staging,
CC   monitoring and prognosing diseases of the human heart and vascular system
CC   e.g. cardiovascular disease, hypertension, cardiac arrhythmias and
CC   congenital heart disease.
CC   Note: The sequence data for this patent did not form part of the printed
CC   specification, but was obtained in electronic format directly from WIPO
CC   at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence 219 BP; 43 A; 55 C; 60 G; 61 T; 0 other;

Alignment Scores:
Pred. No.:              1.86e-65        Length:         219
Score:                  72.00           Matches:        72
Percent Similarity:     100.00%         Conservative:   0
Best Local Similarity:  100.00%         Mismatches:     0
Query Match:            29.15%          Indels:         0
DB:                     22              Gaps:           0
```

```
US-09-705-500A-3 (1-247) x ABA35989 (1-219)

Qy         88 GlyLysAlaPheValLysGluSerLeuLysCysIleAlaAsnGlyValThrSerLysVal 107
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        219 GGAAAAGCATTCGTCAAAGAGAGCTTAAAATGCATCGCCAACGGGGTCACCTCCAAGGTC 160

Qy        108 PheLeuAlaIleArgArgCysSerThrPheGlnArgMetIleAlaGluValGlnGluGlu 127
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        159 TTCCTCGCCATTCGGAGGTGCTCCACTTTCCAAAGGATGATTGCTGAGGTGCAGGAAGAG 100

Qy        128 CysTyrSerLysLeuAsnValCysSerIleAlaLysArgAsnProGluAlaIleThrGlu 147
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         99 TGCTACAGCAAGCTGAATGTGTGCAGCATCGCCAAGCGGAACCCTGAAGCCATCACTGAG 40

Qy        148 ValValGlnLeuProAsnHisPheSerAsnArgTyr 159
              |||||||||||||||||||||||||||||||||||||
Db         39 GTCGTCCAGCTGCCCAATCACTTCTCCAACAGGTAC 4

RESULT 13
AAK17358/c
ID   AAK17358 standard; DNA; 219 BP.
XX
AC   AAK17358;
XX
DT   05-NOV-2001  (first entry)
XX
DE   Human brain expressed single exon probe SEQ ID NO: 17349.
XX
KW   Human; brain expressed exon; gene expression analysis; probe;
KW   microarray; Alzheimer's disease; multiple sclerosis; schizophrenia;
KW   epilepsy; cancer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200157275-A2.
XX
PD   09-AUG-2001.
XX
PF   30-JAN-2001; 2001WO-US00667.
XX
PR   04-FEB-2000; 2000US-0180312.
PR   26-MAY-2000; 2000US-0207456.
PR   30-JUN-2000; 2000US-0608408.
PR   03-AUG-2000; 2000US-0632366.
PR   21-SEP-2000; 2000US-0234687.
PR   27-SEP-2000; 2000US-0236359.
PR   04-OCT-2000; 2000GB-0024263.
XX
PA   (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI   Penn SG,  Hanzel DK,  Chen W,  Rank DR;
XX
DR   WPI; 2001-483446/52.
XX
PT   Single exon nucleic acid probes for analyzing gene expression in human
PT   brains -
XX
PS   Example 4; SEQ ID NO: 17349; 650pp + Sequence Listing; English.
XX
CC   The present invention provides a number of single exon nucleic acid
CC   probes which are derived from genomic sequences expressed in the human
CC   brain. They can be used to measure gene expression in brain cell samples,
CC   which may enable the diagnosis and improved treatment of nervous system
CC   diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia,
CC   epilepsy and cancers. The present sequence is one of the probes of the
CC   invention.
XX
SQ   Sequence 219 BP; 43 A; 55 C; 60 G; 61 T; 0 other;

Alignment Scores:
Pred. No.:              1.86e-65        Length:         219
Score:                  72.00           Matches:        72
Percent Similarity:     100.00%         Conservative:   0
Best Local Similarity:  100.00%         Mismatches:     0
Query Match:            29.15%          Indels:         0
DB:                     22              Gaps:           0

US-09-705-500A-3 (1-247) x AAK17358 (1-219)

Qy         88 GlyLysAlaPheValLysGluSerLeuLysCysIleAlaAsnGlyValThrSerLysVal 107
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        219 GGAAAAGCATTCGTCAAAGAGAGCTTAAAATGCATCGCCAACGGGGTCACCTCCAAGGTC 160

Qy        108 PheLeuAlaIleArgArgCysSerThrPheGlnArgMetIleAlaGluValGlnGluGlu 127
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        159 TTCCTCGCCATTCGGAGGTGCTCCACTTTCCAAAGGATGATTGCTGAGGTGCAGGAAGAG 100

Qy        128 CysTyrSerLysLeuAsnValCysSerIleAlaLysArgAsnProGluAlaIleThrGlu 147
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         99 TGCTACAGCAAGCTGAATGTGTGCAGCATCGCCAAGCGGAACCCTGAAGCCATCACTGAG 40

Qy        148 ValValGlnLeuProAsnHisPheSerAsnArgTyr 159
              |||||||||||||||||||||||||||||||||||||
Db         39 GTCGTCCAGCTGCCCAATCACTTCTCCAACAGGTAC 4

RESULT 14
AAK43155/c
ID   AAK43155 standard; DNA; 219 BP.
XX
AC   AAK43155;
XX
DT   06-NOV-2001  (first entry)
XX
DE   Human bone marrow expressed single exon probe SEQ ID NO: 17712.
XX
KW   Human; bone marrow expressed exon; gene expression analysis; probe;
KW   microarray; cancer; leukaemia; lymphoma; myeloma; ss.
XX
OS   Homo sapiens.
XX
PN   WO200157276-A2.
XX
PD   09-AUG-2001.
XX
PF   30-JAN-2001; 2001WO-US00668.
XX
PR   04-FEB-2000; 2000US-0180312.
PR   26-MAY-2000; 2000US-0207456.
PR   30-JUN-2000; 2000US-0608408.
PR   03-AUG-2000; 2000US-0632366.
PR   21-SEP-2000; 2000US-0234687.
PR   27-SEP-2000; 2000US-0236359.
PR   04-OCT-2000; 2000GB-0024263.
XX
PA   (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI   Penn SG,  Hanzel DK,  Chen W,  Rank DR;
XX
DR   WPI; 2001-488900/53.
XX
PT   Human genome-derived single exon nucleic acid probes useful for
PT   analyzing gene expression in human bone marrow -
XX
PS   Example 4; SEQ ID NO: 17712; 658pp + Sequence Listing; English.
XX
CC   The present invention provides a number of single exon nucleic acid
CC   probes which are derived from genomic sequences expressed in the human
CC   bone marrow. They can be used to measure gene expression in bone marrow
CC   samples, which may enable the improved diagnosis and treatment of cancers
CC   such as lymphoma, leukaemia and myeloma. The present sequence is one of
CC   the probes of the invention.
XX
SQ   Sequence 219 BP; 43 A; 55 C; 60 G; 61 T; 0 other;

Alignment Scores:
Pred. No.:              1.86e-65        Length:         219
```

```
Score:                  72.00       Matches:       72
Percent Similarity:     100.00%     Conservative:  0
Best Local Similarity:  100.00%     Mismatches:    0
Query Match:            29.15%      Indels:        0
DB:                     22          Gaps:          0

US-09-705-500A-3 (1-247) x AAK43155 (1-219)

Qy         88 GlyLysAlaPheValLysGluSerLeuLysCysIleAlaAsnGlyValThrSerLysVal 107
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        219 GGAAAAGCATTCGTCAAAGAGAGCTTAAAATGCATCGCCAACGGGGTCACCTCCAAGGTC 160

Qy        108 PheLeuAlaIleArgArgCysSerThrPheGlnArgMetIleAlaGluValGlnGluGlu 127
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        159 TTCCTCGCCATTCGGAGGTGCTCCACTTTCCAAAGGATGATTGCTGAGGTGCAGGAAGAG 100

Qy        128 CysTyrSerLysLeuAsnValCysSerIleAlaLysArgAsnProGluAlaIleThrGlu 147
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         99 TGCTACAGCAAGCTGAATGTGTGCAGCATCGCCAAGCGGAACCCTGAAGCCATCACTGAG 40

Qy        148 ValValGlnLeuProAsnHisPheSerAsnArgTyr 159
              ||||||||||||||||||||||||||||||||||||
Db         39 GTCGTCCAGCTGCCCAATCACTTCTCCAACAGGTAC 4

RESULT 15
AAI23927/c
ID   AAI23927 standard; DNA; 219 BP.
XX
AC   AAI23927;
XX
DT   12-OCT-2001  (first entry)
XX
DE   Probe #13860 for gene expression analysis in human cervical cell sample.
XX
KW   Probe; human; microarray; gene expression; cervical epithelial cell;
KW   cervical cancer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200157278-A2.
XX
PD   09-AUG-2001.
XX
PF   30-JAN-2001; 2001WO-US00670.
XX
PR   04-FEB-2000; 2000US-0180312.
PR   26-MAY-2000; 2000US-0207456.
PR   30-JUN-2000; 2000US-0608408.
PR   03-AUG-2000; 2000US-0632366.
PR   21-SEP-2000; 2000US-0234687.
PR   27-SEP-2000; 2000US-0236359.
PR   04-OCT-2000; 2000GB-0024263.
XX
PA   (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI   Penn SG,  Hanzel DK,  Chen W,  Rank DR;
XX
DR   WPI; 2001-488901/53.
XX
PT   Human genome-derived single exon nucleic acid probes useful for
PT   analyzing gene expression in human cervical epithelial cells -
XX
PS   Claim 25; SEQ ID No 13860; 487pp; English.
XX
CC   The present invention relates to human single exon nucleic acid probes
CC   (SENP). The present sequence is one such probe. The SENPs are derived
CC   from human HeLa cells. The SENPs can be used to produce a single exon
CC   microarray, which can be used for measuring human gene expression in a
CC   sample derived from human cervical epithelial cells. By measuring gene
CC   expression, the probes are therefore useful in grading and/or staging
CC   of diseases of the cervix, notably cervical cancer.
CC   Note: The sequence data for this patent did not form part of the printed
CC   specification, but was obtained in electronic format directly from WIPO
CC   at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence 219 BP; 43 A; 55 C; 60 G; 61 T; 0 other;

Alignment Scores:
Pred. No.:              1.86e-65    Length:        219
Score:                  72.00       Matches:       72
Percent Similarity:     100.00%     Conservative:  0
Best Local Similarity:  100.00%     Mismatches:    0
Query Match:            29.15%      Indels:        0
DB:                     22          Gaps:          0

US-09-705-500A-3 (1-247) x AAI23927 (1-219)

Qy         88 GlyLysAlaPheValLysGluSerLeuLysCysIleAlaAsnGlyValThrSerLysVal 107
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        219 GGAAAAGCATTCGTCAAAGAGAGCTTAAAATGCATCGCCAACGGGGTCACCTCCAAGGTC 160

Qy        108 PheLeuAlaIleArgArgCysSerThrPheGlnArgMetIleAlaGluValGlnGluGlu 127
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        159 TTCCTCGCCATTCGGAGGTGCTCCACTTTCCAAAGGATGATTGCTGAGGTGCAGGAAGAG 100

Qy        128 CysTyrSerLysLeuAsnValCysSerIleAlaLysArgAsnProGluAlaIleThrGlu 147
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         99 TGCTACAGCAAGCTGAATGTGTGCAGCATCGCCAAGCGGAACCCTGAAGCCATCACTGAG 40

Qy        148 ValValGlnLeuProAsnHisPheSerAsnArgTyr 159
              ||||||||||||||||||||||||||||||||||||
Db         39 GTCGTCCAGCTGCCCAATCACTTCTCCAACAGGTAC 4


Search completed: June 12, 2003, 22:09:56
Job time : 268 secs
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GenCore version 5.1.6

OM protein - nucleic search, using frame_plus_p2n model

Run on: June 12, 2003, 22:03:00 ; Search time 67 Seconds
(without alignments)
1130.584 Million cell updates/sec

Title: US-09-705-500A-3
Perfect score: 247
Sequence: 1 MLQNSAVLLVLVISASATHE.....NLRGEEDSPSHIKRTSHESA 247

Scoring table: OLIGO
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Ygapop 60.0 , Ygapext 60.0
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 441362 seqs, 153338381 residues

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
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	2	247	100.0	771	2	US-09-038-597A-1	Sequence 1, Appli
	3	247	100.0	771	2	US-08-431-117A-1	Sequence 1, Appli
	4	8	3.2	77	4	US-09-364-539-181	Sequence 181, App
	5	8	3.2	3153	4	US-09-175-928-9	Sequence 9, Appli
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	10	7	2.8	27	2	US-09-038-597A-3	Sequence 3, Appli
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	18	7	2.8	213	4	US-08-998-416-74	Sequence 74, Appl
	19	7	2.8	297	3	US-08-513-974B-308	Sequence 308, App
	20	7	2.8	297	4	US-08-776-971-125	Sequence 125, App
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	36	7	2.8	888	4	US-09-955-597-6	Sequence 6, Appli
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241	6	2.4	501	3	US-09-004-053-5	Sequence 5, Appli
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c 243	6	2.4	505	3	US-09-069-434-23	Sequence 23, Appl
244	6	2.4	507	4	US-09-404-879A-282	Sequence 282, App
245	6	2.4	509	1	US-08-151-391A-1	Sequence 1, Appli
c 246	6	2.4	515	1	US-08-275-370-21	Sequence 21, Appl
c 247	6	2.4	515	1	US-08-367-968-21	Sequence 21, Appl
c 248	6	2.4	515	1	US-08-665-484-21	Sequence 21, Appl
c 249	6	2.4	524	2	US-08-459-135A-9	Sequence 9, Appli
c 250	6	2.4	524	3	US-08-495-559-9	Sequence 9, Appli
c 251	6	2.4	531	1	US-08-340-539A-5	Sequence 5, Appli
c 252	6	2.4	531	2	US-08-461-592B-5	Sequence 5, Appli
c 253	6	2.4	536	2	US-08-459-135A-11	Sequence 11, Appl
c 254	6	2.4	536	3	US-08-495-559-11	Sequence 11, Appl
c 255	6	2.4	537	1	US-08-367-968-32	Sequence 32, Appl
c 256	6	2.4	537	1	US-08-665-484-32	Sequence 32, Appl
257	6	2.4	539	3	US-08-545-809A-18	Sequence 18, Appl
c 258	6	2.4	540	1	US-08-367-968-30	Sequence 30, Appl
c 259	6	2.4	540	1	US-08-665-484-30	Sequence 30, Appl
260	6	2.4	540	4	US-09-125-642C-1	Sequence 1, Appli
c 261	6	2.4	543	1	US-08-422-655-1	Sequence 1, Appli
c 262	6	2.4	543	4	US-09-387-919A-3	Sequence 3, Appli
c 263	6	2.4	546	2	US-08-459-135A-5	Sequence 5, Appli
c 264	6	2.4	546	3	US-08-495-559-5	Sequence 5, Appli
c 265	6	2.4	558	1	US-08-259-000-1	Sequence 1, Appli
c 266	6	2.4	558	1	US-08-729-767-1	Sequence 1, Appli
267	6	2.4	558	2	US-08-770-544-17	Sequence 17, Appl
c 268	6	2.4	587	1	US-08-375-241-3	Sequence 3, Appli
c 269	6	2.4	587	5	PCT-US92-06617A-3	Sequence 3, Appli
c 270	6	2.4	599	4	US-09-242-901-4	Sequence 4, Appli
c 271	6	2.4	599	4	US-09-222-575-173	Sequence 173, App
c 272	6	2.4	608	1	US-08-386-495-11	Sequence 11, Appl
c 273	6	2.4	608	5	PCT-US96-02331-11	Sequence 11, Appl
c 274	6	2.4	615	1	US-08-367-968-28	Sequence 28, Appl
c 275	6	2.4	615	1	US-08-665-484-28	Sequence 28, Appl
c 276	6	2.4	622	4	US-08-998-416-895	Sequence 895, App
277	6	2.4	624	4	US-08-998-416-1151	Sequence 1151, Ap
c 278	6	2.4	624	4	US-08-998-416-1151	Sequence 1151, Ap
279	6	2.4	624	4	US-09-199-637A-210	Sequence 210, App
c 280	6	2.4	625	3	US-09-004-113-11	Sequence 11, Appl
c 281	6	2.4	626	4	US-09-328-111-839	Sequence 839, App
282	6	2.4	630	1	US-08-220-379B-3	Sequence 3, Appli
c 283	6	2.4	633	2	US-08-969-106-12	Sequence 12, Appl
284	6	2.4	640	2	US-08-805-117-2	Sequence 2, Appli
285	6	2.4	640	4	US-09-199-838-2	Sequence 2, Appli
c 286	6	2.4	642	4	US-09-134-001C-1132	Sequence 1132, Ap
287	6	2.4	647	4	US-09-605-785-634	Sequence 634, App
c 288	6	2.4	648	1	US-08-451-409A-2	Sequence 2, Appli
c 289	6	2.4	648	1	US-08-451-409A-3	Sequence 3, Appli
c 290	6	2.4	648	1	US-08-451-409A-4	Sequence 4, Appli
c 291	6	2.4	657	4	US-09-081-689-5	Sequence 5, Appli
c 292	6	2.4	657	4	US-09-305-984-15	Sequence 15, Appl
c 293	6	2.4	657	4	US-09-073-541A-15	Sequence 15, Appl
294	6	2.4	658	4	US-09-641-638-402	Sequence 402, App
295	6	2.4	669	3	US-08-513-974B-314	Sequence 314, App
296	6	2.4	669	4	US-08-776-971-99	Sequence 99, Appl
c 297	6	2.4	672	4	US-08-998-416-141	Sequence 141, App
c 298	6	2.4	674	3	US-08-881-094-13	Sequence 13, Appl
299	6	2.4	674	4	US-09-328-111-76	Sequence 76, Appl
c 300	6	2.4	679	4	US-08-998-416-1071	Sequence 1071, Ap
c 301	6	2.4	685	3	US-08-881-094-14	Sequence 14, Appl
302	6	2.4	688	1	US-08-840-683-2	Sequence 2, Appli
303	6	2.4	688	2	US-08-555-722-2	Sequence 2, Appli
304	6	2.4	688	4	US-09-384-301-2	Sequence 2, Appli
c 305	6	2.4	693	2	US-08-690-849-1	Sequence 1, Appli
306	6	2.4	693	2	US-08-690-849-3	Sequence 3, Appli
c 307	6	2.4	693	3	US-09-004-053-1	Sequence 1, Appli
308	6	2.4	693	3	US-09-004-053-3	Sequence 3, Appli
c 309	6	2.4	699	4	US-08-998-416-717	Sequence 717, App
c 310	6	2.4	711	4	US-09-134-001C-2545	Sequence 2545, Ap
c 311	6	2.4	716	4	US-08-991-789A-37	Sequence 37, Appl
c 312	6	2.4	716	4	US-09-062-451-37	Sequence 37, Appl
c 313	6	2.4	716	4	US-09-598-326-37	Sequence 37, Appl
314	6	2.4	721	4	US-08-896-164-30	Sequence 30, Appl
c 315	6	2.4	722	4	US-09-280-116-128	Sequence 128, App
c 316	6	2.4	724	4	US-08-998-416-627	Sequence 627, App
c 317	6	2.4	727	1	US-08-367-968-27	Sequence 27, Appl
c 318	6	2.4	727	1	US-08-665-484-27	Sequence 27, Appl
319	6	2.4	732	4	US-08-998-416-860	Sequence 860, App
c 320	6	2.4	737	2	US-08-861-549-2	Sequence 2, Appli
321	6	2.4	740	4	US-09-451-117-1	Sequence 1, Appli
322	6	2.4	749	1	US-08-080-255-1	Sequence 1, Appli
323	6	2.4	749	3	US-08-465-713-1	Sequence 1, Appli
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c 326	6	2.4	760	3	US-09-146-249A-78	Sequence 78, Appl
c 327	6	2.4	760	3	US-08-206-188B-78	Sequence 78, Appl
c 328	6	2.4	762	4	US-08-991-789A-31	Sequence 31, Appl
c 329	6	2.4	762	4	US-09-062-451-31	Sequence 31, Appl
c 330	6	2.4	762	4	US-09-598-326-31	Sequence 31, Appl
331	6	2.4	767	4	US-09-227-357-85	Sequence 85, Appl
332	6	2.4	767	4	US-09-221-017B-28	Sequence 28, Appl
333	6	2.4	768	4	US-09-528-760A-1	Sequence 1, Appli
c 334	6	2.4	777	4	US-08-998-416-218	Sequence 218, App
335	6	2.4	780	4	US-09-125-642C-10	Sequence 10, Appl
336	6	2.4	784	4	US-09-276-531-131	Sequence 131, App
337	6	2.4	793	4	US-09-040-984-78	Sequence 78, Appl
338	6	2.4	793	4	US-09-123-912-78	Sequence 78, Appl
339	6	2.4	793	4	US-09-643-597-78	Sequence 78, Appl
340	6	2.4	801	4	US-09-459-956-7	Sequence 7, Appli
c 341	6	2.4	802	4	US-08-441-507-18	Sequence 18, Appl
c 342	6	2.4	802	4	US-07-969-875A-18	Sequence 18, Appl
c 343	6	2.4	804	4	US-08-998-416-881	Sequence 881, App
c 344	6	2.4	804	4	US-09-134-001C-2575	Sequence 2575, Ap
345	6	2.4	806	4	US-08-998-416-344	Sequence 344, App
346	6	2.4	811	3	US-08-961-083-63	Sequence 63, Appl
347	6	2.4	820	4	US-08-998-416-282	Sequence 282, App
348	6	2.4	822	4	US-09-134-001C-1080	Sequence 1080, Ap
c 349	6	2.4	832	4	US-08-441-507-19	Sequence 19, Appl
350	6	2.4	832	4	US-09-025-769B-287	Sequence 287, App
c 351	6	2.4	832	4	US-07-969-875A-19	Sequence 19, Appl
352	6	2.4	841	4	US-09-182-145-39	Sequence 39, Appl
c 353	6	2.4	843	2	US-08-969-106-10	Sequence 10, Appl
c 354	6	2.4	848	4	US-09-221-017B-385	Sequence 385, App
355	6	2.4	849	4	US-08-482-918-41	Sequence 41, Appl
356	6	2.4	849	4	US-09-224-681-41	Sequence 41, Appl
357	6	2.4	849	4	US-08-336-728A-41	Sequence 41, Appl
358	6	2.4	852	4	US-08-930-285-19	Sequence 19, Appl
359	6	2.4	854	4	US-09-247-155-67	Sequence 67, Appl
360	6	2.4	867	4	US-08-697-826A-16	Sequence 16, Appl
361	6	2.4	872	1	US-09-384-327-20	Sequence 20, Appl
362	6	2.4	872	1	US-08-458-372-20	Sequence 20, Appl
363	6	2.4	874	6	5506118-10	Patent No. 5506118
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c 365	6	2.4	878	1	US-08-469-667-8	Sequence 8, Appli
c 366	6	2.4	878	4	US-09-224-110-8	Sequence 8, Appli
c 367	6	2.4	878	4	US-09-288-143-25	Sequence 25, Appl
c 368	6	2.4	878	5	PCT-US95-07289-8	Sequence 8, Appli
c 369	6	2.4	879	1	US-08-243-545-1	Sequence 1, Appli
c 370	6	2.4	879	2	US-08-993-962-1	Sequence 1, Appli
c 371	6	2.4	879	4	US-09-160-841-1	Sequence 1, Appli
c 372	6	2.4	879	5	PCT-US94-05365-1	Sequence 1, Appli
c 373	6	2.4	882	1	US-08-489-141A-5	Sequence 5, Appli
374	6	2.4	888	4	US-09-215-694-30	Sequence 30, Appl
375	6	2.4	900	4	US-09-125-642C-5	Sequence 5, Appli
376	6	2.4	913	4	US-09-561-756-23	Sequence 23, Appl
377	6	2.4	913	4	US-09-227-721-23	Sequence 23, Appl

	378	6	2.4	916	4	US-09-239-909-3	Sequence 3, Appli
	379	6	2.4	920	3	US-09-058-489-49	Sequence 49, Appl
	380	6	2.4	921	4	US-09-377-648-4	Sequence 4, Appli
c	381	6	2.4	924	2	US-08-216-894-5	Sequence 5, Appli
c	382	6	2.4	924	4	US-09-115-746-5	Sequence 5, Appli
	383	6	2.4	924	4	US-09-221-017B-262	Sequence 262, App
	384	6	2.4	926	4	US-09-561-497-3	Sequence 3, Appli
	385	6	2.4	939	4	US-09-641-638-403	Sequence 403, App
	386	6	2.4	950	2	US-08-901-200A-14	Sequence 14, Appl
	387	6	2.4	950	3	US-09-219-391-14	Sequence 14, Appl
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c	389	6	2.4	951	2	US-08-308-887A-2	Sequence 2, Appli
c	390	6	2.4	951	3	US-08-881-094-2	Sequence 2, Appli
c	391	6	2.4	954	2	US-09-066-075-1	Sequence 1, Appli
c	392	6	2.4	954	2	US-08-518-615A-1	Sequence 1, Appli
c	393	6	2.4	954	3	US-08-951-889-1	Sequence 1, Appli
c	394	6	2.4	954	4	US-09-472-857-1	Sequence 1, Appli
	395	6	2.4	954	4	US-09-134-001C-1700	Sequence 1700, Ap
c	396	6	2.4	959	4	US-09-221-017B-942	Sequence 942, App
	397	6	2.4	961	4	US-08-846-826A-3	Sequence 3, Appli
	398	6	2.4	963	4	US-09-134-001C-631	Sequence 631, App
c	399	6	2.4	966	4	US-09-134-001C-1789	Sequence 1789, Ap
c	400	6	2.4	975	4	US-09-134-001C-2159	Sequence 2159, Ap
c	401	6	2.4	975	6	5340934-10	Patent No. 5340934
c	402	6	2.4	977	6	5340934-9	Patent No. 5340934
c	403	6	2.4	984	1	US-08-423-691-1	Sequence 1, Appli
c	404	6	2.4	984	3	US-08-867-260-1	Sequence 1, Appli
c	405	6	2.4	986	4	US-09-501-192-8	Sequence 8, Appli
c	406	6	2.4	987	1	US-08-230-047-6	Sequence 6, Appli
	407	6	2.4	987	4	US-09-221-017B-1115	Sequence 1115, Ap
c	408	6	2.4	988	1	US-08-489-141A-1	Sequence 1, Appli
	409	6	2.4	993	4	US-09-134-001C-1491	Sequence 1491, Ap
c	410	6	2.4	1001	4	US-09-641-638-78	Sequence 78, Appl
	411	6	2.4	1001	4	US-09-641-638-180	Sequence 180, App
c	412	6	2.4	1001	4	US-09-641-638-575	Sequence 575, App
c	413	6	2.4	1002	4	US-09-230-637-9	Sequence 9, Appli
c	414	6	2.4	1002	4	US-09-257-179-27	Sequence 27, Appl
	415	6	2.4	1011	4	US-09-134-001C-2258	Sequence 2258, Ap
c	416	6	2.4	1017	5	PCT-US94-05150-21	Sequence 21, Appl
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	418	6	2.4	1024	4	US-09-414-276-5	Sequence 5, Appli
	419	6	2.4	1026	4	US-09-275-384B-4	Sequence 4, Appli
	420	6	2.4	1029	4	US-09-116-498-5	Sequence 5, Appli
	421	6	2.4	1029	4	US-09-449-437A-1	Sequence 1, Appli
	422	6	2.4	1032	4	US-09-257-179-21	Sequence 21, Appl
	423	6	2.4	1034	4	US-09-072-596-312	Sequence 312, App
	424	6	2.4	1037	4	US-09-116-498-3	Sequence 3, Appli
	425	6	2.4	1042	4	US-08-960-780-24	Sequence 24, Appl
	426	6	2.4	1042	4	US-09-073-898-24	Sequence 24, Appl
	427	6	2.4	1045	4	US-08-960-780-20	Sequence 20, Appl
	428	6	2.4	1045	4	US-09-073-898-20	Sequence 20, Appl
	429	6	2.4	1046	4	US-08-960-780-41	Sequence 41, Appl
	430	6	2.4	1046	4	US-09-073-898-41	Sequence 41, Appl
	431	6	2.4	1048	4	US-08-195-967-3	Sequence 3, Appli
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	433	6	2.4	1057	1	US-08-471-770-45	Sequence 45, Appl
	434	6	2.4	1057	2	US-08-468-059-45	Sequence 45, Appl
c	435	6	2.4	1059	4	US-08-476-102A-3	Sequence 3, Appli
	436	6	2.4	1076	4	US-09-615-192A-255	Sequence 255, App
c	437	6	2.4	1080	2	US-09-205-922-1	Sequence 1, Appli
	438	6	2.4	1086	2	US-08-985-090-6	Sequence 6, Appli
	439	6	2.4	1086	3	US-09-165-543-33	Sequence 33, Appl
	440	6	2.4	1091	2	US-08-418-071-5	Sequence 5, Appli
	441	6	2.4	1096	2	US-08-418-071-4	Sequence 4, Appli
	442	6	2.4	1101	3	US-08-987-904A-3	Sequence 3, Appli
	443	6	2.4	1104	3	US-08-454-295-1	Sequence 1, Appli
	444	6	2.4	1104	4	US-09-431-500A-1	Sequence 1, Appli
	445	6	2.4	1104	4	US-09-431-498-1	Sequence 1, Appli
	446	6	2.4	1104	4	US-09-431-499-1	Sequence 1, Appli
	447	6	2.4	1110	3	US-08-513-974B-31	Sequence 31, Appl
	448	6	2.4	1110	4	US-08-776-971-26	Sequence 26, Appl
	449	6	2.4	1110	4	US-09-414-276-2	Sequence 2, Appli
	450	6	2.4	1113	4	US-09-172-353-1	Sequence 1, Appli
	451	6	2.4	1116	4	US-08-776-971-139	Sequence 139, App
c	452	6	2.4	1124	3	US-08-945-056-1	Sequence 1, Appli
	453	6	2.4	1128	1	US-08-205-719-1	Sequence 1, Appli
	454	6	2.4	1128	3	US-08-746-883-2	Sequence 2, Appli
	455	6	2.4	1128	4	US-09-170-769A-9	Sequence 9, Appli
	456	6	2.4	1135	4	US-08-936-165A-135	Sequence 135, App
	457	6	2.4	1146	4	US-08-991-789A-9	Sequence 9, Appli
c	458	6	2.4	1146	4	US-08-991-789A-9	Sequence 9, Appli
	459	6	2.4	1146	4	US-09-062-451-9	Sequence 9, Appli
c	460	6	2.4	1146	4	US-09-062-451-9	Sequence 9, Appli
	461	6	2.4	1146	4	US-09-598-326-9	Sequence 9, Appli
c	462	6	2.4	1146	4	US-09-598-326-9	Sequence 9, Appli
	463	6	2.4	1147	4	US-08-061-376-2	Sequence 2, Appli
c	464	6	2.4	1149	4	US-09-134-001C-928	Sequence 928, App
	465	6	2.4	1158	1	US-08-178-606-5	Sequence 5, Appli
c	466	6	2.4	1164	4	US-09-134-001C-1245	Sequence 1245, Ap
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c	468	6	2.4	1173	3	US-08-740-644-1	Sequence 1, Appli
c	469	6	2.4	1196	2	US-08-864-799-2	Sequence 2, Appli
	470	6	2.4	1198	1	US-08-020-245A-3	Sequence 3, Appli
	471	6	2.4	1198	1	US-08-396-957A-3	Sequence 3, Appli
c	472	6	2.4	1200	4	US-09-204-117B-2	Sequence 2, Appli
c	473	6	2.4	1201	2	US-08-169-948B-13	Sequence 13, Appl
c	474	6	2.4	1201	2	US-08-448-873-13	Sequence 13, Appl
c	475	6	2.4	1201	4	US-08-382-452D-13	Sequence 13, Appl
	476	6	2.4	1206	4	US-09-446-047A-20	Sequence 20, Appl
	477	6	2.4	1209	4	US-09-276-531-14	Sequence 14, Appl
	478	6	2.4	1215	4	US-08-936-165A-63	Sequence 63, Appl
	479	6	2.4	1215	4	US-09-134-001C-1424	Sequence 1424, Ap
	480	6	2.4	1216	4	US-09-071-035-3	Sequence 3, Appli
	481	6	2.4	1218	4	US-08-943-731-89	Sequence 89, Appl
c	482	6	2.4	1227	1	US-09-031-485-17	Sequence 17, Appl
	483	6	2.4	1227	1	US-09-031-485-18	Sequence 18, Appl
c	484	6	2.4	1227	1	US-08-847-429A-17	Sequence 17, Appl
	485	6	2.4	1227	1	US-08-847-429A-18	Sequence 18, Appl
c	486	6	2.4	1227	3	US-09-065-474-17	Sequence 17, Appl
	487	6	2.4	1227	3	US-09-065-474-18	Sequence 18, Appl
	488	6	2.4	1227	4	US-09-315-793-31	Sequence 31, Appl
c	489	6	2.4	1227	4	US-09-557-034-17	Sequence 17, Appl
	490	6	2.4	1227	4	US-09-557-034-18	Sequence 18, Appl
c	491	6	2.4	1228	1	US-09-031-485-14	Sequence 14, Appl
	492	6	2.4	1228	1	US-09-031-485-16	Sequence 16, Appl
c	493	6	2.4	1228	1	US-08-847-429A-14	Sequence 14, Appl
	494	6	2.4	1228	1	US-08-847-429A-16	Sequence 16, Appl
c	495	6	2.4	1228	3	US-09-065-474-14	Sequence 14, Appl
	496	6	2.4	1228	3	US-09-065-474-16	Sequence 16, Appl
c	497	6	2.4	1228	4	US-09-557-034-14	Sequence 14, Appl
	498	6	2.4	1228	4	US-09-557-034-16	Sequence 16, Appl
c	499	6	2.4	1235	2	US-08-530-569B-12	Sequence 12, Appl
c	500	6	2.4	1239	4	US-09-134-001C-1407	Sequence 1407, Ap
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c	502	6	2.4	1248	1	US-08-110-286A-5	Sequence 5, Appli
	503	6	2.4	1251	4	US-09-330-611-7	Sequence 7, Appli
c	504	6	2.4	1251	4	US-09-134-001C-2539	Sequence 2539, Ap
c	505	6	2.4	1252	2	US-08-588-983-43	Sequence 43, Appl
c	506	6	2.4	1252	2	US-08-588-976-43	Sequence 43, Appl
c	507	6	2.4	1252	3	US-08-589-028-13	Sequence 13, Appl
c	508	6	2.4	1252	3	US-08-784-582-13	Sequence 13, Appl
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c	511	6	2.4	1259	4	US-09-295-306-3	Sequence 3, Appli
c	512	6	2.4	1259	4	US-09-734-719-3	Sequence 3, Appli
c	513	6	2.4	1266	3	US-09-065-474-141	Sequence 141, App
	514	6	2.4	1266	3	US-09-065-474-143	Sequence 143, App
c	515	6	2.4	1266	4	US-09-557-034-141	Sequence 141, App
	516	6	2.4	1266	4	US-09-557-034-143	Sequence 143, App
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	518	6	2.4	1288	1	US-08-142-897-4	Sequence 4, Appli
	519	6	2.4	1293	4	US-09-182-145-13	Sequence 13, Appl
c	520	6	2.4	1293	4	US-09-182-145-14	Sequence 14, Appl
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526	6	2.4	1312	4	US-09-059-769-3	Sequence 3, Appli
527	6	2.4	1314	2	US-08-440-845D-9	Sequence 9, Appli
c 528	6	2.4	1314	3	US-08-392-794A-1	Sequence 1, Appli
529	6	2.4	1314	3	US-08-868-458-9	Sequence 9, Appli
530	6	2.4	1314	4	US-09-134-001C-2505	Sequence 2505, Ap
c 531	6	2.4	1329	4	US-09-134-001C-2296	Sequence 2296, Ap
532	6	2.4	1331	3	US-08-513-974B-322	Sequence 322, App
533	6	2.4	1331	4	US-08-776-971-103	Sequence 103, App
534	6	2.4	1338	3	US-09-165-543-6	Sequence 6, Appli
535	6	2.4	1347	4	US-09-071-035-1	Sequence 1, Appli
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c 541	6	2.4	1356	1	US-08-520-519-5	Sequence 5, Appli
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c 583	6	2.4	1476	2	US-08-993-581B-4	Sequence 4, Appli
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590	6	2.4	1497	4	US-09-565-538-41	Sequence 41, Appl
591	6	2.4	1497	4	US-09-661-468-41	Sequence 41, Appl
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639	6	2.4	1662	1	US-08-785-048-1	Sequence 1, Appli
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c 645	6	2.4	1672	2	US-08-474-379C-34	Sequence 34, Appl
c 646	6	2.4	1672	3	US-09-146-249A-34	Sequence 34, Appl
c 647	6	2.4	1672	3	US-08-206-188B-34	Sequence 34, Appl
c 648	6	2.4	1672	5	PCT-US91-02714-33	Sequence 33, Appl
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c 721	6	2.4	1876	2	US-08-485-938A-24	Sequence 24, Appl
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c 723	6	2.4	1876	3	US-09-328-474-24	Sequence 24, Appl
c 724	6	2.4	1876	3	US-09-100-546-24	Sequence 24, Appl
c 725	6	2.4	1876	3	US-09-010-715-24	Sequence 24, Appl
c 726	6	2.4	1876	4	US-09-577-758-24	Sequence 24, Appl
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c 732	6	2.4	1890	2	US-08-785-396-1	Sequence 1, Appli
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762	6	2.4	2012	5	PCT-US94-02233-2	Sequence 2, Appli
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767	6	2.4	2050	3	US-08-993-722A-101	Sequence 101, App
768	6	2.4	2050	3	US-08-993-170A-101	Sequence 101, App
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ALIGNMENTS

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RESULT 1
US-08-208-005C-1
; Sequence 1, Application US/08208005C
; Patent No. 5837498
;  GENERAL INFORMATION:
;    APPLICANT:  OLSEN, ET AL.
;    TITLE OF INVENTION:  Corpuscles of Stannius Protein, Stanniocalcin
;    NUMBER OF SEQUENCES:  5
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  CARELLA, BYRNE, BAIN, GILFILLAN,
;      ADDRESSEE:  CECCHI, STEWART & OLSTEIN
;      STREET:  6 BECKER FARM ROAD
;      CITY:  ROSELAND
;      STATE:  NEW JERSEY
;      COUNTRY:  USA
;      ZIP:  07068
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5 INCH DISKETTE
;      COMPUTER:  IBM PS/2
;      OPERATING SYSTEM:  MS-DOS
;      SOFTWARE:  WORD PERFECT 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/208,005C
;      FILING DATE:  8 MARCH 1994
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  FERRARO, GREGORY D.
;      REGISTRATION NUMBER:  36,134
;      REFERENCE/DOCKET NUMBER:  325800-78
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  201-994-1700
;      TELEFAX:  201-994-1744
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  771 BASE PAIRS
;      TYPE:  NUCLEIC ACID
;      STRANDEDNESS:  SINGLE
;      TOPOLOGY:  LINEAR
;    MOLECULE TYPE:  cDNA
US-08-208-005C-1

Alignment Scores:
Pred. No.:                1.24e-249      Length:          771
Score:                    247.00         Matches:         247
Percent Similarity:       100.00%        Conservative:    0
Best Local Similarity:    100.00%        Mismatches:      0
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US-09-705-500A-3 (1-247) x US-08-208-005C-1 (1-771)

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Db         16 ATGCTCCAAAACTCAGCAGTGCTTCTGGTGCTGGTGATCAGTGCTTCTGCAACCCATGAG 75

Qy         21 AlaGluGlnAsnAspSerValSerProArgLysSerArgValAlaAlaGlnAsnSerAla 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         76 GCGGAGCAGAATGACTCTGTGAGCCCCAGGAAATCCCGAGTGGCGGCCCAAAACTCAGCT 135

Qy         41 GluValValArgCysLeuAsnSerAlaLeuGlnValGlyCysGlyAlaPheAlaCysLeu 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        136 GAAGTGGTTCGTTGCCTCAACAGTGCTCTACAGGTCGGCTGCGGGGCTTTTGCATGCCTG 195

Qy         61 GluAsnSerThrCysAspThrAspGlyMetTyrAspIleCysLysSerPheLeuTyrSer 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        196 GAAAACTCCACCTGTGACACAGATGGGATGTATGACATCTGTAAATCCTTCTTGTACAGC 255

Qy         81 AlaAlaLysPheAspThrGlnGlyLysAlaPheValLysGluSerLeuLysCysIleAla 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        256 GCTGCTAAATTTGACACTCAGGGAAAAGCATTCGTCAAAGAGAGCTTAAAATGCATCGCC 315

Qy        101 AsnGlyValThrSerLysValPheLeuAlaIleArgCysSerThrPheGlnArgMet 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        316 AACGGGGTCACCTCCAAGGTCTTCCTCGCCATTCGGAGGTGCTCCACTTTCCAAAGGATG 375

Qy        121 IleAlaGluValGlnGluGluCysTyrSerLysLeuAsnValCysSerIleAlaLysArg 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        376 ATTGCTGAGGTGCAGGAAGAGTGCTACAGCAAGCTGAATGTGTGCAGCATCGCCAAGCGG 435

Qy        141 AsnProGluAlaIleThrGluValValGlnLeuProAsnHisPheSerAsnArgTyrTyr 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        436 AACCCTGAAGCCATCACTGAGGTCGTCCAGCTGCCCAATCACTTCTCCAACAGATACTAT 495

Qy        161 AsnArgLeuValArgSerLeuLeuGluCysAspGluAspThrValSerThrIleArgAsp 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        496 AACAGACTTGTCCGAAGCCTGCTGGAATGTGATGAAGACACAGTCAGCACAATCAGAGAC 555

Qy        181 SerLeuMetGluLysIleGlyProAsnMetAlaSerLeuPheHisIleLeuGlnThrAsp 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        556 AGCCTGATGGAGAAAATTGGGCCTAACATGGCCAGCCTCTTCCACATCCTGCAGACAGAC 615

Qy        201 HisCysAlaGlnThrHisProArgAlaAspPheAsnArgArgArgThrAsnGluProGln 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        616 CACTGTGCCCAAACACACCCACGAGCTGACTTCAACAGGAGACGCACCAATGAGCCGCAG 675

Qy        221 LysLeuLysValLeuLeuArgAsnLeuArgGlyGluGluAspSerProSerHisIleLys 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        676 AAGCTGAAAGTCCTCCTCAGGAACCTCCGAGGTGAGGAGGACTCTCCCTCCCACATCAAA 735

Qy        241 ArgThrSerHisGluSerAla 247
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Db        736 CGCACATCCCATGAGAGTGCA 756

RESULT 2
US-09-038-597A-1
; Sequence 1, Application US/09038597A
; Patent No. 5877290
;  GENERAL INFORMATION:
;    APPLICANT:  OLSEN, ET AL.
;    TITLE OF INVENTION:  Corpuscles of Stannius Protein,
;    TITLE OF INVENTION:  Stanniocalcin
;    NUMBER OF SEQUENCES:  5
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  CARELLA, BYRNE, BAIN, GILFILLAN,
;      ADDRESSEE:  CECCHI, STEWART & OLSTEIN
;      STREET:  6 BECKER FARM ROAD
;      CITY:  ROSELAND
;      STATE:  NEW JERSEY
;      COUNTRY:  USA
;      ZIP:  07068
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5 INCH DISKETTE
;      COMPUTER:  IBM PS/2
;      OPERATING SYSTEM:  MS-DOS
;      SOFTWARE:  WORD PERFECT 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/038,597A
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/208,005
;      FILING DATE:  8-MARCH-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  FERRARO, GREGORY D.
;      REGISTRATION NUMBER:  36,134
;      REFERENCE/DOCKET NUMBER:  325800-78
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  201-994-1700
;      TELEFAX:  201-994-1744
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  771 BASE PAIRS
;      TYPE:  NUCLEIC ACID
;      STRANDEDNESS:  SINGLE
;      TOPOLOGY:  LINEAR
;    MOLECULE TYPE:  cDNA
US-09-038-597A-1

Alignment Scores:
Pred. No.:              1.24e-249      Length:          771
Score:                  247.00         Matches:         247
Percent Similarity:     100.00%        Conservative:    0
Best Local Similarity:  100.00%        Mismatches:      0
Query Match:            100.00%        Indels:          0
DB:                     2              Gaps:            0

US-09-705-500A-3 (1-247) x US-09-038-597A-1 (1-771)

Qy          1 MetLeuGlnAsnSerAlaValLeuLeuValLeuValIleSerAlaSerAlaThrHisGlu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         16 ATGCTCCAAAACTCAGCAGTGCTTCTGGTGCTGGTGATCAGTGCTTCTGCAACCCATGAG 75

Qy         21 AlaGluGlnAsnAspSerValSerProArgLysSerArgValAlaAlaGlnAsnSerAla 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         76 GCGGAGCAGAATGACTCTGTGAGCCCCAGGAAATCCCGAGTGGCGGCCCAAAACTCAGCT 135

Qy         41 GluValValArgCysLeuAsnSerAlaLeuGlnValGlyCysGlyAlaPheAlaCysLeu 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        136 GAAGTGGTTCGTTGCCTCAACAGTGCTCTACAGGTCGGCTGCGGGGCTTTTGCATGCCTG 195

Qy         61 GluAsnSerThrCysAspThrAspGlyMetTyrAspIleCysLysSerPheLeuTyrSer 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        196 GAAAACTCCACCTGTGACACAGATGGGATGTATGACATCTGTAAATCCTTCTTGTACAGC 255

Qy         81 AlaAlaLysPheAspThrGlnGlyLysAlaPheValLysGluSerLeuLysCysIleAla 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        256 GCTGCTAAATTTGACACTCAGGGAAAAGCATTCGTCAAAGAGAGCTTAAAATGCATCGCC 315

Qy        101 AsnGlyValThrSerLysValPheLeuAlaIleArgArgCysSerThrPheGlnArgMet 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        316 AACGGGGTCACCTCCAAGGTCTTCCTCGCCATTCGGAGGTGCTCCACTTTCCAAAGGATG 375

Qy        121 IleAlaGluValGlnGluGluCysTyrSerLysLeuAsnValCysSerIleAlaLysArg 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        376 ATTGCTGAGGTGCAGGAAGAGTGCTACAGCAAGCTGAATGTGTGCAGCATCGCCAAGCGG 435

Qy        141 AsnProGluAlaIleThrGluValValGlnLeuProAsnHisPheSerAsnArgTyrTyr 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        436 AACCCTGAAGCCATCACTGAGGTCGTCCAGCTGCCCAATCACTTCTCCAACAGATACTAT 495

Qy        161 AsnArgLeuValArgSerLeuLeuGluCysAspGluAspThrValSerThrIleArgAsp 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        496 AACAGACTTGTCCGAAGCCTGCTGGAATGTGATGAAGACACAGTCAGCACAATCAGAGAC 555

Qy        181 SerLeuMetGluLysIleGlyProAsnMetAlaSerLeuPheHisIleLeuGlnThrAsp 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        556 AGCCTGATGGAGAAAATTGGGCCTAACATGGCCAGCCTCTTCCACATCCTGCAGACAGAC 615

Qy        201 HisCysAlaGlnThrHisProArgAlaAspPheAsnArgArgArgThrAsnGluProGln 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        616 CACTGTGCCCAAACACACCCACGAGCTGACTTCAACAGGAGACGCACCAATGAGCCGCAG 675

Qy        221 LysLeuLysValLeuLeuArgAsnLeuArgGlyGluGluAspSerProSerHisIleLys 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        676 AAGCTGAAAGTCCTCCTCAGGAACCTCCGAGGTGAGGAGGACTCTCCCTCCCACATCAAA 735

Qy        241 ArgThrSerHisGluSerAla 247
              ||||||||||||||||||||
Db        736 CGCACATCCCATGAGAGTGCA 756

RESULT 3
US-08-431-117A-1
; Sequence 1, Application US/08431117A
; Patent No. 5994301
;  GENERAL INFORMATION:
;    APPLICANT:  OLSEN, ET AL.
;    TITLE OF INVENTION:  Corpuscles of Stannius Protein, Stanniocalcin
;    NUMBER OF SEQUENCES:  8
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  CARELLA, BYRNE, BAIN, GILFILLAN,
;      ADDRESSEE:  CECCHI, STEWART & OLSTEIN
;      STREET:  6 BECKER FARM ROAD
;      CITY:  ROSELAND
;      STATE:  NEW JERSEY
;      COUNTRY:  USA
;      ZIP:  07068
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5 INCH DISKETTE
;      COMPUTER:  IBM PS/2
;      OPERATING SYSTEM:  MS-DOS
;      SOFTWARE:  WORD PERFECT 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/431,117A
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/208,005
;      FILING DATE:  8 MARCH 1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  FERRARO, GREGORY D.
;      REGISTRATION NUMBER:  36,134
;      REFERENCE/DOCKET NUMBER:  325800-296
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  201-994-1700
;      TELEFAX:  201-994-1744
;  INFORMATION FOR SEQ ID NO:  1:
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;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  771 BASE PAIRS
;       TYPE:  NUCLEIC ACID
;       STRANDEDNESS:  SINGLE
;       TOPOLOGY:  LINEAR
;     MOLECULE TYPE:  cDNA
US-08-431-117A-1

Alignment Scores:
Pred. No.:              1.24e-249       Length:         771
Score:                  247.00          Matches:        247
Percent Similarity:     100.00%         Conservative:   0
Best Local Similarity:  100.00%         Mismatches:     0
Query Match:            100.00%         Indels:         0
DB:                     2               Gaps:           0

US-09-705-500A-3 (1-247) x US-08-431-117A-1 (1-771)

Qy          1 MetLeuGlnAsnSerAlaValLeuLeuValLeuValIleSerAlaSerAlaThrHisGlu 20
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         16 ATGCTCCAAAACTCAGCAGTGCTTCTGGTGCTGGTGATCAGTGCTTCTGCAACCCATGAG 75

Qy         21 AlaGluGlnAsnAspSerValSerProArgLysSerArgValAlaAlaGlnAsnSerAla 40
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         76 GCGGAGCAGAATGACTCTGTGAGCCCCAGGAAATCCCGAGTGGCGGCCCAAAACTCAGCT 135

Qy         41 GluValValArgCysLeuAsnSerAlaLeuGlnValGlyCysGlyAlaPheAlaCysLeu 60
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        136 GAAGTGGTTCGTTGCCTCAACAGTGCTCTACAGGTCGGCTGCGGGGCTTTTGCATGCCTG 195

Qy         61 GluAsnSerThrCysAspThrAspGlyMetTyrAspIleCysLysSerPheLeuTyrSer 80
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        196 GAAAACTCCACCTGTGACACAGATGGGATGTATGACATCTGTAAATCCTTCTTGTACAGC 255

Qy         81 AlaAlaLysPheAspThrGlnGlyLysAlaPheValLysGluSerLeuLysCysIleAla 100
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        256 GCTGCTAAATTTGACACTCAGGGAAAAGCATTCGTCAAAGAGAGCTTAAAATGCATCGCC 315

Qy        101 AsnGlyValThrSerLysValPheLeuAlaIleArgArgCysSerThrPheGlnArgMet 120
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        316 AACGGGGTCACCTCCAAGGTCTTCCTCGCCATTCGGAGGTGCTCCACTTTCCAAAGGATG 375

Qy        121 IleAlaGluValGlnGluGluCysTyrSerLysLeuAsnValCysSerIleAlaLysArg 140
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        376 ATTGCTGAGGTGCAGGAAGAGTGCTACAGCAAGCTGAATGTGTGCAGCATCGCCAAGCGG 435

Qy        141 AsnProGluAlaIleThrGluValValGlnLeuProAsnHisPheSerAsnArgTyrTyr 160
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        436 AACCCTGAAGCCATCACTGAGGTCGTCCAGCTGCCCAATCACTTCTCCAACAGATACTAT 495

Qy        161 AsnArgLeuValArgSerLeuLeuGluCysAspGluAspThrValSerThrIleArgAsp 180
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        496 AACAGACTTGTCCGAAGCCTGCTGGAATGTGATGAAGACACAGTCAGCACAATCAGAGAC 555

Qy        181 SerLeuMetGluLysIleGlyProAsnMetAlaSerLeuPheHisIleLeuGlnThrAsp 200
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        556 AGCCTGATGGAGAAAATTGGGCCTAACATGGCCAGCCTCTTCCACATCCTGCAGACAGAC 615

Qy        201 HisCysAlaGlnThrHisProArgAlaAspPheAsnArgArgArgThrAsnGluProGln 220
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        616 CACTGTGCCCAAACACACCCACGAGCTGACTTCAACAGGAGACGCACCAATGAGCCGCAG 675

Qy        221 LysLeuLysValLeuLeuArgAsnLeuArgGlyGluGluAspSerProSerHisIleLys 240
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        676 AAGCTGAAAGTCCTCCTCAGGAACCTCCGAGGTGAGGAGGACTCTCCCTCCCACATCAAA 735

Qy        241 ArgThrSerHisGluSerAla 247
              |||||||||||||||||||||
Db        736 CGCACATCCCATGAGAGTGCA 756

RESULT 4
US-09-364-539-181
; Sequence 181, Application US/09364539B
; Patent No. 6344321
; GENERAL INFORMATION:
;  APPLICANT: Rabin, Ross
;  APPLICANT: Lochrie, Michael
;  APPLICANT: Janjic, Nebojsa
;  APPLICANT: Gold, Larry
;  TITLE OF INVENTION: Nucleic Acid Ligands Which Bind to Hepatocyte Growth
;  TITLE OF INVENTION: Factor/Scatter Factor (HGF/SF) or its Receptor C-Met
;  FILE REFERENCE: NEX83
;  CURRENT APPLICATION NUMBER: US/09/364,539B
;  CURRENT FILING DATE: 1999-07-29
;  NUMBER OF SEQ ID NOS: 192
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 181
;   LENGTH: 77
;   TYPE: RNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;   OTHER INFORMATION: Sequence
;   FEATURE:
;   NAME/KEY: modified_base
;   LOCATION: (1)..(77)
;   OTHER INFORMATION: All pyrimidines are 2'F.
US-09-364-539-181

Alignment Scores:
Pred. No.:              2.59            Length:         77
Score:                  8.00            Matches:        8
Percent Similarity:     100.00%         Conservative:   0
Best Local Similarity:  100.00%         Mismatches:     0
Query Match:            3.24%           Indels:         0
DB:                     4               Gaps:           0

US-09-705-500A-3 (1-247) x US-09-364-539-181 (1-77)

Qy        222 LeuLysValLeuLeuArgAsnLeu 229
              |||||||||||||||||||||||||
Db         19 CUCAAGGUGCUCCUUAGGAACUUG 42

RESULT 5
US-09-175-928-9
; Sequence 9, Application US/09175928A
; Patent No. 6312921
; GENERAL INFORMATION:
;  APPLICANT: Jacobs, Kenneth
;  APPLICANT: McCoy, John M.
;  APPLICANT: LaVallie, Edward R.
;  APPLICANT: Collins-Racie, Lisa A.
;  APPLICANT: Evans, Cheryl
;  APPLICANT: Merberg, David
;  APPLICANT: Treacy, Maurice
;  APPLICANT: Mi, Sha
;  APPLICANT: Genetics Institute, Inc.
;  TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM
;  FILE REFERENCE: 6006B.AJ172A
;  CURRENT APPLICATION NUMBER: US/09/175,928A
;  CURRENT FILING DATE: 1998-10-20
;  NUMBER OF SEQ ID NOS: 62
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
;   LENGTH: 3153
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-175-928-9

Alignment Scores:
Pred. No.:              104             Length:         3153
Score:                  8.00            Matches:        8
Percent Similarity:     100.00%         Conservative:   0
Best Local Similarity:  100.00%         Mismatches:     0
Query Match:            3.24%           Indels:         0
DB:                     4               Gaps:           0
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US-09-705-500A-3 (1-247) x US-09-175-928-9 (1-3153)

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Qy        219 ProGlnLysLeuLysValLeuLeu 226
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Db       2448 CCCCAGAAGCTGAAAGTCCTCTTG 2471
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RESULT 6
US-08-804-227C-7
; Sequence 7, Application US/08804227C
; Patent No. 5876991
; GENERAL INFORMATION:
; APPLICANT: DeHoff, Bradley S.
; APPLICANT: Kuhstoss, Stuart A.
; APPLICANT: Rosteck, Paul R., Jr.
; APPLICANT: Sutton, Kimberly L.
; TITLE OF INVENTION: POLYKETIDE SYNTHASE GENES
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: THOMAS G. PLANT 1501
; STREET: LILLY CORPORATE CENTER
; CITY: INDIANAPOLIS
; STATE: IN
; COUNTRY: USA
; ZIP: 46285
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: ASCI(DOS) Text only
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/804,227C
; FILING DATE: February 21, 1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Plant, Thomas, G.
; REGISTRATION NUMBER: 35,784
; REFERENCE/DOCKET NUMBER: X-8231
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 317-276-2459
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 44377 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 350..14002
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 14046..20036
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 20110..31284
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 31329..36071
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 36155..41830
US-08-804-227C-7

Alignment Scores:

Pred. No.:	1.44e+03	Length:	44377
Score:	8.00	Matches:	8
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	3.24%	Indels:	0
DB:	2	Gaps:	0

US-09-705-500A-3 (1-247) x US-08-804-227C-7 (1-44377)

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Qy        162 ArgLeuValArgSerLeuLeuGlu 169
              |||||||||||||||||||||||
Db      23686 CGACTGGTCCGGTCCCTCCTCGAG 23709
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RESULT 7
US-08-804-198-1
; Sequence 1, Application US/08804198
; Patent No. 5945320
; GENERAL INFORMATION:
; APPLICANT: Burgett, Stanley G.
; APPLICANT: Kuhstoss, Stuart A.
; APPLICANT: Rao, Nagaraja R.
; APPLICANT: Richardson, Mark A.
; APPLICANT: Rosteck, Paul R., Jr.
; TITLE OF INVENTION: PLATENOLIDE SYNTHASE GENE
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PAUL R. CANTRELL 1138
; STREET: LILLY CORPORATE CENTER
; CITY: INDIANAPOLIS
; STATE: IN
; COUNTRY: USA
; ZIP: 46285
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Macintosh
; OPERATING SYSTEM: Macintosh 7.0
; SOFTWARE: Microsoft Word 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/804,198
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: CANTRELL, PAUL R.
; REGISTRATION NUMBER: 36,470
; REFERENCE/DOCKET NUMBER: P9113
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 317-276-3885
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 44377 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 350..14002
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 14046..20036
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 20110..31284
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 31329..36071
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 36155..41830
US-08-804-198-1

Alignment Scores:

Pred. No.:	1.44e+03	Length:	44377
Score:	8.00	Matches:	8
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	3.24%	Indels:	0
DB:	2	Gaps:	0

US-09-705-500A-3 (1-247) x US-08-804-198-1 (1-44377)

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Qy        162 ArgLeuValArgSerLeuLeuGlu 169
              ||||||||||||||||||||||||||
Db      23686 CGACTGGTCCGGTCCCTCCTCGAG 23709

RESULT 8
US-08-325-553-30/c
; Sequence 30, Application US/08325553
; Patent No. 5538866
;  GENERAL INFORMATION:
;    APPLICANT:  Israeli, Ron S.
;    APPLICANT:  Heston, Warren D.W.
;    APPLICANT:  Fair, William R.
;    TITLE OF INVENTION:  THE PROSTATE-SPECIFIC MEMBRANE ANTIGEN
;    NUMBER OF SEQUENCES:  38
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Cooper & Dunham
;      STREET:  30 Rockefeller Plaza
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  United States of America
;      ZIP:  10112
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/325,553
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/973,337A
;      FILING DATE:  05 NOV 1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  White, John P.
;      REGISTRATION NUMBER:  28,678
;      REFERENCE/DOCKET NUMBER:  1747/41426
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 977-9550
;      TELEFAX:  (212) 664-0525
;      TELEX:  422523 COOP UI
;  INFORMATION FOR SEQ ID NO:  30:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  27 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    ORIGINAL SOURCE:
;      ORGANISM:  Homo Sapien
;      TISSUE TYPE:  Carcinoma
;    IMMEDIATE SOURCE:
;      CLONE:  Prostate Specific Membrane Antigen
US-08-325-553-30

Alignment Scores:
Pred. No.:              10.2          Length:         27
Score:                  7.00          Matches:        7
Percent Similarity:     100.00%       Conservative:   0
Best Local Similarity:  100.00%       Mismatches:     0
Query Match:            2.83%         Indels:         0
DB:                     1             Gaps:           0

US-09-705-500A-3 (1-247) x US-08-325-553-30 (1-27)

Qy        221 LysLeuLysValLeuLeuArg 227
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Db         21 AAGCTGAAAGTTTTGCTCCGT 1

RESULT 9
US-08-208-005C-3
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; Sequence 3, Application US/08208005C
; Patent No. 5837498
;  GENERAL INFORMATION:
;    APPLICANT:  OLSEN, ET AL.
;    TITLE OF INVENTION:  Corpuscles of Stannius Protein, Stanniocalcin
;    NUMBER OF SEQUENCES:  5
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  CARELLA, BYRNE, BAIN, GILFILLAN,
;      ADDRESSEE:  CECCHI, STEWART & OLSTEIN
;      STREET:  6 BECKER FARM ROAD
;      CITY:  ROSELAND
;      STATE:  NEW JERSEY
;      COUNTRY:  USA
;      ZIP:  07068
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5 INCH DISKETTE
;      COMPUTER:  IBM PS/2
;      OPERATING SYSTEM:  MS-DOS
;      SOFTWARE:  WORD PERFECT 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/208,005C
;      FILING DATE:  8 MARCH 1994
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  FERRARO, GREGORY D.
;      REGISTRATION NUMBER:  36,134
;      REFERENCE/DOCKET NUMBER:  325800-78
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  201-994-1700
;      TELEFAX:  201-994-1744
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  27 BASE PAIRS
;      TYPE:  NUCLEIC ACID
;      STRANDEDNESS:  SINGLE
;      TOPOLOGY:  LINEAR
;    MOLECULE TYPE:  Oligonucleotide
US-08-208-005C-3

Alignment Scores:
Pred. No.:              10.2          Length:         27
Score:                  7.00          Matches:        7
Percent Similarity:     100.00%       Conservative:   0
Best Local Similarity:  100.00%       Mismatches:     0
Query Match:            2.83%         Indels:         0
DB:                     2             Gaps:           0

US-09-705-500A-3 (1-247) x US-08-208-005C-3 (1-27)

Qy          1 MetLeuGlnAsnSerAlaVal 7
              |||||||||||||||||||||
Db          7 ATGCTCCAAAACTCAGCAGTG 27

RESULT 10
US-09-038-597A-3
; Sequence 3, Application US/09038597A
; Patent No. 5877290
;  GENERAL INFORMATION:
;    APPLICANT:  OLSEN, ET AL.
;    TITLE OF INVENTION:  Corpuscles of Stannius Protein,
;    TITLE OF INVENTION:  Stanniocalcin
;    NUMBER OF SEQUENCES:  5
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  CARELLA, BYRNE, BAIN, GILFILLAN,
;      ADDRESSEE:  CECCHI, STEWART & OLSTEIN
;      STREET:  6 BECKER FARM ROAD
;      CITY:  ROSELAND
;      STATE:  NEW JERSEY
;      COUNTRY:  USA
;      ZIP:  07068
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;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5 INCH DISKETTE
;      COMPUTER:  IBM PS/2
;      OPERATING SYSTEM:  MS-DOS
;      SOFTWARE:  WORD PERFECT 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/038,597A
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/208,005
;      FILING DATE:  8-MARCH-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  FERRARO, GREGORY D.
;      REGISTRATION NUMBER:  36,134
;      REFERENCE/DOCKET NUMBER:  325800-78
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  201-994-1700
;      TELEFAX:  201-994-1744
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  27 BASE PAIRS
;      TYPE:  NUCLEIC ACID
;      STRANDEDNESS:  SINGLE
;      TOPOLOGY:  LINEAR
;    MOLECULE TYPE:  Oligonucleotide
US-09-038-597A-3

Alignment Scores:
Pred. No.:                10.2          Length:          27
Score:                    7.00          Matches:         7
Percent Similarity:       100.00%       Conservative:    0
Best Local Similarity:    100.00%       Mismatches:      0
Query Match:              2.83%         Indels:          0
DB:                       2             Gaps:            0

US-09-705-500A-3 (1-247) x US-09-038-597A-3 (1-27)

Qy          1 MetLeuGlnAsnSerAlaVal 7
              |||||||||||||||||||||
Db          7 ATGCTCCAAAACTCAGCAGTG 27

RESULT 11
US-08-394-152A-30/c
; Sequence 30, Application US/08394152A
; Patent No. 5935818
;  GENERAL INFORMATION:
;    APPLICANT:  Israeli, Ron S.
;    APPLICANT:  Heston, Warren D.W.
;    APPLICANT:  Fair, William R.
;    TITLE OF INVENTION:  PROSTATE-SPECIFIC MEMBRANE ANTIGEN AND
;    TITLE OF INVENTION:  USES THEREOF
;    NUMBER OF SEQUENCES:  48
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Cooper & Dunham LLP
;      STREET:  1185 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  United States of America
;      ZIP:  10036
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM 330 466 DX2
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/394,152A
;      FILING DATE:  24-FEB-95
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  White, John P.
;      REGISTRATION NUMBER:  28,678
;      REFERENCE/DOCKET NUMBER:  41426-B
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 278-0400
;      TELEFAX:  (212) 391-0525
;  INFORMATION FOR SEQ ID NO:  30:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  27 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    ORIGINAL SOURCE:
;      ORGANISM:  Homo Sapien
;      TISSUE TYPE:  Carcinoma
;    IMMEDIATE SOURCE:
;      CLONE:  Prostate Specific Membrane Antigen
US-08-394-152A-30

Alignment Scores:
Pred. No.:                10.2          Length:          27
Score:                    7.00          Matches:         7
Percent Similarity:       100.00%       Conservative:    0
Best Local Similarity:    100.00%       Mismatches:      0
Query Match:              2.83%         Indels:          0
DB:                       2             Gaps:            0

US-09-705-500A-3 (1-247) x US-08-394-152A-30 (1-27)

Qy          221 LysLeuLysValLeuLeuArg 227
                ||||||||||||||||||||||
Db           21 AAGCTGAAAGTTTTGCTCCGT 1

RESULT 12
US-08-431-117A-3
; Sequence 3, Application US/08431117A
; Patent No. 5994301
;  GENERAL INFORMATION:
;    APPLICANT:  OLSEN, ET AL.
;    TITLE OF INVENTION:  Corpuscles of Stannius Protein, Stanniocalcin
;    NUMBER OF SEQUENCES:  8
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  CARELLA, BYRNE, BAIN, GILFILLAN,
;      ADDRESSEE:  CECCHI, STEWART & OLSTEIN
;      STREET:  6 BECKER FARM ROAD
;      CITY:  ROSELAND
;      STATE:  NEW JERSEY
;      COUNTRY:  USA
;      ZIP:  07068
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5 INCH DISKETTE
;      COMPUTER:  IBM PS/2
;      OPERATING SYSTEM:  MS-DOS
;      SOFTWARE:  WORD PERFECT 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/431,117A
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/208,005
;      FILING DATE:  8 MARCH 1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  FERRARO, GREGORY D.
;      REGISTRATION NUMBER:  36,134
;      REFERENCE/DOCKET NUMBER:  325800-296
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  201-994-1700
;      TELEFAX:  201-994-1744
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  27 BASE PAIRS
;      TYPE:  NUCLEIC ACID
;      STRANDEDNESS:  SINGLE
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;      TOPOLOGY:  LINEAR
;    MOLECULE TYPE:  Oligonucleotide
US-08-431-117A-3

Alignment Scores:
Pred. No.:              10.2          Length:         27
Score:                  7.00          Matches:        7
Percent Similarity:     100.00%       Conservative:   0
Best Local Similarity:  100.00%       Mismatches:     0
Query Match:            2.83%         Indels:         0
DB:                     2             Gaps:           0

US-09-705-500A-3 (1-247) x US-08-431-117A-3 (1-27)

Qy          1 MetLeuGlnAsnSerAlaVal 7
              |||||||||||||||||||
Db          7 ATGCTCCAAAACTCAGCAGTG 27

RESULT 13
US-08-208-005C-4/c
; Sequence 4, Application US/08208005C
; Patent No. 5837498
;  GENERAL INFORMATION:
;    APPLICANT:  OLSEN, ET AL.
;    TITLE OF INVENTION:  Corpuscles of Stannius Protein, Stanniocalcin
;    NUMBER OF SEQUENCES:  5
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  CARELLA, BYRNE, BAIN, GILFILLAN,
;      ADDRESSEE:  CECCHI, STEWART & OLSTEIN
;      STREET:  6 BECKER FARM ROAD
;      CITY:  ROSELAND
;      STATE:  NEW JERSEY
;      COUNTRY:  USA
;      ZIP:  07068
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5 INCH DISKETTE
;      COMPUTER:  IBM PS/2
;      OPERATING SYSTEM:  MS-DOS
;      SOFTWARE:  WORD PERFECT 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/208,005C
;      FILING DATE:  8 MARCH 1994
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  FERRARO, GREGORY D.
;      REGISTRATION NUMBER:  36,134
;      REFERENCE/DOCKET NUMBER:  325800-78
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  201-994-1700
;      TELEFAX:  201-994-1744
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  31 BASE PAIRS
;      TYPE:  NUCLEIC ACID
;      STRANDEDNESS:  SINGLE
;      TOPOLOGY:  LINEAR
;    MOLECULE TYPE:  Oligonucleotide
US-08-208-005C-4

Alignment Scores:
Pred. No.:              11.7          Length:         31
Score:                  7.00          Matches:        7
Percent Similarity:     100.00%       Conservative:   0
Best Local Similarity:  100.00%       Mismatches:     0
Query Match:            2.83%         Indels:         0
DB:                     2             Gaps:           0

US-09-705-500A-3 (1-247) x US-08-208-005C-4 (1-31)

Qy          241 ArgThrSerHisGluSerAla 247
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Db           31 CGCACATCCCATGAGAGTGCA 11

RESULT 14
US-09-038-597A-4/c
; Sequence 4, Application US/09038597A
; Patent No. 5877290
;  GENERAL INFORMATION:
;    APPLICANT:  OLSEN, ET AL.
;    TITLE OF INVENTION:  Corpuscles of Stannius Protein,
;    TITLE OF INVENTION:  Stanniocalcin
;    NUMBER OF SEQUENCES:  5
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  CARELLA, BYRNE, BAIN, GILFILLAN,
;      ADDRESSEE:  CECCHI, STEWART & OLSTEIN
;      STREET:  6 BECKER FARM ROAD
;      CITY:  ROSELAND
;      STATE:  NEW JERSEY
;      COUNTRY:  USA
;      ZIP:  07068
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5 INCH DISKETTE
;      COMPUTER:  IBM PS/2
;      OPERATING SYSTEM:  MS-DOS
;      SOFTWARE:  WORD PERFECT 5.1
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;      APPLICATION NUMBER:  US/09/038,597A
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/208,005
;      FILING DATE:  8-MARCH-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  FERRARO, GREGORY D.
;      REGISTRATION NUMBER:  36,134
;      REFERENCE/DOCKET NUMBER:  325800-78
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  201-994-1700
;      TELEFAX:  201-994-1744
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  31 BASE PAIRS
;      TYPE:  NUCLEIC ACID
;      STRANDEDNESS:  SINGLE
;      TOPOLOGY:  LINEAR
;    MOLECULE TYPE:  Oligonucleotide
US-09-038-597A-4

Alignment Scores:
Pred. No.:              11.7          Length:         31
Score:                  7.00          Matches:        7
Percent Similarity:     100.00%       Conservative:   0
Best Local Similarity:  100.00%       Mismatches:     0
Query Match:            2.83%         Indels:         0
DB:                     2             Gaps:           0

US-09-705-500A-3 (1-247) x US-09-038-597A-4 (1-31)

Qy          241 ArgThrSerHisGluSerAla 247
                |||||||||||||||||||
Db           31 CGCACATCCCATGAGAGTGCA 11

RESULT 15
US-08-431-117A-4/c
; Sequence 4, Application US/08431117A
; Patent No. 5994301
;  GENERAL INFORMATION:
;    APPLICANT:  OLSEN, ET AL.
;    TITLE OF INVENTION:  Corpuscles of Stannius Protein, Stanniocalcin
;    NUMBER OF SEQUENCES:  8
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  CARELLA, BYRNE, BAIN, GILFILLAN,
;      ADDRESSEE:  CECCHI, STEWART & OLSTEIN
```

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;       STREET:  6 BECKER FARM ROAD
;       CITY:  ROSELAND
;       STATE:  NEW JERSEY
;       COUNTRY:  USA
;       ZIP:  07068
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  3.5 INCH DISKETTE
;       COMPUTER:  IBM PS/2
;       OPERATING SYSTEM:  MS-DOS
;       SOFTWARE:  WORD PERFECT 5.1
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/431,117A
;       FILING DATE:
;       CLASSIFICATION:  435
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  08/208,005
;       FILING DATE:  8 MARCH 1994
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  FERRARO, GREGORY D.
;       REGISTRATION NUMBER:  36,134
;       REFERENCE/DOCKET NUMBER:  325800-296
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  201-994-1700
;       TELEFAX:  201-994-1744
;   INFORMATION FOR SEQ ID NO:  4:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  31 BASE PAIRS
;       TYPE:  NUCLEIC ACID
;       STRANDEDNESS:  SINGLE
;       TOPOLOGY:  LINEAR
;     MOLECULE TYPE:  Oligonucleotide
US-08-431-117A-4

Alignment Scores:
Pred. No.:              11.7            Length:         31
Score:                  7.00            Matches:        7
Percent Similarity:     100.00%         Conservative:   0
Best Local Similarity:  100.00%         Mismatches:     0
Query Match:            2.83%           Indels:         0
DB:                     2               Gaps:           0

US-09-705-500A-3 (1-247) x US-08-431-117A-4 (1-31)

Qy        241 ArgThrSerHisGluSerAla 247
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Db         31 CGCACATCCCATGAGAGTGCA 11


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Job time : 107 secs
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GenCore version 5.1.6

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Ygapop 60.0 , Ygapext 60.0
Fgapop 6.0 , Fgapext 7.0
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Searched: 870385 seqs, 699768693 residues

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-MAXLEN=2000000000 -USER=US09705500_@CGN_1_1_104_@runat_06062003_113647_8081
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-LONGLOG -DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	247	100.0	1283	10	US-09-840-989A-1	Sequence 1, Appli
3	247	100.0	3765	12	US-10-044-090-638	Sequence 638, App
4	247	100.0	3897	9	US-10-198-846-13651	Sequence 13651, A
5	184	74.5	2572	10	US-09-925-300-486	Sequence 486, App
6	160	64.8	585	10	US-09-778-320-149	Sequence 149, App
7	160	64.8	585	10	US-09-910-689-149	Sequence 149, App
8	160	64.8	585	12	US-10-010-742-149	Sequence 149, App
c 9	132	53.4	473	9	US-10-060-036-2677	Sequence 2677, Ap
10	76	30.8	436	9	US-09-918-995-33032	Sequence 33032, A
c 11	72	29.1	219	10	US-09-864-761-21309	Sequence 21309, A
c 12	41	16.6	362	10	US-09-864-761-4563	Sequence 4563, Ap
13	40	16.2	420	10	US-09-778-320-141	Sequence 141, App
14	40	16.2	420	10	US-09-910-689-141	Sequence 141, App
15	40	16.2	420	12	US-10-010-742-141	Sequence 141, App
16	8	3.2	324	9	US-10-169-048-45	Sequence 45, Appl
17	8	3.2	416	9	US-09-854-133-398	Sequence 398, App
18	8	3.2	416	10	US-09-738-973-398	Sequence 398, App
19	8	3.2	3153	9	US-10-114-893-138	Sequence 138, App
20	8	3.2	3153	9	US-10-016-249-9	Sequence 9, Appli
21	8	3.2	3776	10	US-09-900-237-3	Sequence 3, Appli
22	8	3.2	7525	10	US-09-967-552A-72	Sequence 72, Appl
23	8	3.2	8911	10	US-09-764-853-895	Sequence 895, App
c 24	8	3.2	10302	10	US-09-782-378A-23	Sequence 23, Appl
c 25	8	3.2	14286	10	US-09-070-927A-162	Sequence 162, App
26	8	3.2	32768	10	US-09-070-927A-399	Sequence 399, App
c 27	8	3.2	1830121	9	US-10-329-960-1	Sequence 1, Appli
28	7	2.8	27	10	US-09-840-989A-5	Sequence 5, Appli
29	7	2.8	27	12	US-10-116-051-3	Sequence 3, Appli
30	7	2.8	28	9	US-09-934-020A-3	Sequence 3, Appli
31	7	2.8	28	9	US-09-934-020A-6	Sequence 6, Appli
32	7	2.8	28	9	US-09-934-020A-8	Sequence 8, Appli
33	7	2.8	28	9	US-09-934-020A-10	Sequence 10, Appl
c 34	7	2.8	31	10	US-09-840-989A-6	Sequence 6, Appli
c 35	7	2.8	31	12	US-10-116-051-4	Sequence 4, Appli
36	7	2.8	37	10	US-09-840-989A-7	Sequence 7, Appli
37	7	2.8	37	10	US-09-840-989A-9	Sequence 9, Appli
38	7	2.8	37	12	US-10-116-051-5	Sequence 5, Appli
39	7	2.8	37	12	US-10-116-051-7	Sequence 7, Appli
40	7	2.8	106	10	US-09-864-761-27322	Sequence 27322, A
c 41	7	2.8	154	10	US-09-864-761-23903	Sequence 23903, A
c 42	7	2.8	155	10	US-09-783-590-12295	Sequence 12295, A
c 43	7	2.8	182	10	US-09-815-242-2990	Sequence 2990, Ap
c 44	7	2.8	182	10	US-09-815-242-3355	Sequence 3355, Ap
45	7	2.8	186	9	US-10-044-359-13	Sequence 13, Appl
c 46	7	2.8	238	10	US-09-923-876-2920	Sequence 2920, Ap
c 47	7	2.8	264	10	US-09-923-876-626	Sequence 626, App
48	7	2.8	277	10	US-09-867-701-8578	Sequence 8578, Ap
c 49	7	2.8	289	10	US-09-878-574-1957	Sequence 1957, Ap
50	7	2.8	292	9	US-09-796-692-6712	Sequence 6712, Ap
51	7	2.8	292	9	US-10-040-862-6712	Sequence 6712, Ap
c 52	7	2.8	293	10	US-09-867-701-6991	Sequence 6991, Ap
c 53	7	2.8	294	10	US-09-974-300-7499	Sequence 7499, Ap
c 54	7	2.8	297	10	US-09-867-550-125	Sequence 125, App
55	7	2.8	297	12	US-10-044-592-63	Sequence 63, Appl
c 56	7	2.8	317	9	US-09-796-692-7679	Sequence 7679, Ap
c 57	7	2.8	317	9	US-10-040-862-7679	Sequence 7679, Ap
58	7	2.8	345	10	US-09-815-242-9104	Sequence 9104, Ap
c 59	7	2.8	361	9	US-09-809-391-71	Sequence 71, Appl
60	7	2.8	381	9	US-09-738-626-1527	Sequence 1527, Ap
61	7	2.8	384	10	US-09-960-352-577	Sequence 577, App
62	7	2.8	389	10	US-09-960-352-1972	Sequence 1972, Ap
c 63	7	2.8	395	9	US-09-918-995-4663	Sequence 4663, Ap
64	7	2.8	398	9	US-09-796-692-2804	Sequence 2804, Ap
65	7	2.8	398	9	US-10-040-862-2804	Sequence 2804, Ap
c 66	7	2.8	403	10	US-09-864-761-3640	Sequence 3640, Ap
67	7	2.8	413	10	US-09-867-701-1633	Sequence 1633, Ap
c 68	7	2.8	421	9	US-09-796-692-8115	Sequence 8115, Ap
c 69	7	2.8	421	9	US-10-040-862-8115	Sequence 8115, Ap
70	7	2.8	447	10	US-09-770-444-767	Sequence 767, App
71	7	2.8	450	9	US-09-764-868-404	Sequence 404, App
72	7	2.8	450	9	US-10-103-313-135	Sequence 135, App
73	7	2.8	450	9	US-10-103-313-258	Sequence 258, App
c 74	7	2.8	454	9	US-09-918-995-11842	Sequence 11842, A
c 75	7	2.8	454	10	US-09-728-445-494	Sequence 494, App
c 76	7	2.8	463	9	US-09-918-995-19660	Sequence 19660, A
77	7	2.8	463	10	US-09-864-761-5708	Sequence 5708, Ap

	78	7	2.8	466	9	US-09-918-995-14339	Sequence 14339, A
c	79	7	2.8	466	10	US-09-864-864-97	Sequence 97, Appl
c	80	7	2.8	467	10	US-09-864-761-5409	Sequence 5409, Ap
c	81	7	2.8	467	10	US-09-864-761-5918	Sequence 5918, Ap
	82	7	2.8	469	9	US-10-178-213-313	Sequence 313, App
c	83	7	2.8	475	10	US-09-864-761-189	Sequence 189, App
	84	7	2.8	476	10	US-09-864-761-10674	Sequence 10674, A
	85	7	2.8	478	9	US-09-918-995-21127	Sequence 21127, A
	86	7	2.8	485	9	US-09-764-891-8018	Sequence 8018, Ap
c	87	7	2.8	486	10	US-09-969-708-515	Sequence 515, App
	88	7	2.8	492	10	US-09-815-242-8120	Sequence 8120, Ap
	89	7	2.8	515	9	US-09-918-995-5520	Sequence 5520, Ap
	90	7	2.8	517	9	US-09-918-995-20243	Sequence 20243, A
c	91	7	2.8	523	10	US-09-867-701-5640	Sequence 5640, Ap
	92	7	2.8	530	9	US-10-219-220-16	Sequence 16, Appl
	93	7	2.8	537	10	US-09-815-242-4479	Sequence 4479, Ap
	94	7	2.8	540	10	US-09-864-761-22470	Sequence 22470, A
	95	7	2.8	549	9	US-09-991-936-1777	Sequence 1777, Ap
	96	7	2.8	549	9	US-09-991-936-1791	Sequence 1791, Ap
c	97	7	2.8	553	10	US-09-864-761-13169	Sequence 13169, A
c	98	7	2.8	565	9	US-09-764-891-108	Sequence 108, App
c	99	7	2.8	569	10	US-09-864-761-7542	Sequence 7542, Ap
c	100	7	2.8	570	9	US-09-918-995-12139	Sequence 12139, A
c	101	7	2.8	570	10	US-09-879-536-544	Sequence 544, App
	102	7	2.8	578	10	US-09-867-701-1450	Sequence 1450, Ap
	103	7	2.8	589	10	US-09-764-864-227	Sequence 227, App
c	104	7	2.8	600	10	US-09-864-761-7172	Sequence 7172, Ap
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c	108	7	2.8	648	10	US-09-946-805-5	Sequence 5, Appli
c	109	7	2.8	663	10	US-09-879-536-401	Sequence 401, App
	110	7	2.8	708	10	US-09-764-864-656	Sequence 656, App
c	111	7	2.8	720	10	US-09-974-300-5207	Sequence 5207, Ap
c	112	7	2.8	758	10	US-09-866-562-34	Sequence 34, Appl
	113	7	2.8	830	9	US-10-198-846-7541	Sequence 7541, Ap
c	114	7	2.8	903	10	US-09-815-242-2092	Sequence 2092, Ap
	115	7	2.8	904	9	US-10-228-794-59	Sequence 59, Appl
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c	121	7	2.8	918	9	US-10-175-737-475	Sequence 475, App
c	122	7	2.8	918	9	US-10-173-706-475	Sequence 475, App
c	123	7	2.8	918	9	US-10-175-738-475	Sequence 475, App
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c	147	7	2.8	918	9	US-10-176-993-475	Sequence 475, App
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c	155	7	2.8	918	9	US-10-173-705-475	Sequence 475, App
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c 563	7	2.8	1164	9	US-10-174-582-221	Sequence 221, App
c 564	7	2.8	1164	9	US-10-174-588-221	Sequence 221, App
c 565	7	2.8	1164	9	US-10-175-739-221	Sequence 221, App
c 566	7	2.8	1164	9	US-10-175-740-221	Sequence 221, App
c 567	7	2.8	1164	9	US-10-175-743-221	Sequence 221, App
c 568	7	2.8	1164	9	US-10-176-488-221	Sequence 221, App
c 569	7	2.8	1164	9	US-10-176-492-221	Sequence 221, App
c 570	7	2.8	1164	9	US-10-176-747-221	Sequence 221, App
c 571	7	2.8	1164	9	US-10-176-750-221	Sequence 221, App
c 572	7	2.8	1164	9	US-10-176-985-221	Sequence 221, App
c 573	7	2.8	1164	9	US-10-176-987-221	Sequence 221, App
c 574	7	2.8	1164	9	US-10-176-991-221	Sequence 221, App
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c 578	7	2.8	1164	9	US-09-990-711-294	Sequence 294, App
c 579	7	2.8	1164	9	US-10-173-695-221	Sequence 221, App
c 580	7	2.8	1164	9	US-10-173-697-221	Sequence 221, App
c 581	7	2.8	1164	9	US-10-173-705-221	Sequence 221, App
c 582	7	2.8	1164	9	US-10-174-576-221	Sequence 221, App
c 583	7	2.8	1164	9	US-10-174-585-221	Sequence 221, App
c 584	7	2.8	1164	9	US-10-174-586-221	Sequence 221, App
c 585	7	2.8	1164	9	US-10-175-747-221	Sequence 221, App
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c 592	7	2.8	1164	9	US-10-176-919-221	Sequence 221, App
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ALIGNMENTS

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; Sequence 1, Application US/10116051
; Patent No. US20020146791A1
; GENERAL INFORMATION:
;  APPLICANT: Olsen et al.
;  TITLE OF INVENTION: CORPUSCLES OF STANNIUS PROTEIN, STANNIOCALCIN
;  FILE REFERENCE: PF108P1D1C1
;  CURRENT APPLICATION NUMBER: US/10/116,051
;  CURRENT FILING DATE:  2002-04-05
;  PRIOR APPLICATION NUMBER: 09/312,610
;  PRIOR FILING DATE: 1999-05-17
;  PRIOR APPLICATION NUMBER: 08/431,117
;  PRIOR FILING DATE: 1995-04-28
;  PRIOR APPLICATION NUMBER: 08/208,005
;  PRIOR FILING DATE: 1994-03-08
;  NUMBER OF SEQ ID NOS: 10
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
;  LENGTH: 771
;  TYPE: DNA
;  ORGANISM: Homo sapiens
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US-10-116-051-1

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Percent Similarity:     100.00%        Conservative:    0
Best Local Similarity:  100.00%        Mismatches:      0
Query Match:            100.00%        Indels:          0
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US-09-705-500A-3 (1-247) x US-10-116-051-1 (1-771)

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RESULT 2
US-09-840-989A-1
; Sequence 1, Application US/09840989A
; Patent No. US20020042372A1
; GENERAL INFORMATION:
;  APPLICANT: Olsen et al.
;  TITLE OF INVENTION: Stanniocalcin Polynucleotides, Polypeptides, and Methods Based The
;  FILE REFERENCE: PF108P2
;  CURRENT APPLICATION NUMBER: US/09/840,989A
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;  CURRENT FILING DATE:  2001-04-25
;  PRIOR APPLICATION NUMBER: PCT/US00/29432
;  PRIOR FILING DATE: 2000-10-26
;  PRIOR APPLICATION NUMBER: US 60/161,740
;  PRIOR FILING DATE: 1999-10-27
;  NUMBER OF SEQ ID NOS: 12
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;   ORGANISM: Homo sapiens
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;   OTHER INFORMATION: n is equal to a, t, c, or g.
US-09-840-989A-1

Alignment Scores:
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Score:                    247.00          Matches:        247
Percent Similarity:       100.00%         Conservative:   0
Best Local Similarity:    100.00%         Mismatches:     0
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US-09-705-500A-3 (1-247) x US-09-840-989A-1 (1-1283)

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Qy         41 GluValValArgCysLeuAsnSerAlaLeuGlnValGlyCysGlyAlaPheAlaCysLeu 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        165 GAAGTGGTTCGTTGCCTCAACAGTGCTCTACAGGTCGGCTGCGGGGCTTTTGCATGCCTG 224

Qy         61 GluAsnSerThrCysAspThrAspGlyMetTyrAspIleCysLysSerPheLeuTyrSer 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        225 GAAAACTCCACCTGTGACACAGATGGGATGTATGACATCTGTAAATCCTTCTTGTACAGC 284

Qy         81 AlaAlaLysPheAspThrGlnGlyLysAlaPheValLysGluSerLeuLysCysIleAla 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        285 GCTGCTAAATTTGACACTCAGGGAAAAGCATTCGTCAAAGAGAGCTTAAAATGCATCGCC 344

Qy        101 AsnGlyValThrSerLysValPheLeuAlaIleArgArgCysSerThrPheGlnArgMet 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        345 AACGGGGTCACCTCCAAGGTCTTCCTCGCCATTCGGAGGTGCTCCACTTTCCAAAGGATG 404

Qy        121 IleAlaGluValGlnGluGluCysTyrSerLysLeuAsnValCysSerIleAlaLysArg 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        405 ATTGCTGAGGTGCAGGAAGAGTGCTACAGCAAGCTGAATGTGTGCAGCATCGCCAAGCGG 464

Qy        141 AsnProGluAlaIleThrGluValValGlnLeuProAsnHisPheSerAsnArgTyrTyr 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        465 AACCCTGAAGCCATCACTGAGGTCGTCCAGCTGCCCAATCACTTCTCCAACAGATACTAT 524

Qy        161 AsnArgLeuValArgSerLeuLeuGluCysAspGluAspThrValSerThrIleArgAsp 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        525 AACAGACTTGTCCGAAGCCTGCTGGAATGTGATGAAGACACAGTCAGCACAATCAGAGAC 584

Qy        181 SerLeuMetGluLysIleGlyProAsnMetAlaSerLeuPheHisIleLeuGlnThrAsp 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        585 AGCCTGATGGAGAAAATTGGGCCTAACATGGCCAGCCTCTTCCACATCCTGCAGACAGAC 644

Qy        201 HisCysAlaGlnThrHisProArgAlaAspPheAsnArgArgArgThrAsnGluProGln 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        645 CACTGTGCCCAAACACACCCACGAGCTGACTTCAACAGGAGACGCACCAATGAGCCGCAG 704

Qy        221 LysLeuLysValLeuLeuArgAsnLeuArgGlyGluGluAspSerProSerHisIleLys 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        705 AAGCTGAAAGTCCTCCTCAGGAACCTCCGAGGTGAGGAGGACTCTCCCTCCCACATCAAA 764

Qy        241 ArgThrSerHisGluSerAla 247
              |||||||||||||||||||||
Db        765 CGCACATCCCATGAGAGTGCA 785

RESULT 3
US-10-044-090-638
; Sequence 638, Application US/10044090
; Patent No. US20020137081A1
; GENERAL INFORMATION:
;  APPLICANT: Olga Bandman
;  TITLE OF INVENTION: GENES DIFFERENTIALLY EXPRESSED IN VASCULAR TISSUE ACTIVATION
;  FILE REFERENCE: PA-0028 US
;  CURRENT APPLICATION NUMBER: US/10/044,090
;  CURRENT FILING DATE:  2002-01-09
;  NUMBER OF SEQ ID NOS: 850
;  SOFTWARE: PERL Program
; SEQ ID NO 638
;   LENGTH: 3765
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: Incyte ID No. US20020137081A1 331181.1
;   NAME/KEY: unsure
;   LOCATION: 2378, 3184, 3187, 3194
;   OTHER INFORMATION: a, t, c, g, or other
US-10-044-090-638

Alignment Scores:
Pred. No.:                5.6e-249        Length:         3765
Score:                    247.00          Matches:        247
Percent Similarity:       100.00%         Conservative:   0
Best Local Similarity:    100.00%         Mismatches:     0
Query Match:              100.00%         Indels:         0
DB:                       12              Gaps:           0

US-09-705-500A-3 (1-247) x US-10-044-090-638 (1-3765)

Qy          1 MetLeuGlnAsnSerAlaValLeuLeuValLeuValIleSerAlaSerAlaThrHisGlu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        174 ATGCTCCAAAACTCAGCAGTGCTTCTGGTGCTGGTGATCAGTGCTTCTGCAACCCATGAG 233

Qy         21 AlaGluGlnAsnAspSerValSerProArgLysSerArgValAlaAlaGlnAsnSerAla 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        234 GCGGAGCAGAATGACTCTGTGAGCCCCAGGAAATCCCGAGTGGCGGCTCAAAACTCAGCT 293

Qy         41 GluValValArgCysLeuAsnSerAlaLeuGlnValGlyCysGlyAlaPheAlaCysLeu 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        294 GAAGTGGTTCGTTGCCTCAACAGTGCTCTACAGGTCGGCTGCGGGGCTTTTGCATGCCTG 353

Qy         61 GluAsnSerThrCysAspThrAspGlyMetTyrAspIleCysLysSerPheLeuTyrSer 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        354 GAAAACTCCACCTGTGACACAGATGGGATGTATGACATCTGTAAATCCTTCTTGTACAGC 413

Qy         81 AlaAlaLysPheAspThrGlnGlyLysAlaPheValLysGluSerLeuLysCysIleAla 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        414 GCTGCTAAATTTGACACTCAGGGAAAAGCATTCGTCAAAGAGAGCTTAAAATGCATCGCC 473

Qy        101 AsnGlyValThrSerLysValPheLeuAlaIleArgArgCysSerThrPheGlnArgMet 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        474 AACGGGGTCACCTCCAAGGTCTTCCTCGCCATTCGGAGGTGCTCCACTTTCCAAAGGATG 533
```

```
Qy        121 IleAlaGluValGlnGluGluCysTyrSerLysLeuAsnValCysSerIleAlaLysArg 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        534 ATTGCTGAGGTGCAGGAAGAGTGCTACAGCAAGCTGAATGTGTGCAGCATCGCCAAGCGG 593

Qy        141 AsnProGluAlaIleThrGluValValGlnLeuProAsnHisPheSerAsnArgTyrTyr 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        594 AACCCTGAAGCCATCACTGAGGTCGTCCAGCTGCCCAATCACTTCTCCAACAGATACTAT 653

Qy        161 AsnArgLeuValArgSerLeuLeuGluCysAspGluAspThrValSerThrIleArgAsp 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        654 AACAGACTTGTCCGAAGCCTGCTGGAATGTGATGAAGACACAGTCAGCACAATCAGAGAC 713

Qy        181 SerLeuMetGluLysIleGlyProAsnMetAlaSerLeuPheHisIleLeuGlnThrAsp 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        714 AGCCTGATGGAGAAAATTGGGCCTAACATGGCCAGCCTCTTCCACATCCTGCAGACAGAC 773

Qy        201 HisCysAlaGlnThrHisProArgAlaAspPheAsnArgArgArgThrAsnGluProGln 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        774 CACTGTGCCCAAACACACCCACGAGCTGACTTCAACAGGAGACGCACCAATGAGCCGCAG 833

Qy        221 LysLeuLysValLeuLeuArgAsnLeuArgGlyGluGluAspSerProSerHisIleLys 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        834 AAGCTGAAAGTCCTCCTCAGGAACCTCCGAGGTGAGGAGGACTCTCCCTCCCACATCAAA 893

Qy        241 ArgThrSerHisGluSerAla 247
              ||||||||||||||||||||
Db        894 CGCACATCCCATGAGAGTGCA 914

RESULT 4
US-10-198-846-13651
; Sequence 13651, Application US/10198846
; Publication No. US20030099974A1
; GENERAL INFORMATION:
;  APPLICANT: Lillie, James
;  APPLICANT:  Xu, Yongyao
;  APPLICANT:  Wang, Youzhen
;  APPLICANT:  Steinmann, Kathleen
;  TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS
;  TITLE OF INVENTION:  FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
;  TITLE OF INVENTION:  THERAPY OF BREAST CANCER
;  FILE REFERENCE: MRI-049
;  CURRENT APPLICATION NUMBER: US/10/198,846
;  CURRENT FILING DATE:  2002-07-18
;  PRIOR APPLICATION NUMBER: 60/306,220
;  PRIOR FILING DATE: 2001-07-18
;  NUMBER OF SEQ ID NOS: 14084
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 13651
;   LENGTH: 3897
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: 3878, 3879, 3880, 3881, 3882, 3883, 3884, 3885, 3886, 3887,
;   LOCATION: 3888, 3889, 3890, 3891, 3892, 3893, 3894, 3895, 3896, 3897
;   OTHER INFORMATION: n = A,T,C or G
US-10-198-846-13651

Alignment Scores:
Pred. No.:              5.79e-249       Length:         3897
Score:                  247.00          Matches:        247
Percent Similarity:     100.00%         Conservative:   0
Best Local Similarity:  100.00%         Mismatches:     0
Query Match:            100.00%         Indels:         0
DB:                     9               Gaps:           0

US-09-705-500A-3 (1-247) x US-10-198-846-13651 (1-3897)

Qy          1 MetLeuGlnAsnSerAlaValLeuLeuValLeuValIleSerAlaSerAlaThrHisGlu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        285 ATGCTCCAAAACTCAGCAGTGCTTCTGGTGCTGGTGATCAGTGCTTCTGCAACCCATGAG 344

Qy         21 AlaGluGlnAsnAspSerValSerProArgLysSerArgValAlaAlaGlnAsnSerAla 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        345 GCGGAGCAGAATGACTCTGTGAGCCCCAGGAAATCCCGAGTGGCGGCTCAAAACTCAGCT 404

Qy         41 GluValValArgCysLeuAsnSerAlaLeuGlnValGlyCysGlyAlaPheAlaCysLeu 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        405 GAAGTGGTTCGTTGCCTCAACAGTGCTCTACAGGTCGGCTGCGGGGCTTTTGCATGCCTG 464

Qy         61 GluAsnSerThrCysAspThrAspGlyMetTyrAspIleCysLysSerPheLeuTyrSer 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        465 GAAAACTCCACCTGTGACACAGATGGGATGTATGACATCTGTAAATCCTTCTTGTACAGC 524

Qy         81 AlaAlaLysPheAspThrGlnGlyLysAlaPheValLysGluSerLeuLysCysIleAla 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        525 GCTGCTAAATTTGACACTCAGGGAAAAGCATTCGTCAAAGAGAGCTTAAAATGCATCGCC 584

Qy        101 AsnGlyValThrSerLysValPheLeuAlaIleArgArgCysSerThrPheGlnArgMet 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        585 AACGGGGTCACCTCCAAGGTCTTCCTCGCCATTCGGAGGTGCTCCACTTTCCAAAGGATG 644

Qy        121 IleAlaGluValGlnGluGluCysTyrSerLysLeuAsnValCysSerIleAlaLysArg 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        645 ATTGCTGAGGTGCAGGAAGAGTGCTACAGCAAGCTGAATGTGTGCAGCATCGCCAAGCGG 704

Qy        141 AsnProGluAlaIleThrGluValValGlnLeuProAsnHisPheSerAsnArgTyrTyr 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        705 AACCCTGAAGCCATCACTGAGGTCGTCCAGCTGCCCAATCACTTCTCCAACAGATACTAT 764

Qy        161 AsnArgLeuValArgSerLeuLeuGluCysAspGluAspThrValSerThrIleArgAsp 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        765 AACAGACTTGTCCGAAGCCTGCTGGAATGTGATGAAGACACAGTCAGCACAATCAGAGAC 824

Qy        181 SerLeuMetGluLysIleGlyProAsnMetAlaSerLeuPheHisIleLeuGlnThrAsp 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        825 AGCCTGATGGAGAAAATTGGGCCTAACATGGCCAGCCTCTTCCACATCCTGCAGACAGAC 884

Qy        201 HisCysAlaGlnThrHisProArgAlaAspPheAsnArgArgArgThrAsnGluProGln 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        885 CACTGTGCCCAAACACACCCACGAGCTGACTTCAACAGGAGACGCACCAATGAGCCGCAG 944

Qy        221 LysLeuLysValLeuLeuArgAsnLeuArgGlyGluGluAspSerProSerHisIleLys 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        945 AAGCTGAAAGTCCTCCTCAGGAACCTCCGAGGTGAGGAGGACTCTCCCTCCCACATCAAA 1004

Qy        241 ArgThrSerHisGluSerAla 247
              ||||||||||||||||||||
Db       1005 CGCACATCCCATGAGAGTGCA 1025

RESULT 5
US-09-925-300-486
; Sequence 486, Application US/09925300
; Patent No. US20020151681A1
; GENERAL INFORMATION:
;  APPLICANT: Craig Rosen,
;  APPLICANT:  Steve Ruben
;  TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
;  FILE REFERENCE: PA101
;  CURRENT APPLICATION NUMBER: US/09/925,300
;  CURRENT FILING DATE:  2001-08-10
;  PRIOR APPLICATION NUMBER: PCT/US00/05988
;  PRIOR FILING DATE: 2000-03-08
;  PRIOR APPLICATION NUMBER: 60/124,270
;  PRIOR FILING DATE: 1999-03-12
;  NUMBER OF SEQ ID NOS: 1890
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 486
;   LENGTH: 2572
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc feature
;   LOCATION: (823)
;   OTHER INFORMATION: n equals a,t,g, or c
US-09-925-300-486
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Alignment Scores:
Pred. No.:              4.29e-183       Length:         2572
Score:                  184.00          Matches:        246
Percent Similarity:     98.80%          Conservative:   0
Best Local Similarity:  98.80%          Mismatches:     1
Query Match:            74.49%          Indels:         3
DB:                     10              Gaps:           0

US-09-705-500A-3 (1-247) x US-09-925-300-486 (1-2572)

Qy          1 MetLeuGlnAsnSerAlaValLeuLeuValLeuValIleSerAlaSerAlaThrHisGlu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        265 ATGCTCCAAAACTCAGCAGTGCTTCTGGTGCTGGTGATCAGTGCTTCTGCAACCCATGAG 324

Qy         21 AlaGluGlnAsnAspSerValSerProArgLysSerArgValAlaAlaGlnAsnSerAla 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        325 GCGGAGCAGAATGACTCTGTGAGCCCCAGGAAATCCCGAGTGGCGGCTCAAAACTCAGCT 384

Qy         41 GluValValArgCysLeuAsnSerAlaLeuGlnValGlyCysGlyAlaPheAlaCysLeu 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        385 GAAGTGGTTCGTTGCCTCAACAGTGCTCTACAGGTCGGCTGCGGGGCTTTTGCATGCCTG 444

Qy         61 GluAsnSerThrCysAspThrAspGlyMetTyrAspIleCysLysSerPheLeuTyrSer 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        445 GAAAACTCCACCTGTGACACAGATGGGATGTATGACATCTGTAAATCCTTCTTGTACAGC 504

Qy         81 AlaAlaLysPheAspThrGlnGlyLysAlaPheValLysGluSerLeuLysCysIleAla 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        505 GCTGCTAAATTTGACACTCAGGGAAAAGCATTCGTCAAAGAGAGCTTAAAATGCATCGCC 564

Qy        101 AsnGlyValThrSerLysValPheLeuAlaIleArgArgCysSerThrPheGlnArgMet 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        565 AACGGGGTCACCTCCAAGGTCTTCCTCGCCATTCGGAGGTGCTCCACTTTCCAAAGGATG 624

Qy        121 IleAlaGluValGlnGluGluCysTyrSerLysLeuAsnValCysSerIleAlaLysArg 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        625 ATTGCTGAGGTGCAGGAAGAGTGCTACAGCAAGCTGAATGTGTGCAGCATCGCCAAGCGG 684

Qy        141 AsnProGluAlaIleThrGluValValGlnLeuProAsnHisPheSerAsnArgTyrTyr 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        685 AACCCTGAAGCCATCACTGAGGTCGTCCAGCTGCCCAATCACTTCTCCAACAGATACTAT 744

Qy        161 AsnArgLeuValArgSerLeuLeuGluCysAspGluAspThrValSerThrIleArgAsp 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        745 AACAGACTTGTCCGAAGCCTGCTGGAATGTGATGAAGACACAGTCAGCACAATCAGAGAC 804

Qy        181 SerLeuMetGluLys-Ile-GlyProAsnMetAlaSerLeuPheHisIleLeuGlnThrA 200
              |||||||||||     ||| ||||||||||||||||||||||||||||||||||||||
Db        805 AGCCTGATGGAGRA-AATTNGGGCCTAACATGGCCAGCCTCTTCCACATCCTGCAGACAG 863

Qy        200 spHisCysAlaGlnThrHisProArgAlaAspPheAsnArgArgArgThrAsnGluProG 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        864 ACCACTGTGCCCAAACACACCCACGAGCTGACTTCAACAGGAGACGCACCAATGAGCCGC 923

Qy        220 lnLysLeuLysValLeuLeuArgAsnLeuArgGlyGluGluAspSerProSerHisIleL 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        924 AGAAGCTGAAAGTCCTCCTCAGGAACCTCCGAGGTGAGGAGGACTCTCCCTCCCACATCA 983

Qy        240 ysArgThrSerHisGluSerAla 247
              |||||||||||||||||||||||
Db        984 AACGCACATCCCATGAGAGTGCA 1006

RESULT 6
US-09-778-320-149
; Sequence 149, Application US/09778320
; Patent No. US20010034052A1
; GENERAL INFORMATION:
;  APPLICANT:  Dillon, Davin C.
;  APPLICANT:  Day, Craig H.
;  APPLICANT:  Jiang, Yuqiu
;  APPLICANT:  Houghton, Raymond L.
;  APPLICANT:  Mitcham, Jennifer
;  APPLICANT:  Wang, TongTong
;  APPLICANT:  McNeill, Patricia D.
;  TITLE OF INVENTION:  COMPOSITIONS AND METHODS FOR THE THERAPY AND
;  TITLE OF INVENTION:  DIAGNOSIS OF BREAST CANCER
;  FILE REFERENCE:  210121.491C5
;  CURRENT APPLICATION NUMBER: US/09/778,320
;  CURRENT FILING DATE:  2001-02-06
;  NUMBER OF SEQ ID NOS:  301
;  SOFTWARE:  FastSEQ for Windows Version 3.0
; SEQ ID NO 149
;   LENGTH: 585
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(585)
;   OTHER INFORMATION: n=A,T,C or G
US-09-778-320-149

Alignment Scores:
Pred. No.:              1.49e-158       Length:         585
Score:                  160.00          Matches:        160
Percent Similarity:     100.00%         Conservative:   0
Best Local Similarity:  100.00%         Mismatches:     0
Query Match:            64.78%          Indels:         0
DB:                     10              Gaps:           0

US-09-705-500A-3 (1-247) x US-09-778-320-149 (1-585)

Qy         88 GlyLysAlaPheValLysGluSerLeuLysCysIleAlaAsnGlyValThrSerLysVal 107
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         33 GGAAAAGCATTCGTCAAAGAGAGCTTAAAATGCATCGCCAACGGGGTCACCTCCAAGGTC 92

Qy        108 PheLeuAlaIleArgArgCysSerThrPheGlnArgMetIleAlaGluValGlnGluGlu 127
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         93 TTCCTCGCCATTCGGAGGTGCTCCACTTTCCAAAGGATGATTGCTGAGGTGCAGGAAGAG 152

Qy        128 CysTyrSerLysLeuAsnValCysSerIleAlaLysArgAsnProGluAlaIleThrGlu 147
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        153 TGCTACAGCAAGCTGAATGTGTGCAGCATCGCCAAGCGGAACCCTGAAGCCATCACTGAG 212

Qy        148 ValValGlnLeuProAsnHisPheSerAsnArgTyrTyrAsnArgLeuValArgSerLeu 167
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        213 GTCGTCCAGCTGCCCAATCACTTCTCCAACAGATACTATAACAGACTTGTCCGAAGCCTG 272

Qy        168 LeuGluCysAspGluAspThrValSerThrIleArgAspSerLeuMetGluLysIleGly 187
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        273 CTGGAATGTGATGAAGACACAGTCAGCACAATCAGAGACAGCCTGATGGAGAAAATTGGG 332

Qy        188 ProAsnMetAlaSerLeuPheHisIleLeuGlnThrAspHisCysAlaGlnThrHisPro 207
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        333 CCTAACATGGCCAGCCTCTTCCACATCCTGCAGACAGACCACTGTGCCCAAACACACCCA 392

Qy        208 ArgAlaAspPheAsnArgArgArgThrAsnGluProGlnLysLeuLysValLeuLeuArg 227
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        393 CGAGCTGACTTCAACAGGAGACGCACCAATGAGCCGCAGAAGCTGAAAGTCCTCCTCAGG 452

Qy        228 AsnLeuArgGlyGluGluAspSerProSerHisIleLysArgThrSerHisGluSerAla 247
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        453 AACCTCCGAGGTGAGGAGGACTCTCCCTCCCACATCAAACGCACATCCCATGAGAGTGCA 512

RESULT 7
US-09-910-689-149
; Sequence 149, Application US/09910689
; Patent No. US20020081609A1
; GENERAL INFORMATION:
;  APPLICANT: Dillon, Davin C.
;  APPLICANT:  Day, Craig H.
;  APPLICANT:  Jiang, Yuqiu
;  APPLICANT:  Houghton, Raymond L.
;  APPLICANT:  Mitcham, Jennifer
;  APPLICANT:  Wang, Tongtong
;  APPLICANT:  McNeill, Patricia D.
```

```
;  APPLICANT:  Harlocker, Susan L.
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
;  TITLE OF INVENTION:  DIAGNOSIS OF BREAST CANCER
;  FILE REFERENCE: 210121.491C6
;  CURRENT APPLICATION NUMBER: US/09/910,689
;  CURRENT FILING DATE:  2001-07-20
;  NUMBER OF SEQ ID NOS: 307
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 149
;   LENGTH: 585
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: 10, 30, 32, 527, 565
;   OTHER INFORMATION: n = A,T,C or G
US-09-910-689-149

Alignment Scores:
Pred. No.:              1.49e-158       Length:         585
Score:                  160.00          Matches:        160
Percent Similarity:     100.00%         Conservative:   0
Best Local Similarity:  100.00%         Mismatches:     0
Query Match:            64.78%          Indels:         0
DB:                     10              Gaps:           0

US-09-705-500A-3 (1-247) x US-09-910-689-149 (1-585)

Qy         88 GlyLysAlaPheValLysGluSerLeuLysCysIleAlaAsnGlyValThrSerLysVal 107
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         33 GGAAAAGCATTCGTCAAAGAGAGCTTAAAATGCATCGCCAACGGGGTCACCTCCAAGGTC 92

Qy        108 PheLeuAlaIleArgArgCysSerThrPheGlnArgMetIleAlaGluValGlnGluGlu 127
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         93 TTCCTCGCCATTCGGAGGTGCTCCACTTTCCAAAGGATGATTGCTGAGGTGCAGGAAGAG 152

Qy        128 CysTyrSerLysLeuAsnValCysSerIleAlaLysArgAsnProGluAlaIleThrGlu 147
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        153 TGCTACAGCAAGCTGAATGTGTGCAGCATCGCCAAGCGGAACCCTGAAGCCATCACTGAG 212

Qy        148 ValValGlnLeuProAsnHisPheSerAsnArgTyrTyrAsnArgLeuValArgSerLeu 167
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        213 GTCGTCCAGCTGCCCAATCACTTCTCCAACAGATACTATAACAGACTTGTCCGAAGCCTG 272

Qy        168 LeuGluCysAspGluAspThrValSerThrIleArgAspSerLeuMetGluLysIleGly 187
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        273 CTGGAATGTGATGAAGACACAGTCAGCACAATCAGAGACAGCCTGATGGAGAAAATTGGG 332

Qy        188 ProAsnMetAlaSerLeuPheHisIleLeuGlnThrAspHisCysAlaGlnThrHisPro 207
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        333 CCTAACATGGCCAGCCTCTTCCACATCCTGCAGACAGACCACTGTGCCCAAACACACCCA 392

Qy        208 ArgAlaAspPheAsnArgArgArgThrAsnGluProGlnLysLeuLysValLeuLeuArg 227
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        393 CGAGCTGACTTCAACAGGAGACGCACCAATGAGCCGCAGAAGCTGAAAGTCCTCCTCAGG 452

Qy        228 AsnLeuArgGlyGluGluAspSerProSerHisIleLysArgThrSerHisGluSerAla 247
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        453 AACCTCCGAGGTGAGGAGGACTCTCCCTCCCACATCAAACGCACATCCCATGAGAGTGCA 512

RESULT 8
US-10-010-742-149
; Sequence 149, Application US/10010742
; Patent No. US20020146727A1
; GENERAL INFORMATION:
;  APPLICANT: Dillon, Davin C.
;  APPLICANT:  Day, Craig H.
;  APPLICANT:  Jiang, Yuqiu
;  APPLICANT:  Houghton, Raymond L.
;  APPLICANT:  Mitcham, Jennifer L.
;  APPLICANT:  Wang, Tongtong
;  APPLICANT:  McNeill, Patricia D.
;  APPLICANT:  Harlocker, Susan L.
;  APPLICANT:  Bennington, Angela Ann
;  APPLICANT:  Zehentner, Barbara
;  APPLICANT:  Fanger, Gary R.
;  APPLICANT:  Retter, Marc W.
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
;  TITLE OF INVENTION:  DIAGNOSIS OF BREAST CANCER
;  FILE REFERENCE: 210121.491C7
;  CURRENT APPLICATION NUMBER: US/10/010,742
;  CURRENT FILING DATE:  2001-11-30
;  NUMBER OF SEQ ID NOS: 307
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 149
;   LENGTH: 585
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: 10, 30, 32, 527, 565
;   OTHER INFORMATION: n = A,T,C or G
US-10-010-742-149

Alignment Scores:
Pred. No.:              1.49e-158       Length:         585
Score:                  160.00          Matches:        160
Percent Similarity:     100.00%         Conservative:   0
Best Local Similarity:  100.00%         Mismatches:     0
Query Match:            64.78%          Indels:         0
DB:                     12              Gaps:           0

US-09-705-500A-3 (1-247) x US-10-010-742-149 (1-585)

Qy         88 GlyLysAlaPheValLysGluSerLeuLysCysIleAlaAsnGlyValThrSerLysVal 107
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         33 GGAAAAGCATTCGTCAAAGAGAGCTTAAAATGCATCGCCAACGGGGTCACCTCCAAGGTC 92

Qy        108 PheLeuAlaIleArgArgCysSerThrPheGlnArgMetIleAlaGluValGlnGluGlu 127
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         93 TTCCTCGCCATTCGGAGGTGCTCCACTTTCCAAAGGATGATTGCTGAGGTGCAGGAAGAG 152

Qy        128 CysTyrSerLysLeuAsnValCysSerIleAlaLysArgAsnProGluAlaIleThrGlu 147
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        153 TGCTACAGCAAGCTGAATGTGTGCAGCATCGCCAAGCGGAACCCTGAAGCCATCACTGAG 212

Qy        148 ValValGlnLeuProAsnHisPheSerAsnArgTyrTyrAsnArgLeuValArgSerLeu 167
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        213 GTCGTCCAGCTGCCCAATCACTTCTCCAACAGATACTATAACAGACTTGTCCGAAGCCTG 272

Qy        168 LeuGluCysAspGluAspThrValSerThrIleArgAspSerLeuMetGluLysIleGly 187
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        273 CTGGAATGTGATGAAGACACAGTCAGCACAATCAGAGACAGCCTGATGGAGAAAATTGGG 332

Qy        188 ProAsnMetAlaSerLeuPheHisIleLeuGlnThrAspHisCysAlaGlnThrHisPro 207
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        333 CCTAACATGGCCAGCCTCTTCCACATCCTGCAGACAGACCACTGTGCCCAAACACACCCA 392

Qy        208 ArgAlaAspPheAsnArgArgArgThrAsnGluProGlnLysLeuLysValLeuLeuArg 227
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        393 CGAGCTGACTTCAACAGGAGACGCACCAATGAGCCGCAGAAGCTGAAAGTCCTCCTCAGG 452

Qy        228 AsnLeuArgGlyGluGluAspSerProSerHisIleLysArgThrSerHisGluSerAla 247
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        453 AACCTCCGAGGTGAGGAGGACTCTCCCTCCCACATCAAACGCACATCCCATGAGAGTGCA 512

RESULT 9
US-10-060-036-2677/c
; Sequence 2677, Application US/10060036
; Publication No. US20030073144A1
; GENERAL INFORMATION:
;  APPLICANT: Benson, Darin R.
;  APPLICANT:  Kalos, Michael D.
;  APPLICANT:  Lodes, Michael J.
;  APPLICANT:  Persing, David H.
;  APPLICANT:  Hepler, William T.
```

```
;  APPLICANT:  Jiang, Yuqiu
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
;  TITLE OF INVENTION:  AND DIAGNOSIS OF PANCREATIC CANCER
;  FILE REFERENCE: 210121.566
;  CURRENT APPLICATION NUMBER: US/10/060,036
;  CURRENT FILING DATE:  2002-01-30
;  NUMBER OF SEQ ID NOS: 4560
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2677
;   LENGTH: 473
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-060-036-2677

Alignment Scores:
Pred. No.:              2.73e-129       Length:         473
Score:                  132.00          Matches:        132
Percent Similarity:     100.00%         Conservative:   0
Best Local Similarity:  100.00%         Mismatches:     0
Query Match:            53.44%          Indels:         0
DB:                     9               Gaps:           0

US-09-705-500A-3 (1-247) x US-10-060-036-2677 (1-473)

Qy        116 ThrPheGlnArgMetIleAlaGluValGlnGluGluCysTyrSerLysLeuAsnValCys 135
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        472 ACTTTCCAAAGGATGATTGCTGAGGTGCAGGAAGAGTGCTACAGCAAGCTGAATGTGTGC 413

Qy        136 SerIleAlaLysArgAsnProGluAlaIleThrGluValValGlnLeuProAsnHisPhe 155
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        412 AGCATCGCCAAGCGGAACCCTGAAGCCATCACTGAGGTCGTCCAGCTGCCCAATCACTTC 353

Qy        156 SerAsnArgTyrTyrAsnArgLeuValArgSerLeuLeuGluCysAspGluAspThrVal 175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        352 TCCAACAGATACTATAACAGACTTGTCCGAAGCCTGCTGGAATGTGATGAAGACACAGTC 293

Qy        176 SerThrIleArgAspSerLeuMetGluLysIleGlyProAsnMetAlaSerLeuPheHis 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        292 AGCACAATCAGAGACAGCCTGATGGAGAAAATTGGGCCTAACATGGCCAGCCTCTTCCAC 233

Qy        196 IleLeuGlnThrAspHisCysAlaGlnThrHisProArgAlaAspPheAsnArgArgArg 215
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        232 ATCCTGCAGACAGACCACTGTGCCCAAACACACCCACGAGCTGACTTCAACAGGAGACGC 173

Qy        216 ThrAsnGluProGlnLysLeuLysValLeuLeuArgAsnLeuArgGlyGluGluAspSer 235
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        172 ACCAATGAGCCGCAGAAGCTGAAAGTCCTCCTCAGGAACCTCCGAGGTGAGGAGGACTCT 113

Qy        236 ProSerHisIleLysArgThrSerHisGluSerAla 247
              ||||||||||||||||||||||||||||||||||||||
Db        112 CCCTCCCACATCAAACGCACATCCCATGAGAGTGCA 77

RESULT 10
US-09-918-995-33032
; Sequence 33032, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
;  APPLICANT: Hyseq, Inc.
;  TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
;  TITLE OF INVENTION:  FROM VARIOUS cDNA LIBRARIES
;  FILE REFERENCE: 20411-756
;  CURRENT APPLICATION NUMBER: US/09/918,995
;  CURRENT FILING DATE:  2001-07-30
;  PRIOR APPLICATION NUMBER: US/09/235,076
;  PRIOR FILING DATE: 1999-01-20
;  NUMBER OF SEQ ID NOS: 38054
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 33032
;   LENGTH: 436
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-918-995-33032

Alignment Scores:
Pred. No.:              1.28e-70        Length:         436
Score:                  76.00           Matches:        76
Percent Similarity:     100.00%         Conservative:   0
Best Local Similarity:  100.00%         Mismatches:     0
Query Match:            30.77%          Indels:         0
DB:                     9               Gaps:           0

US-09-705-500A-3 (1-247) x US-09-918-995-33032 (1-436)

Qy        172 GluAspThrValSerThrIleArgAspSerLeuMetGluLysIleGlyProAsnMetAla 191
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 GAAGACACAGTCAGCACAATCAGAGACAGCCTGATGGAGAAAATTGGGCCTAACATGGCC 61

Qy        192 SerLeuPheHisIleLeuGlnThrAspHisCysAlaGlnThrHisProArgAlaAspPhe 211
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 AGCCTCTTCCACATCCTGCAGACAGACCACTGTGCCCAAACACACCCACGAGCTGACTTC 121

Qy        212 AsnArgArgArgThrAsnGluProGlnLysLeuLysValLeuLeuArgAsnLeuArgGly 231
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        122 AACAGGAGACGCACCAATGAGCCGCAGAAGCTGAAAGTCCTCCTCAGGAACCTCCGAGGT 181

Qy        232 GluGluAspSerProSerHisIleLysArgThrSerHisGluSerAla 247
              ||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 GAGGAGGACTCTCCCTCCCACATCAAACGCACATCCCATGAGAGTGCA 229

RESULT 11
US-09-864-761-21309/c
; Sequence 21309, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
;  APPLICANT: Penn, Sharron G.
;  APPLICANT:  Rank, David R.
;  APPLICANT:  Hanzel, David K.
;  APPLICANT:  Chen, Wensheng
;  TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
;  TITLE OF INVENTION:  GENE EXPRESSION ANALYSIS BY MICROARRAY
;  FILE REFERENCE: Aeomica-X-1
;  CURRENT APPLICATION NUMBER: US/09/864,761
;  CURRENT FILING DATE:  2001-05-23
;  PRIOR APPLICATION NUMBER: US 60/180,312
;  PRIOR FILING DATE: 2000-02-04
;  PRIOR APPLICATION NUMBER: US 60/207,456
;  PRIOR FILING DATE: 2000-05-26
;  PRIOR APPLICATION NUMBER: US 09/632,366
;  PRIOR FILING DATE: 2000-08-03
;  PRIOR APPLICATION NUMBER: GB 24263.6
;  PRIOR FILING DATE: 2000-10-04
;  PRIOR APPLICATION NUMBER: US 60/236,359
;  PRIOR FILING DATE: 2000-09-27
;  PRIOR APPLICATION NUMBER: PCT/US01/00666
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00667
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00664
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00669
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00665
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00668
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00663
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00662
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00661
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00670
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: US 60/234,687
;  PRIOR FILING DATE: 2000-09-21
;  PRIOR APPLICATION NUMBER: US 09/608,408
```

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;  PRIOR FILING DATE: 2000-06-30
;  PRIOR APPLICATION NUMBER: US 09/774,203
;  PRIOR FILING DATE: 2001-01-29
;  NUMBER OF SEQ ID NOS: 49117
;  SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 21309
;   LENGTH: 219
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: MAP TO AC012119.1
;   OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.7
;   OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 2.4
;   OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 2.8
;   OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 2.8
;   OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 2.4
;   OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 3.1
;   OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 1.8
;   OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.7
;   OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 2.2
;   OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 2.7
;   OTHER INFORMATION: SWISSPROT HIT: P52823, EVALUE 2.00e-36
;   OTHER INFORMATION: NT HIT: AF098463.1, EVALUE 1.00e-120
;   OTHER INFORMATION: EST_HUMAN HIT: AW954342.1, EVALUE 1.00e-116
US-09-864-761-21309

Alignment Scores:
Pred. No.:              1.03e-66        Length:         219
Score:                  72.00           Matches:        72
Percent Similarity:     100.00%         Conservative:   0
Best Local Similarity:  100.00%         Mismatches:     0
Query Match:            29.15%          Indels:         0
DB:                     10              Gaps:           0

US-09-705-500A-3 (1-247) x US-09-864-761-21309 (1-219)

Qy          88 GlyLysAlaPheValLysGluSerLeuLysCysIleAlaAsnGlyValThrSerLysVal 107
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         219 GGAAAAGCATTCGTCAAAGAGAGCTTAAAATGCATCGCCAACGGGGTCACCTCCAAGGTC 160

Qy         108 PheLeuAlaIleArgArgCysSerThrPheGlnArgMetIleAlaGluValGlnGluGlu 127
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         159 TTCCTCGCCATTCGGAGGTGCTCCACTTTCCAAAGGATGATTGCTGAGGTGCAGGAAGAG 100

Qy         128 CysTyrSerLysLeuAsnValCysSerIleAlaLysArgAsnProGluAlaIleThrGlu 147
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          99 TGCTACAGCAAGCTGAATGTGTGCAGCATCGCCAAGCGGAACCCTGAAGCCATCACTGAG 40

Qy         148 ValValGlnLeuProAsnHisPheSerAsnArgTyr 159
               |||||||||||||||||||||||||||||||||||||
Db          39 GTCGTCCAGCTGCCCAATCACTTCTCCAACAGGTAC 4

RESULT 12
US-09-864-761-4563/c
; Sequence 4563, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
;  APPLICANT: Penn, Sharron G.
;  APPLICANT:  Rank, David R.
;  APPLICANT:  Hanzel, David K.
;  APPLICANT:  Chen, Wensheng
;  TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
;  TITLE OF INVENTION:  GENE EXPRESSION ANALYSIS BY MICROARRAY
;  FILE REFERENCE: Aeomica-X-1
;  CURRENT APPLICATION NUMBER: US/09/864,761
;  CURRENT FILING DATE:  2001-05-23
;  PRIOR APPLICATION NUMBER: US 60/180,312
;  PRIOR FILING DATE: 2000-02-04
;  PRIOR APPLICATION NUMBER: US 60/207,456
;  PRIOR FILING DATE: 2000-05-26
;  PRIOR APPLICATION NUMBER: US 09/632,366
;  PRIOR FILING DATE: 2000-08-03
;  PRIOR APPLICATION NUMBER: GB 24263.6
;  PRIOR FILING DATE: 2000-10-04
;  PRIOR APPLICATION NUMBER: US 60/236,359
;  PRIOR FILING DATE: 2000-09-27
;  PRIOR APPLICATION NUMBER: PCT/US01/00666
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00667
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00664
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00669
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00665
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00668
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00663
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00662
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00661
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00670
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: US 60/234,687
;  PRIOR FILING DATE: 2000-09-21
;  PRIOR APPLICATION NUMBER: US 09/608,408
;  PRIOR FILING DATE: 2000-06-30
;  PRIOR APPLICATION NUMBER: US 09/774,203
;  PRIOR FILING DATE: 2001-01-29
;  NUMBER OF SEQ ID NOS: 49117
;  SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 4563
;   LENGTH: 362
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: MAP TO AC012119.1
;   OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.7
;   OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 2.4
;   OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 2.8
;   OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 2.8
;   OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 2.4
;   OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 3.1
;   OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 1.8
;   OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.7
;   OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 2.2
;   OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 2.7
US-09-864-761-4563

Alignment Scores:
Pred. No.:              5.26e-34        Length:         362
Score:                  41.00           Matches:        41
Percent Similarity:     100.00%         Conservative:   0
Best Local Similarity:  100.00%         Mismatches:     0
Query Match:            16.60%          Indels:         0
DB:                     10              Gaps:           0

US-09-705-500A-3 (1-247) x US-09-864-761-4563 (1-362)

Qy         119 ArgMetIleAlaGluValGlnGluGluCysTyrSerLysLeuAsnValCysSerIleAla 138
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         361 AGGATGATTGCTGAGGTGCAGGAAGAGTGCTACAGCAAGCTGAATGTGTGCAGCATCGCC 302

Qy         139 LysArgAsnProGluAlaIleThrGluValValGlnLeuProAsnHisPheSerAsnArg 158
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         301 AAGCGGAACCCTGAAGCCATCACTGAGGTCGTCCAGCTGCCCAATCACTTCTCCAACAGG 242

Qy         159 Tyr 159
               |||
Db         241 TAC 239

RESULT 13
US-09-778-320-141
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```
; Sequence 141, Application US/09778320
; Patent No. US20010034052A1
; GENERAL INFORMATION:
;  APPLICANT:  Dillon, Davin C.
;  APPLICANT:  Day, Craig H.
;  APPLICANT:  Jiang, Yuqiu
;  APPLICANT:  Houghton, Raymond L.
;  APPLICANT:  Mitcham, Jennifer
;  APPLICANT:  Wang, TongTong
;  APPLICANT:  McNeill, Patricia D.
;  TITLE OF INVENTION:  COMPOSITIONS AND METHODS FOR THE THERAPY AND
;  TITLE OF INVENTION:  DIAGNOSIS OF BREAST CANCER
;  FILE REFERENCE:  210121.491C5
;  CURRENT APPLICATION NUMBER: US/09/778,320
;  CURRENT FILING DATE:  2001-02-06
;  NUMBER OF SEQ ID NOS:  301
;  SOFTWARE:  FastSEQ for Windows Version 3.0
; SEQ ID NO 141
;   LENGTH: 420
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(420)
;   OTHER INFORMATION: n = A,T,C or G
US-09-778-320-141

Alignment Scores:
Pred. No.:                6.78e-33        Length:         420
Score:                    40.00           Matches:        40
Percent Similarity:       100.00%         Conservative:   0
Best Local Similarity:    100.00%         Mismatches:     0
Query Match:              16.19%          Indels:         0
DB:                       10              Gaps:           0

US-09-705-500A-3 (1-247) x US-09-778-320-141 (1-420)

Qy         95 SerLeuLysCysIleAlaAsnGlyValThrSerLysValPheLeuAlaIleArgArgCys 114
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         31 AGCTTAAAATGCATCGCCAACGGGGTCACCTCCAAGGTCTTCCTCGCCATTCGGAGGTGC 90

Qy        115 SerThrPheGlnArgMetIleAlaGluValGlnGluGluCysTyrSerLysLeuAsnVal 134
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Db         91 TCCACTTTCCAAAGGATGATTGCTGAGGTGCAGGAAGAGTGCTACAGCAAGCTGAATGTG 150

RESULT 14
US-09-910-689-141
; Sequence 141, Application US/09910689
; Patent No. US20020081609A1
; GENERAL INFORMATION:
;  APPLICANT: Dillon, Davin C.
;  APPLICANT:  Day, Craig H.
;  APPLICANT:  Jiang, Yuqiu
;  APPLICANT:  Houghton, Raymond L.
;  APPLICANT:  Mitcham, Jennifer
;  APPLICANT:  Wang, Tongtong
;  APPLICANT:  McNeill, Patricia D.
;  APPLICANT:  Harlocker, Susan L.
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
;  TITLE OF INVENTION:  DIAGNOSIS OF BREAST CANCER
;  FILE REFERENCE: 210121.491C6
;  CURRENT APPLICATION NUMBER: US/09/910,689
;  CURRENT FILING DATE:  2001-07-20
;  NUMBER OF SEQ ID NOS: 307
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 141
;   LENGTH: 420
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: 20, 21, 23, 28, 155, 174, 221, 239, 240, 258, 265, 302, 307,
;   LOCATION: 316, 342, 346, 374, 387, 388, 402, 418
;   OTHER INFORMATION: n = A,T,C or G
US-09-910-689-141

Alignment Scores:
Pred. No.:                6.78e-33        Length:         420
Score:                    40.00           Matches:        40
Percent Similarity:       100.00%         Conservative:   0
Best Local Similarity:    100.00%         Mismatches:     0
Query Match:              16.19%          Indels:         0
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US-09-705-500A-3 (1-247) x US-09-910-689-141 (1-420)

Qy         95 SerLeuLysCysIleAlaAsnGlyValThrSerLysValPheLeuAlaIleArgArgCys 114
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Db         31 AGCTTAAAATGCATCGCCAACGGGGTCACCTCCAAGGTCTTCCTCGCCATTCGGAGGTGC 90

Qy        115 SerThrPheGlnArgMetIleAlaGluValGlnGluGluCysTyrSerLysLeuAsnVal 134
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Db         91 TCCACTTTCCAAAGGATGATTGCTGAGGTGCAGGAAGAGTGCTACAGCAAGCTGAATGTG 150

RESULT 15
US-10-010-742-141
; Sequence 141, Application US/10010742
; Patent No. US20020146727A1
; GENERAL INFORMATION:
;  APPLICANT: Dillon, Davin C.
;  APPLICANT:  Day, Craig H.
;  APPLICANT:  Jiang, Yuqiu
;  APPLICANT:  Houghton, Raymond L.
;  APPLICANT:  Mitcham, Jennifer L.
;  APPLICANT:  Wang, Tongtong
;  APPLICANT:  McNeill, Patricia D.
;  APPLICANT:  Harlocker, Susan L.
;  APPLICANT:  Bennington, Angela Ann
;  APPLICANT:  Zehentner, Barbara
;  APPLICANT:  Fanger, Gary R.
;  APPLICANT:  Retter, Marc W.
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
;  TITLE OF INVENTION:  DIAGNOSIS OF BREAST CANCER
;  FILE REFERENCE: 210121.491C7
;  CURRENT APPLICATION NUMBER: US/10/010,742
;  CURRENT FILING DATE:  2001-11-30
;  NUMBER OF SEQ ID NOS: 307
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 141
;   LENGTH: 420
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: 20, 21, 23, 28, 155, 174, 221, 239, 240, 258, 265, 302, 307,
;   LOCATION: 316, 342, 346, 374, 387, 388, 402, 418
;   OTHER INFORMATION: n = A,T,C or G
US-10-010-742-141

Alignment Scores:
Pred. No.:                6.78e-33        Length:         420
Score:                    40.00           Matches:        40
Percent Similarity:       100.00%         Conservative:   0
Best Local Similarity:    100.00%         Mismatches:     0
Query Match:              16.19%          Indels:         0
DB:                       12              Gaps:           0

US-09-705-500A-3 (1-247) x US-10-010-742-141 (1-420)

Qy         95 SerLeuLysCysIleAlaAsnGlyValThrSerLysValPheLeuAlaIleArgArgCys 114
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         31 AGCTTAAAATGCATCGCCAACGGGGTCACCTCCAAGGTCTTCCTCGCCATTCGGAGGTGC 90

Qy        115 SerThrPheGlnArgMetIleAlaGluValGlnGluGluCysTyrSerLysLeuAsnVal 134
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Db         91 TCCACTTTCCAAAGGATGATTGCTGAGGTGCAGGAAGAGTGCTACAGCAAGCTGAATGTG 150
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Job time : 164 secs

OM protein - nucleic search, using frame_plus_p2n model

Run on: June 12, 2003, 21:52:10 ; Search time 1418 Seconds
(without alignments)
2821.076 Million cell updates/sec

Title: US-09-705-500A-3
Perfect score: 247
Sequence: 1 MLQNSAVLLVLVISASATHE.....NLRGEEDSPSHIKRTSHESA 247

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Ygapop 60.0 , Ygapext 60.0
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Delop 6.0 , Delext 7.0

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Word size: 1

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Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

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-FGAPEXT=7 -YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7

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8: em_htc:*
9: gb_est1:*
10: gb_est2:*
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12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
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22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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	6	168	68.0	646	10	AW954342	AW954342 EST366412
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	17	90	36.4	524	14	BM708153	BM708153 UI-E-CI1-
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	50	18	7.3	879	13	BI769460	BI769460 603054789
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c	62	9	3.6	375	10	AV952436	AV952436 AV952436
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	124	9	3.6	886	17	AZ205753	AZ205753 SP_0101_B
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	129	8	3.2	185	17	AZ094382	AZ094382 RPCI-23-4
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	146	8	3.2	370	9	AV216495	AV216495 AV216495
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c	182	8	3.2	503	17	AQ802079	AQ802079 HS_3132_A
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c	187	8	3.2	513	17	AZ994502	AZ994502 2M0280C05
c	188	8	3.2	516	17	AQ433423	AQ433423 HS_5052_B
	189	8	3.2	517	17	AZ397157	AZ397157 1M0162F01
	190	8	3.2	521	13	BI131816	BI131816 G126P13Y
	191	8	3.2	523	14	BQ902484	BQ902484 Ta03_04h1
	192	8	3.2	524	10	BB853154	BB853154 BB853154
c	193	8	3.2	525	14	BQ169089	BQ169089 WHE2165_H
c	194	8	3.2	526	10	AW215576	AW215576 up06b01.x
c	195	8	3.2	526	17	AQ433422	AQ433422 HS_5052_B
	196	8	3.2	531	9	AA764381	AA764381 vp08d04.r
	197	8	3.2	539	13	BJ411277	BJ411277 BJ411277
c	198	8	3.2	545	17	AZ421259	AZ421259 1M0199M23
	199	8	3.2	553	17	BH099397	BH099397 RPCI-24-2
c	200	8	3.2	555	17	AQ616892	AQ616892 HS_5157_A
	201	8	3.2	557	13	BJ065937	BJ065937 BJ065937
	202	8	3.2	563	13	BI590135	BI590135 RH03715.5
c	203	8	3.2	567	13	BJ107919	BJ107919 BJ107919
c	204	8	3.2	567	14	BQ398973	BQ398973 NISC_mp01
	205	8	3.2	570	13	BG942705	BG942705 ax28e07.x
c	206	8	3.2	571	14	BQ784635	BQ784635 SnEST4a78
	207	8	3.2	572	13	BJ417141	BJ417141 BJ417141
	208	8	3.2	572	13	BJ417811	BJ417811 BJ417811
c	209	8	3.2	574	12	BG904449	BG904449 TaLr1132C
	210	8	3.2	576	17	AZ947697	AZ947697 2M0210D05

	211	8	3.2	577	13	BJ411667	BJ411667 BJ411667		284	8	3.2	663	13	BJ410966	BJ410966 BJ410966
	212	8	3.2	579	13	BJ414306	BJ414306 BJ414306		285	8	3.2	663	13	BJ416388	BJ416388 BJ416388
	213	8	3.2	580	13	BJ412066	BJ412066 BJ412066	c	286	8	3.2	663	14	BQ864445	BQ864445 QGC26L17.
	214	8	3.2	580	13	BJ419924	BJ419924 BJ419924		287	8	3.2	664	13	BJ416100	BJ416100 BJ416100
c	215	8	3.2	581	10	AW399627	AW399627 EST310127		288	8	3.2	665	13	BJ416884	BJ416884 BJ416884
	216	8	3.2	583	13	BJ413263	BJ413263 BJ413263	c	289	8	3.2	665	13	BJ430187	BJ430187 BJ430187
	217	8	3.2	584	13	BJ417331	BJ417331 BJ417331		290	8	3.2	667	10	BB622512	BB622512 BB622512
	218	8	3.2	585	13	BJ415102	BJ415102 BJ415102		291	8	3.2	668	13	BJ424526	BJ424526 BJ424526
	219	8	3.2	585	13	BJ416726	BJ416726 BJ416726		292	8	3.2	670	10	BB643827	BB643827 BB643827
	220	8	3.2	586	13	BJ414051	BJ414051 BJ414051	c	293	8	3.2	673	13	BJ428475	BJ428475 BJ428475
	221	8	3.2	590	13	BJ414074	BJ414074 BJ414074		294	8	3.2	674	10	BB649732	BB649732 BB649732
c	222	8	3.2	592	17	AZ610940	AZ610940 1M0436H03	c	295	8	3.2	676	14	BQ859701	BQ859701 QGC13M04.
	223	8	3.2	593	13	BJ074964	BJ074964 BJ074964		296	8	3.2	677	10	BB641961	BB641961 BB641961
	224	8	3.2	595	13	BI865598	BI865598 ft22e09.y	c	297	8	3.2	678	13	BJ432196	BJ432196 BJ432196
	225	8	3.2	597	13	BJ412222	BJ412222 BJ412222	c	298	8	3.2	678	14	BQ839084	BQ839084 WHE3589_B
	226	8	3.2	601	17	AZ599038	AZ599038 1M0414J07		299	8	3.2	681	13	BJ468212	BJ468212 BJ468212
	227	8	3.2	603	13	BJ411184	BJ411184 BJ411184		300	8	3.2	682	13	BJ413304	BJ413304 BJ413304
c	228	8	3.2	603	17	CNS01WG9	AL170370 Tetraodon		301	8	3.2	684	17	AG115948	AG115948 Pan trogl
	229	8	3.2	606	13	BJ412577	BJ412577 BJ412577		302	8	3.2	685	13	BI570121	BI570121 RH02376.5
	230	8	3.2	607	10	AW222838	AW222838 EST299649	c	303	8	3.2	693	17	AQ961058	AQ961058 LERFI87TF
c	231	8	3.2	607	14	C79063	C79063 C79063 Mous	c	304	8	3.2	705	13	BJ430989	BJ430989 BJ430989
	232	8	3.2	608	13	BJ414516	BJ414516 BJ414516		305	8	3.2	706	13	BJ485819	BJ485819 BJ485819
	233	8	3.2	609	13	BJ413067	BJ413067 BJ413067	c	306	8	3.2	708	13	BJ435162	BJ435162 BJ435162
	234	8	3.2	609	13	BJ416310	BJ416310 BJ416310	c	307	8	3.2	710	17	AQ658216	AQ658216 Sheared D
	235	8	3.2	610	13	BJ410929	BJ410929 BJ410929	c	308	8	3.2	713	13	BJ433245	BJ433245 BJ433245
	236	8	3.2	611	13	BJ417640	BJ417640 BJ417640	c	309	8	3.2	713	13	BJ433906	BJ433906 BJ433906
	237	8	3.2	612	13	BJ410630	BJ410630 BJ410630	c	310	8	3.2	716	13	BJ432890	BJ432890 BJ432890
	238	8	3.2	613	10	BB622271	BB622271 BB622271	c	311	8	3.2	716	13	BJ434692	BJ434692 BJ434692
	239	8	3.2	613	13	BI617500	BI617500 RH47857.5	c	312	8	3.2	716	13	BJ435000	BJ435000 BJ435000
	240	8	3.2	613	13	BJ415030	BJ415030 BJ415030	c	313	8	3.2	717	13	BJ429726	BJ429726 BJ429726
	241	8	3.2	616	10	BE401916	BE401916 CSB002E06	c	314	8	3.2	718	17	AZ337721	AZ337721 1M0068E06
	242	8	3.2	616	14	BQ607570	BQ607570 BRY_3464	c	315	8	3.2	720	12	BF845571	BF845571 134T3 Tet
	243	8	3.2	617	13	BJ411340	BJ411340 BJ411340		316	8	3.2	724	14	BQ853408	BQ853408 QGB20G22.
	244	8	3.2	621	17	DR3L3T	AL737555 Danio rer		317	8	3.2	728	13	BJ415708	BJ415708 BJ415708
	245	8	3.2	625	13	BJ413594	BJ413594 BJ413594	c	318	8	3.2	728	14	BQ863310	BQ863310 QGC23I15.
c	246	8	3.2	626	17	AQ461934	AQ461934 HS_5098_A	c	319	8	3.2	733	13	BJ432487	BJ432487 BJ432487
	247	8	3.2	631	13	BJ416040	BJ416040 BJ416040	c	320	8	3.2	738	13	BJ434660	BJ434660 BJ434660
	248	8	3.2	631	17	AQ483808	AQ483808 RPCI-11-2	c	321	8	3.2	738	13	BJ436326	BJ436326 BJ436326
	249	8	3.2	632	13	BJ412227	BJ412227 BJ412227		322	8	3.2	741	14	BQ180118	BQ180118 UI-M-EW0-
c	250	8	3.2	634	13	BJ053505	BJ053505 BJ053505		323	8	3.2	741	17	AZ199988	AZ199988 SP_1040_B
c	251	8	3.2	636	13	BJ436083	BJ436083 BJ436083		324	8	3.2	746	17	BH049863	BH049863 RPCI-24-2
	252	8	3.2	637	13	BI960353	BI960353 HVSMEn002	c	325	8	3.2	749	13	BJ429394	BJ429394 BJ429394
	253	8	3.2	640	10	AW640966	AW640966 cm01h04.w	c	326	8	3.2	749	13	BJ432170	BJ432170 BJ432170
	254	8	3.2	640	10	BB633489	BB633489 BB633489	c	327	8	3.2	750	13	BJ433376	BJ433376 BJ433376
c	255	8	3.2	640	12	BG905886	BG905886 TaLr1143C		328	8	3.2	752	17	BH437101	BH437101 BOHFJ56TF
	256	8	3.2	640	13	BJ414703	BJ414703 BJ414703	c	329	8	3.2	762	17	BH125003	BH125003 RPCI-24-3
c	257	8	3.2	640	14	BQ861914	BQ861914 QGC19O20.	c	330	8	3.2	763	17	AQ739627	AQ739627 HS_5384_B
	258	8	3.2	641	17	CNS03VWG	AL262969 Tetraodon	c	331	8	3.2	766	17	AZ979871	AZ979871 2M0256O10
	259	8	3.2	644	12	BF708291	BF708291 A1105_LE	c	332	8	3.2	773	13	BJ432652	BJ432652 BJ432652
	260	8	3.2	644	13	BJ311120	BJ311120 BJ311120	c	333	8	3.2	787	13	BJ432686	BJ432686 BJ432686
	261	8	3.2	645	13	BJ417498	BJ417498 BJ417498		334	8	3.2	805	17	BH490187	BH490187 BOHBN89TR
	262	8	3.2	646	14	BQ867110	BQ867110 QGC9N02.y	c	335	8	3.2	813	13	BJ428796	BJ428796 BJ428796
	263	8	3.2	647	10	BB650700	BB650700 BB650700	c	336	8	3.2	813	13	BJ434250	BJ434250 BJ434250
	264	8	3.2	648	13	BJ410319	BJ410319 BJ410319	c	337	8	3.2	816	12	BG369452	BG369452 HVSMEi002
	265	8	3.2	648	13	BJ411936	BJ411936 BJ411936	c	338	8	3.2	828	17	AG110971	AG110971 Pan trogl
	266	8	3.2	648	13	BJ426412	BJ426412 BJ426412	c	339	8	3.2	835	14	BQ736005	BQ736005 AGENCOURT
	267	8	3.2	649	13	BJ412540	BJ412540 BJ412540		340	8	3.2	852	12	BF217002	BF217002 601884071
	268	8	3.2	650	13	BJ416019	BJ416019 BJ416019	c	341	8	3.2	854	17	CNS03M9O	AL250485 Tetraodon
	269	8	3.2	652	13	BJ415109	BJ415109 BJ415109	c	342	8	3.2	861	13	BM046394	BM046394 603626417
c	270	8	3.2	653	13	BI066230	BI066230 pgf1n.pk0	c	343	8	3.2	892	17	BH135229	BH135229 ENTNE07TR
c	271	8	3.2	654	13	BJ430322	BJ430322 BJ430322		344	8	3.2	904	17	AZ692954	AZ692954 ENTLG27TF
c	272	8	3.2	655	13	BJ435772	BJ435772 BJ435772	c	345	8	3.2	906	12	BE910085	BE910085 601502153
	273	8	3.2	657	13	BJ414465	BJ414465 BJ414465		346	8	3.2	927	12	BF122599	BF122599 601760317
	274	8	3.2	658	13	BJ415976	BJ415976 BJ415976		347	8	3.2	954	10	BB614507	BB614507 BB614507
	275	8	3.2	659	13	BJ416287	BJ416287 BJ416287	c	348	8	3.2	961	17	CNS05ECE	AL333527 Tetraodon
c	276	8	3.2	659	13	BJ433327	BJ433327 BJ433327		349	8	3.2	969	12	BG243614	BG243614 602357701
	277	8	3.2	660	10	AW641013	AW641013 cm02d06.w	c	350	8	3.2	971	12	BF345966	BF345966 602017974
	278	8	3.2	660	13	BJ415603	BJ415603 BJ415603		351	8	3.2	992	14	BQ924064	BQ924064 AGENCOURT
c	279	8	3.2	660	13	BJ430829	BJ430829 BJ430829		352	8	3.2	1022	17	CNS04TFB	AL306416 Tetraodon
c	280	8	3.2	660	13	BJ434806	BJ434806 BJ434806	c	353	8	3.2	1037	17	CNS03KUE	AL248639 Tetraodon
	281	8	3.2	661	13	BJ415162	BJ415162 BJ415162		354	8	3.2	1044	11	AK021133	AK021133 Mus muscu
c	282	8	3.2	662	14	BQ865969	BQ865969 QGC6I15.y	c	355	8	3.2	1062	17	CNS05BUU	AL330303 Tetraodon
	283	8	3.2	662	17	AQ908600	AQ908600 GSSTc0555		356	8	3.2	1088	13	BM554814	BM554814 AGENCOURT

	357	8	3.2	1110	13	BI411920 BI411920 602966595
	358	8	3.2	1117	17	CNS05SFG AL351781 Tetraodon
c	359	8	3.2	1121	17	B11753 B11753 F13O12-T7 I
	360	8	3.2	1211	14	BQ882176 BQ882176 AGENCOURT
c	361	8	3.2	1337	12	BG855749 BG855749 1024043F0
c	362	8	3.2	1515	12	BE901081 BE901081 601674431
c	363	8	3.2	1641	12	BF540589 BF540589 602054670
c	364	8	3.2	1837	12	BF237870 BF237870 601842431
c	365	8	3.2	1873	12	BG324059 BG324059 602423006
	366	8	3.2	1909	11	AK018414 AK018414 Mus muscu
	367	8	3.2	3262	11	AK004797 AK004797 Mus muscu
	368	8	3.2	3783	11	AY104730 AY104730 Zea mays
	369	7	2.8	35	14	N34382 N34382 yy12h04.s1
c	370	7	2.8	51	14	T63178 T63178 yc04f02.r1
	371	7	2.8	61	10	AW988145 AW988145 ug03d07.y
	372	7	2.8	76	14	W41257 W41257 mc48c03.r1
	373	7	2.8	77	17	BH809906 BH809906 SALK_0366
	374	7	2.8	81	12	BG820823 BG820823 602783472
	375	7	2.8	91	9	AA200723 AA200723 mu13f09.r
	376	7	2.8	97	9	AA759750 AA759750 vw57a08.r
c	377	7	2.8	97	9	AA959603 AA959603 vw57a08.s
c	378	7	2.8	97	9	AA960313 AA960313 ub57b09.s
c	379	7	2.8	97	9	AI327346 AI327346 mp79a12.x
c	380	7	2.8	97	9	AA108084 AA108084 ml58d05.r
	381	7	2.8	97	9	AA119505 AA119505 mp79a12.r
c	382	7	2.8	97	9	AI461671 AI461671 vw57a08.x
c	383	7	2.8	97	9	AI646879 AI646879 ub66h10.x
	384	7	2.8	97	9	AA270320 AA270320 vb11h12.r
	385	7	2.8	97	10	AW913215 AW913215 uf50d11.y
	386	7	2.8	97	10	AW985736 AW985736 uf85c09.y
c	387	7	2.8	97	10	AW986604 AW986604 uf85c09.x
c	388	7	2.8	97	10	BE133618 BE133618 ug03d07.x
c	389	7	2.8	97	10	BE135910 BE135910 ug21c04.x
	390	7	2.8	97	10	BE198362 BE198362 ug77g02.y
	391	7	2.8	97	10	BE628937 BE628937 uu30a12.y
	392	7	2.8	97	12	BE850225 BE850225 uw14e07.y
c	393	7	2.8	97	12	BE852121 BE852121 uw23d04.x
	394	7	2.8	104	17	AZ951153 AZ951153 2M0215D04
c	395	7	2.8	109	10	AW639203 AW639203 bl79g08.w
	396	7	2.8	109	14	W96924 W96924 mf60e05.r1
	397	7	2.8	111	9	AI226688 AI226688 uj14e03.y
c	398	7	2.8	111	9	AA388074 AA388074 vc88c07.r
	399	7	2.8	112	13	BI135912 BI135912 F060P29Y
c	400	7	2.8	117	12	BF020805 BF020805 uw14e07.x
c	401	7	2.8	118	14	BQ337706 BQ337706 CM4-NN000
	402	7	2.8	119	17	BH810734 BH810734 SALK_0511
c	403	7	2.8	121	9	AI662126 AI662126 mz89e04.x
	404	7	2.8	121	10	BE689216 BE689216 uw51a07.y
c	405	7	2.8	121	13	BI440162 BI440162 ic50d12.x
c	406	7	2.8	124	9	AL841865 AL841865
	407	7	2.8	127	12	BE847161 BE847161 uw23d04.y
	408	7	2.8	127	17	CNS01UZE AL168467 Tetraodon
	409	7	2.8	131	14	W59932 W59932 EST000451 S
	410	7	2.8	133	9	AI037484 AI037484 ub53f06.r
	411	7	2.8	135	10	AW214926 AW214926 up03e10.y
c	412	7	2.8	139	12	BE831154 BE831154 PM4-MT003
	413	7	2.8	141	10	AV847299 AV847299 AV847299
c	414	7	2.8	141	12	BF772824 BF772824 RC5-IT003
	415	7	2.8	142	10	AW989679 AW989679 uf18g12.y
	416	7	2.8	142	13	BI420358 BI420358 LjNEST56a
c	417	7	2.8	145	14	N68288 N68288 za12f02.s1
	418	7	2.8	147	9	AI121690 AI121690 uc44c09.r
c	419	7	2.8	147	9	AI463126 AI463126 uc44c09.x
	420	7	2.8	147	9	AI528016 AI528016 uj39a05.y
	421	7	2.8	147	17	AZ825224 AZ825224 2M0100K17
	422	7	2.8	149	17	BH020997 BH020997 Hs-8BJ-05
	423	7	2.8	151	9	AA972026 AA972026 op85g11.s
	424	7	2.8	152	12	BF820385 BF820385 MR1-RT004
c	425	7	2.8	153	17	AZ812529 AZ812529 2M0079F14
c	426	7	2.8	154	12	BG266773 BG266773 1000101D0
	427	7	2.8	156	9	AI197039 AI197039 ue50g01.r
	428	7	2.8	157	14	R95499 R95499 EST000056 S
	429	7	2.8	158	9	AA429388 AA429388 zw07e03.r
	430	7	2.8	158	9	AA456663 AA456663 aa01f03.s
c	431	7	2.8	159	13	BI807903 BI807903 B006C01 O
c	432	7	2.8	165	10	BE147288 BE147288 PM3-HT022
c	433	7	2.8	166	10	BE135921 BE135921 ug21d11.x
	434	7	2.8	169	17	AQ555099 AQ555099 RPCI-11-4
c	435	7	2.8	173	12	BF953347 BF953347 MR4-NN018
	436	7	2.8	175	10	AW987001 AW987001 uf93b10.y
	437	7	2.8	175	10	BE689027 BE689027 uw58g06.y
c	438	7	2.8	177	9	AA596365 AA596365 vo30d12.r
	439	7	2.8	178	13	BI812758 BI812758 F013F06 O
c	440	7	2.8	178	13	BM422230 BM422230 U018A03 O
c	441	7	2.8	178	14	BQ358091 BQ358091 RC3-HT086
	442	7	2.8	180	9	AA938808 AA938808 SMTBADA00
c	443	7	2.8	180	17	AZ775198 AZ775198 2M0007B20
c	444	7	2.8	181	9	AV144245 AV144245 AV144245
c	445	7	2.8	182	9	AV287643 AV287643 AV287643
	446	7	2.8	183	10	BE064409 BE064409 RC4-BT031
	447	7	2.8	183	17	AZ056518 AZ056518 RPCI-23-4
	448	7	2.8	184	17	BH366314 BH366314 CH230-156
c	449	7	2.8	185	10	AV316668 AV316668 AV316668
c	450	7	2.8	185	10	BB084364 BB084364 BB084364
c	451	7	2.8	186	10	AV669356 AV669356 AV669356
	452	7	2.8	186	10	BE142767 BE142767 MR0-HT015
	453	7	2.8	186	14	D42214 D42214 D42214 Rice
	454	7	2.8	190	12	BG797814 BG797814 ic07b07.x
c	455	7	2.8	190	14	BQ305222 BQ305222 MR0-BT350
c	456	7	2.8	191	9	AA490645 AA490645 aa01f04.r
c	457	7	2.8	191	17	BH617576 BH617576 SALK_0372
	458	7	2.8	193	9	AI930865 AI930865 sb43e03.y
c	459	7	2.8	193	17	AQ978106 AQ978106 RPCI-23-3
c	460	7	2.8	194	9	AU175975 AU175975 AU175975
	461	7	2.8	195	9	AA360099 AA360099 EST69245
	462	7	2.8	196	14	BQ327532 BQ327532 MR1-RT004
c	463	7	2.8	199	12	BF368154 BF368154 CM3-GN004
	464	7	2.8	200	10	BB575840 BB575840 BB575840
c	465	7	2.8	201	9	AV027610 AV027610 AV027610
c	466	7	2.8	201	10	AW330029 AW330029 TENU4570
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	578	7	2.8	240	13	BI189693 BI189693 g1a01fs.f
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	632	7	2.8	250	17	AZ898348 AZ898348 RPCI-24-1
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	710	7	2.8	264	10	BB461826 BB461826 BB461826
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	730	7	2.8	269	17	BH842208 BH842208 TC3-53A12
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c	742	7	2.8	271	10	BE528028 BE528028 M70C10STM
c	743	7	2.8	271	10	BE530103 BE530103 M76P12STM
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c	751	7	2.8	274	10	AW201305 AW201305 sf01d11.y
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	757	7	2.8	275	10	BE320431 BE320431 NF030G06R
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ALIGNMENTS

RESULT 1
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DEFINITION AGENCOURT_8032625 NIH_MGC_102 Homo sapiens cDNA clone IMAGE:6213518 5', mRNA sequence.
ACCESSION BQ672018
VERSION BQ672018.1 GI:21782852
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 869)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Plate: LLCM2379 row: f column: 15
High quality sequence stop: 673.

FEATURES Location/Qualifiers
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/tissue_type="epidermoid carcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/note="Organ: salivary gland; Vector: pOTB7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."

BASE COUNT 234 a 231 c 214 g 188 t 2 others
ORIGIN

Alignment Scores:

Pred. No.:	2.56e-218	Length:	869
Score:	228.00	Matches:	228
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	92.31%	Indels:	0
DB:	14	Gaps:	0

US-09-705-500A-3 (1-247) x BQ672018 (1-869)

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Db        321 AACGGGGTCACCTCCAAGGTCTTCCTCGCCATTCGGAGGTGCTCCACTTTCCAAAGGATG 380

Qy        121 IleAlaGluValGlnGluGluCysTyrSerLysLeuAsnValCysSerIleAlaLysArg 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db        381 ATTGCTGAGGTGCAGGAAGAGTGCTACAGCAAGCTGAATGTGTGCAGCATCGCCAAGCGG 440

Qy        141 AsnProGluAlaIleThrGluValValGlnLeuProAsnHisPheSerAsnArgTyrTyr 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        441 AACCCTGAAGCCATCACTGAGGTCGTCCAGCTGCCCAATCACTTCTCCAACAGATACTAT 500

Qy        161 AsnArgLeuValArgSerLeuLeuGluCysAspGluAspThrValSerThrIleArgAsp 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        501 AACAGACTTGTCCGAAGCCTGCTGGAATGTGATGAAGACACAGTCAGCACAATCAGAGAC 560

Qy        181 SerLeuMetGluLysIleGlyProAsnMetAlaSerLeuPheHisIleLeuGlnThrAsp 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        561 AGCCTGATGGAGAAAATTGGGCCTAACATGGCCAGCCTCTTCCACATCCTGCAGACAGAC 620

Qy        201 HisCysAlaGlnThrHisProArgAlaAspPheAsnArgArgArgThrAsnGluProGln 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        621 CACTGTGCCCAAACACACCCACGAGCTGACTTCAACAGGAGACGCACCAATGAGCCGCAG 680

Qy        221 LysLeuLysValLeuLeuArgAsn 228
              ||||||||||||||||||||||||
Db        681 AAGCTGAAAGTCCTCCTCAGGAAC 704

RESULT 2
BQ225453
LOCUS       BQ225453                1057 bp    mRNA    linear   EST 02-MAY-2002
DEFINITION  AGENCOURT_7257225 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:5773821
            5', mRNA sequence.
ACCESSION   BQ225453
VERSION     BQ225453.1  GI:20406853
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1057)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: DCTD/DTP/Gazdar
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM12842  row: e  column: 22
            High quality sequence stop: 578.
FEATURES             Location/Qualifiers
     source          1. .1057
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:5773821"
                     /clone_lib="NIH_MGC_68"
                     /tissue_type="large cell carcinoma"
                     /lab_host="DH10B (phage-resistant)"
                     /note="Organ: lung; Vector: pCMV-SPORT6; Site_1: NotI;
                     Site_2: SalI; Cloned unidirectionally.  Primer: Oligo dT.
                     Average insert size 1.8 kb.   Library constructed by Life
                     Technologies. "
BASE COUNT      291 a    293 c    219 g    254 t
ORIGIN

Alignment Scores:
Pred. No.:              3.82e-198      Length:          1057
Score:                  208.00         Matches:         208
Percent Similarity:     100.00%        Conservative:    0
Best Local Similarity:  100.00%        Mismatches:      0
Query Match:            84.21%         Indels:          0
DB:                     14             Gaps:            0

US-09-705-500A-3 (1-247) x BQ225453 (1-1057)

Qy         40 AlaGluValValArgCysLeuAsnSerAlaLeuGlnValGlyCysGlyAlaPheAlaCys 59
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          4 GCTGAAGTGGTTCGTTGCCTCAACAGTGCTCTACAGGTCGGCTGCGGGGCTTTTGCATGC 63

Qy         60 LeuGluAsnSerThrCysAspThrAspGlyMetTyrAspIleCysLysSerPheLeuTyr 79
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         64 CTGGAAAACTCCACCTGTGACACAGATGGGATGTATGACATCTGTAAATCCTTCTTGTAC 123

Qy         80 SerAlaAlaLysPheAspThrGlnGlyLysAlaPheValLysGluSerLeuLysCysIle 99
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        124 AGCGCTGCTAAATTTGACACTCAGGGAAAAGCATTCGTCAAAGAGAGCTTAAAATGCATC 183

Qy        100 AlaAsnGlyValThrSerLysValPheLeuAlaIleArgArgCysSerThrPheGlnArg 119
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        184 GCCAACGGGGTCACCTCCAAGGTCTTCCTCGCCATTCGGAGGTGCTCCACTTTCCAAAGG 243

Qy        120 MetIleAlaGluValGlnGluGluCysTyrSerLysLeuAsnValCysSerIleAlaLys 139
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        244 ATGATTGCTGAGGTGCAGGAAGAGTGCTACAGCAAGCTGAATGTGTGCAGCATCGCCAAG 303

Qy        140 ArgAsnProGluAlaIleThrGluValValGlnLeuProAsnHisPheSerAsnArgTyr 159
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        304 CGGAACCCTGAAGCCATCACTGAGGTCGTCCAGCTGCCCAATCACTTCTCCAACAGATAC 363

Qy        160 TyrAsnArgLeuValArgSerLeuLeuGluCysAspGluAspThrValSerThrIleArg 179
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        364 TATAACAGACTTGTCCGAAGCCTGCTGGAATGTGATGAAGACACAGTCAGCACAATCAGA 423

Qy        180 AspSerLeuMetGluLysIleGlyProAsnMetAlaSerLeuPheHisIleLeuGlnThr 199
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        424 GACAGCCTGATGGAGAAAATTGGGCCTAACATGGCCAGCCTCTTCCACATCCTGCAGACA 483

Qy        200 AspHisCysAlaGlnThrHisProArgAlaAspPheAsnArgArgArgThrAsnGluPro 219
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        484 GACCACTGTGCCCAAACACACCCACGAGCTGACTTCAACAGGAGACGCACCAATGAGCCG 543

Qy        220 GlnLysLeuLysValLeuLeuArgAsnLeuArgGlyGluGluAspSerProSerHisIle 239
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        544 CAGAAGCTGAAAGTCCTCCTCAGGAACCTCCGAGGTGAGGAGGACTCTCCCTCCCACATC 603

Qy        240 LysArgThrSerHisGluSerAla 247
              ||||||||||||||||||||||||
Db        604 AAACGCACATCCCATGAGAGTGCA 627

RESULT 3
BM311682
LOCUS       BM311682                648 bp    mRNA    linear   EST 03-JAN-2002
DEFINITION  ig60f04.x1 HR85 islet Homo sapiens cDNA 3' similar to SW:STC1_HUMAN
            P52823 STANNIOCALCIN 1 PRECURSOR ;, mRNA sequence.
ACCESSION   BM311682
VERSION     BM311682.1  GI:18046027
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 648)
  AUTHORS   Melton,D., Brown,J., Kenty,G., Permutt,A., Lee,C., Kaestner,K.,
            Lemishka,I., Scearce,M., Brestelli,J., Gradwohl,G., Clifton,S.,
            Hillier,L., Marra,M., Pape,D., Wylie,T., Martin,J., Blistain,A.,
            Schmitt,A., Theising,B., Ritter,E., Ronko,I., Bennett,J., Cardenas
            ,M., Gibbons,M., McCann,R., Cole,R., Tsagareishvili,R., Williams,T.
            , Jackson,Y. and Bowers,Y.
  TITLE     Endocrine Pancreas Consortium
  JOURNAL   Unpublished (2000)
COMMENT     Other_ESTs: ig60f04.y1
            Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
            Endocrine Pancreas Consortium
            Harvard University, Howard Hughes Medical Institute
            Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
            MA 02138
            Tel: 617-495-1812
```

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           Fax: 617-495-8557
           Email: dmelton@biohp.harvard.edu
           Library was constructed by Dr. Hiroshi Inoue DNA sequencing by:
           Washington University Genome Sequencing Center For information on
           obtaining a clone please contact: Dr. Hiroshi Inoue
           (hinoue@im.wustl.edu)
           Possible reversed clone: similarity on wrong strand
           Seq primer: -40UP from Gibco
           High quality sequence stop: 475.
FEATURES             Location/Qualifiers
     source          1. .648
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone_lib="HR85 islet"
                     /tissue_type="Purified pancreatic islet"
                     /lab_host="DH10B"
                     /note="Organ: Pancreas; Vector: pBluescript SK(-); Site_1:
                     NotI; Site_2: XhoI; cDNA made by oligo-dT priming.
                     Size-selected on agarose gel. Average insert size ~1kb. 5'
                     XhoI site was destroyed after directional cloning.
                     Amplified once. Contact information: Hiroshi Inoue, MD,
                     Metabolism Div. (Alan Permutt Lab), Washington University
                     School of Medicine, Box 8127, 660 South Euclid Ave., St.
                     Louis, MO 63110, E-mail: hinoue@imgate.wustl.edu, Tel:
                     314-362-1916, Fax: 314-747-2692."
BASE COUNT      175 a    179 c    164 g    130 t
ORIGIN

Alignment Scores:
Pred. No.:              2.18e-197      Length:         648
Score:                  207.00         Matches:        207
Percent Similarity:     100.00%        Conservative:   0
Best Local Similarity:  100.00%        Mismatches:     0
Query Match:            83.81%         Indels:         0
DB:                     13             Gaps:           0

US-09-705-500A-3 (1-247) x BM311682 (1-648)

Qy         13 IleSerAlaSerAlaThrHisGluAlaGluGlnAsnAspSerValSerProArgLysSer 32
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         28 ATCAGTGCTTCTGCAACCCATGAGGCGGAGCAGAATGACTCTGTGAGCCCCAGGAAATCC 87

Qy         33 ArgValAlaAlaGlnAsnSerAlaGluValValArgCysLeuAsnSerAlaLeuGlnVal 52
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         88 CGAGTGGCGGCTCAAAACTCAGCTGAAGTGGTTCGTTGCCTCAACAGTGCTCTACAGGTC 147

Qy         53 GlyCysGlyAlaPheAlaCysLeuGluAsnSerThrCysAspThrAspGlyMetTyrAsp 72
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        148 GGCTGCGGGGCTTTTGCATGCCTGGAAAACTCCACCTGTGACACAGATGGGATGTATGAC 207

Qy         73 IleCysLysSerPheLeuTyrSerAlaAlaLysPheAspThrGlnGlyLysAlaPheVal 92
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        208 ATCTGTAAATCCTTCTTGTACAGCGCTGCTAAATTTGACACTCAGGGAAAAGCATTCGTC 267

Qy         93 LysGluSerLeuLysCysIleAlaAsnGlyValThrSerLysValPheLeuAlaIleArg 112
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        268 AAAGAGAGCTTAAAATGCATCGCCAACGGGGTCACCTCCAAGGTCTTCCTCGCCATTCGG 327

Qy        113 ArgCysSerThrPheGlnArgMetIleAlaGluValGlnGluGluCysTyrSerLysLeu 132
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        328 AGGTGCTCCACTTTCCAAAGGATGATTGCTGAGGTGCAGGAAGAGTGCTACAGCAAGCTG 387

Qy        133 AsnValCysSerIleAlaLysArgAsnProGluAlaIleThrGluValValGlnLeuPro 152
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        388 AATGTGTGCAGCATCGCCAAGCGGAACCCTGAAGCCATCACTGAGGTCGTCCAGCTGCCC 447

Qy        153 AsnHisPheSerAsnArgTyrTyrAsnArgLeuValArgSerLeuLeuGluCysAspGlu 172
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        448 AATCACTTCTCCAACAGATACTATAACAGACTTGTCCGAAGCCTGCTGGAATGTGATGAA 507

Qy        173 AspThrValSerThrIleArgAspSerLeuMetGluLysIleGlyProAsnMetAlaSer 192
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        508 GACACAGTCAGCACAATCAGAGACAGCCTGATGGAGAAAATTGGGCCTAACATGGCCAGC 567

Qy        193 LeuPheHisIleLeuGlnThrAspHisCysAlaGlnThrHisProArgAlaAspPheAsn 212
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        568 CTCTTCCACATCCTGCAGACAGACCACTGTGCCCAAACACACCCACGAGCTGACTTCAAC 627

Qy        213 ArgArgArgThrAsnGluPro 219
              |||||||||||||||||||
Db        628 AGGAGACGCACCAATGAGCCG 648

RESULT 4
BM311087/c
LOCUS       BM311087                617 bp    mRNA    linear   EST 03-JAN-2002
DEFINITION  ig60f04.y1 HR85 islet Homo sapiens cDNA 5' similar to SW:STC1_HUMAN
            P52823 STANNIOCALCIN 1 PRECURSOR ;, mRNA sequence.
ACCESSION   BM311087
VERSION     BM311087.1  GI:18045432
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 617)
  AUTHORS   Melton,D., Brown,J., Kenty,G., Permutt,A., Lee,C., Kaestner,K.,
            Lemishka,I., Scearce,M., Brestelli,J., Gradwohl,G., Clifton,S.,
            Hillier,L., Marra,M., Pape,D., Wylie,T., Martin,J., Blistain,A.,
            Schmitt,A., Theising,B., Ritter,E., Ronko,I., Bennett,J., Cardenas
            ,M., Gibbons,M., McCann,R., Cole,R., Tsagareishvili,R., Williams,T.
            , Jackson,Y. and Bowers,Y.
  TITLE     Endocrine Pancreas Consortium
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
            Endocrine Pancreas Consortium
            Harvard University, Howard Hughes Medical Institute
            Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
            MA 02138
            Tel: 617-495-1812
            Fax: 617-495-8557
            Email: dmelton@biohp.harvard.edu
            Library was constructed by Dr. Hiroshi Inoue DNA sequencing by:
            Washington University Genome Sequencing Center For information on
            obtaining a clone please contact: Dr. Hiroshi Inoue
            (hinoue@im.wustl.edu)
            Possible reversed clone: similarity on wrong strand
            Seq primer: -40RP from Gibco
            High quality sequence stop: 441.
FEATURES             Location/Qualifiers
     source          1. .617
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone_lib="HR85 islet"
                     /tissue_type="Purified pancreatic islet"
                     /lab_host="DH10B"
                     /note="Organ: Pancreas; Vector: pBluescript SK(-); Site_1:
                     NotI; Site_2: XhoI; cDNA made by oligo-dT priming.
                     Size-selected on agarose gel. Average insert size ~1kb. 5'
                     XhoI site was destroyed after directional cloning.
                     Amplified once. Contact information: Hiroshi Inoue, MD,
                     Metabolism Div. (Alan Permutt Lab), Washington University
                     School of Medicine, Box 8127, 660 South Euclid Ave., St.
                     Louis, MO 63110, E-mail: hinoue@imgate.wustl.edu, Tel:
                     314-362-1916, Fax: 314-747-2692."
BASE COUNT      123 a    155 c    168 g    171 t
ORIGIN

Alignment Scores:
Pred. No.:              2.1e-195       Length:         617
Score:                  205.00         Matches:        205
Percent Similarity:     100.00%        Conservative:   0
Best Local Similarity:  100.00%        Mismatches:     0
Query Match:            83.00%         Indels:         0
DB:                     13             Gaps:           0

US-09-705-500A-3 (1-247) x BM311087 (1-617)
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Qy         20 GluAlaGluGlnAsnAspSerValSerProArgLysSerArgValAlaAlaGlnAsnSer 39
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        617 GAGGCGGAGCAGAATGACTCTGTGAGCCCCAGGAAATCCCGAGTGGCGGCTCAAAACTCA 558

Qy         40 AlaGluValValArgCysLeuAsnSerAlaLeuGlnValGlyCysGlyAlaPheAlaCys 59
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        557 GCTGAAGTGGTTCGTTGCCTCAACAGTGCTCTACAGGTCGGCTGCGGGGCTTTTGCATGC 498

Qy         60 LeuGluAsnSerThrCysAspThrAspGlyMetTyrAspIleCysLysSerPheLeuTyr 79
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        497 CTGGAAAACTCCACCTGTGACACAGATGGGATGTATGACATCTGTAAATCCTTCTTGTAC 438

Qy         80 SerAlaAlaLysPheAspThrGlnGlyLysAlaPheValLysGluSerLeuLysCysIle 99
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        437 AGCGCTGCTAAATTTGACACTCAGGGAAAAGCATTCGTCAAAGAGAGCTTAAAATGCATC 378

Qy        100 AlaAsnGlyValThrSerLysValPheLeuAlaIleArgArgCysSerThrPheGlnArg 119
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        377 GCCAACGGGGTCACCTCCAAGGTCTTCCTCGCCATTCGGAGGTGCTCCACTTTCCAAAGG 318

Qy        120 MetIleAlaGluValGlnGluGluCysTyrSerLysLeuAsnValCysSerIleAlaLys 139
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        317 ATGATTGCTGAGGTGCAGGAAGAGTGCTACAGCAAGCTGAATGTGTGCAGCATCGCCAAG 258

Qy        140 ArgAsnProGluAlaIleThrGluValValGlnLeuProAsnHisPheSerAsnArgTyr 159
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        257 CGGAACCCTGAAGCCATCACTGAGGTCGTCCAGCTGCCCAATCACTTCTCCAACAGATAC 198

Qy        160 TyrAsnArgLeuValArgSerLeuLeuGluCysAspGluAspThrValSerThrIleArg 179
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        197 TATAACAGACTTGTCCGAAGCCTGCTGGAATGTGATGAAGACACAGTCAGCACAATCAGA 138

Qy        180 AspSerLeuMetGluLysIleGlyProAsnMetAlaSerLeuPheHisIleLeuGlnThr 199
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        137 GACAGCCTGATGGAGAAAATTGGGCCTAACATGGCCAGCCTCTTCCACATCCTGCAGACA 78

Qy        200 AspHisCysAlaGlnThrHisProArgAlaAspPheAsnArgArgArgThrAsnGluPro 219
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         77 GACCACTGTGCCCAAACACACCCACGAGCTGACTTCAACAGGAGACGCACCAATGAGCCG 18

Qy        220 GlnLysLeuLysVal 224
              |||||||||||||||
Db         17 CAGAAGCTGAAAGTC 3
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RESULT 5
AW965863
LOCUS AW965863 644 bp mRNA linear EST 01-JUN-2000
DEFINITION EST377936 MAGE resequences, MAGI Homo sapiens cDNA, mRNA sequence.
ACCESSION AW965863
VERSION AW965863.1 GI:8155699
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 644)
AUTHORS Hegde,P., Qi,R., Abernathy,K., Dharap,S., Gaspard,R., Gay,C., Holt,I.E., Saeed,A.I., Sharov,V., Lee,N.H., Yeatman,T.J. and Quackenbush,J.
TITLE Assessment of gene expression patterns in a model of colon tumor metastasis using a 19,200 element cDNA microarray
JOURNAL Unpublished (2000)
COMMENT Contact: John Quackenbush
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 3528
Fax: 301 838 0208
Email: johnq@tigr.org
Plate: 220
Seq primer: Reverse.
FEATURES Location/Qualifiers
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="MAGE resequences, MAGI"
/note="Vector: pBluescriptSKm"
BASE COUNT 171 a 175 c 164 g 134 t
ORIGIN

Alignment Scores:

Pred. No.:	2.32e-189	Length:	644
Score:	199.00	Matches:	199
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	80.57%	Indels:	0
DB:	10	Gaps:	0

US-09-705-500A-3 (1-247) x AW965863 (1-644)

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Qy          5 SerAlaValLeuLeuValLeuValIleSerAlaSerAlaThrHisGluAlaGluGlnAsn 24
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 TCAGCAGTGCTTCTGGTGCTGGTGATCAGTGCTTCTGCAACCCATGAGGCGGAGCAGAAT 60

Qy         25 AspSerValSerProArgLysSerArgValAlaAlaGlnAsnSerAlaGluValValArg 44
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GACTCTGTGAGCCCCAGGAAATCCCGAGTGGCGGCTCAAAACTCAGCTGAAGTGGTTCGT 120

Qy         45 CysLeuAsnSerAlaLeuGlnValGlyCysGlyAlaPheAlaCysLeuGluAsnSerThr 64
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TGCCTCAACAGTGCTCTACAGGTCGGCTGCGGGGCTTTTGCATGCCTGGAAAACTCCACC 180

Qy         65 CysAspThrAspGlyMetTyrAspIleCysLysSerPheLeuTyrSerAlaAlaLysPhe 84
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TGTGACACAGATGGGATGTATGACATCTGTAAATCCTTCTTGTACAGCGCTGCTAAATTT 240

Qy         85 AspThrGlnGlyLysAlaPheValLysGluSerLeuLysCysIleAlaAsnGlyValThr 104
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GACACTCAGGGAAAAGCATTCGTCAAAGAGAGCTTAAAATGCATCGCCAACGGGGTCACC 300

Qy        105 SerLysValPheLeuAlaIleArgArgCysSerThrPheGlnArgMetIleAlaGluVal 124
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TCCAAGGTCTTCCTCGCCATTCGGAGGTGCTCCACTTTCCAAAGGATGATTGCTGAGGTG 360

Qy        125 GlnGluGluCysTyrSerLysLeuAsnValCysSerIleAlaLysArgAsnProGluAla 144
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CAGGAAGAGTGCTACAGCAAGCTGAATGTGTGCAGCATCGCCAAGCGGAACCCTGAAGCC 420

Qy        145 IleThrGluValValGlnLeuProAsnHisPheSerAsnArgTyrTyrAsnArgLeuVal 164
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ATCACTGAGGTCGTCCAGCTGCCCAATCACTTCTCCAACAGATACTATAACAGACTGGTC 480

Qy        165 ArgSerLeuLeuGluCysAspGluAspThrValSerThrIleArgAspSerLeuMetGlu 184
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 CGAAGCCTGCTGGAATGTGATGAAGACACAGTCAGCACAATCAGAGACAGCCTGATGGAG 540

Qy        185 LysIleGlyProAsnMetAlaSerLeuPheHisIleLeuGlnThrAspHisCysAla 203
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 AAAATTGGGCCTAACATGGCCAGCCTCTTCCACATCCTGCAGACGGACCATTGTGCC 597
```

RESULT 6
AW954342
LOCUS AW954342 646 bp mRNA linear EST 01-JUN-2000
DEFINITION EST366412 MAGE resequences, MAGC Homo sapiens cDNA, mRNA sequence.
ACCESSION AW954342
VERSION AW954342.1 GI:8144025
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 646)
AUTHORS Hegde,P., Qi,R., Abernathy,K., Dharap,S., Gaspard,R., Gay,C., Holt,I.E., Saeed,A.I., Sharov,V., Lee,N.H., Yeatman,T.J. and Quackenbush,J.
TITLE Assessment of gene expression patterns in a model of colon tumor

```
            metastasis using a 19,200 element cDNA microarray
  JOURNAL   Unpublished (2000)
COMMENT     Contact: John Quackenbush
            The Institute for Genomic Research
            9712 Medical Center Dr., Rockville, MD 20850, USA
            Tel: 301 838 3528
            Fax: 301 838 0208
            Email: johnq@tigr.org
            Plate: 62
            Seq primer: Reverse.
FEATURES             Location/Qualifiers
     source          1. .646
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone_lib="MAGE resequences, MAGC"
                     /note="Vector: pBluescriptSKm"
BASE COUNT      171 a    178 c    161 g    135 t      1 others
ORIGIN

Alignment Scores:
Pred. No.:                3.04e-158      Length:          646
Score:                    168.00         Matches:         168
Percent Similarity:       100.00%        Conservative:    0
Best Local Similarity:    100.00%        Mismatches:      0
Query Match:              68.02%         Indels:          0
DB:                       10             Gaps:            0

US-09-705-500A-3 (1-247) x AW954342 (1-646)

Qy          5 SerAlaValLeuLeuValLeuValIleSerAlaSerAlaThrHisGluAlaGluGlnAsn 24
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 TCAGCAGTGCTTCTGGTGCTGGTGATCAGTGCTTCTGCAACCCATGAGGCGGAGCAGAAT 60

Qy         25 AspSerValSerProArgLysSerArgValAlaAlaGlnAsnSerAlaGluValValArg 44
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GACTCTGTGAGCCCCAGGAAATCCCGAGTGGCGGCTCAAAACTCAGCTGAAGTGGTTCGT 120

Qy         45 CysLeuAsnSerAlaLeuGlnValGlyCysGlyAlaPheAlaCysLeuGluAsnSerThr 64
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TGCCTCAACAGTGCTCTACAGGTCGGCTGCGGGGCTTTTGCATGCCTGGAAAACTCCACC 180

Qy         65 CysAspThrAspGlyMetTyrAspIleCysLysSerPheLeuTyrSerAlaAlaLysPhe 84
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TGTGACACAGATGGGATGTATGACATCTGTAAATCCTTCTTGTACAGCGCTGCTAAATTT 240

Qy         85 AspThrGlnGlyLysAlaPheValLysGluSerLeuLysCysIleAlaAsnGlyValThr 104
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GACACTCAGGGAAAAGCATTCGTCAAAGAGAGCTTAAAATGCATCGCCAACGGGGTCACC 300

Qy        105 SerLysValPheLeuAlaIleArgArgCysSerThrPheGlnArgMetIleAlaGluVal 124
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TCCAAGGTCTTCCTCGCCATTCGGAGGTGCTCCACTTTCCAAAGGATGATTGCTGAGGTG 360

Qy        125 GlnGluGluCysTyrSerLysLeuAsnValCysSerIleAlaLysArgAsnProGluAla 144
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CAGGAAGAGTGCTACAGCAAGCTGAATGTGTGCAGCATCGCCAAGCGGAACCCTGAAGCC 420

Qy        145 IleThrGluValValGlnLeuProAsnHisPheSerAsnArgTyrTyrAsnArgLeuVal 164
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ATCACTGAGGTCGTCCAGCTGCCCAATCACTTCTCCAACAGATACTATAACAGACTTGTC 480

Qy        165 ArgSerLeuLeuGluCysAspGlu 172
              ||||||||||||||||||||||||
Db        481 CGAAGCCTGCTGGAATGTGATGAA 504

RESULT 7
BQ894224
LOCUS       BQ894224                915 bp    mRNA    linear   EST 16-AUG-2002
DEFINITION  AGENCOURT_8489564 Lupski_dorsal_root_ganglion Homo sapiens cDNA
            clone IMAGE:6180797 5', mRNA sequence.
ACCESSION   BQ894224
VERSION     BQ894224.1  GI:22286238
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 915)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. James R. Lupski
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM13564  row: c  column: 06
            High quality sequence stop: 638.
FEATURES             Location/Qualifiers
     source          1. .915
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:6180797"
                     /clone_lib="Lupski_dorsal_root_ganglion"
                     /sex="male"
                     /tissue_type="dorsal root ganglia"
                     /dev_stage="adult, 36 yr"
                     /lab_host="DH10B"
                     /note="Vector: pCMV-SPORT6 (Life Technologies); Site_1:
                     NotI; Site_2: SalI; cDNA made by oligo-dT priming.
                     Directionally cloned using the following adaptors:
                     5'-TCGACCCACGCGTCCG-3' and
                     5'-GACTAGTTCTAGATCGCGAGCGGCCGCCCT(15)-3'. Size selected >
                     1 kb for average insert length 1.7 kb. This is a primary
                     library, non-amplified. Library constructed by Life
                     Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor
                     College of Medicine) and is available through Life
                     Technologies."
BASE COUNT      271 a    247 c    235 g    161 t      1 others
ORIGIN

Alignment Scores:
Pred. No.:                4.56e-158      Length:          915
Score:                    168.00         Matches:         168
Percent Similarity:       100.00%        Conservative:    0
Best Local Similarity:    100.00%        Mismatches:      0
Query Match:              68.02%         Indels:          0
DB:                       14             Gaps:            0

US-09-705-500A-3 (1-247) x BQ894224 (1-915)

Qy          1 MetLeuGlnAsnSerAlaValLeuLeuValLeuValIleSerAlaSerAlaThrHisGlu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        256 ATGCTCCAAAACTCAGCAGTGCTTCTGGTGCTGGTGATCAGTGCTTCTGCAACCCATGAG 315

Qy         21 AlaGluGlnAsnAspSerValSerProArgLysSerArgValAlaAlaGlnAsnSerAla 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        316 GCGGAGCAGAATGACTCTGTGAGCCCCAGGAAATCCCGAGTGGCGGCTCAAAACTCAGCT 375

Qy         41 GluValValArgCysLeuAsnSerAlaLeuGlnValGlyCysGlyAlaPheAlaCysLeu 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        376 GAAGTGGTTCGTTGCCTCAACAGTGCTCTACAGGTCGGCTGCGGGGCTTTTGCATGCCTG 435

Qy         61 GluAsnSerThrCysAspThrAspGlyMetTyrAspIleCysLysSerPheLeuTyrSer 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        436 GAAAACTCCACCTGTGACACAGATGGGATGTATGACATCTGTAAATCCTTCTTGTACAGC 495

Qy         81 AlaAlaLysPheAspThrGlnGlyLysAlaPheValLysGluSerLeuLysCysIleAla 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        496 GCTGCTAAATTTGACACTCAGGGAAAAGCATTCGTCAAAGAGAGCTTAAAATGCATCGCC 555

Qy        101 AsnGlyValThrSerLysValPheLeuAlaIleArgArgCysSerThrPheGlnArgMet 120
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                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        556 AACGGGGTCACCTCCAAGGTCTTCCTCGCCATTCGGAGGTGCTCCACTTTCCAAAGGATG 615

Qy        121 IleAlaGluValGlnGluGluCysTyrSerLysLeuAsnValCysSerIleAlaLysArg 140
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        616 ATTGCTGAGGTGCAGGAAGAGTGCTACAGCAAGCTGAATGTGTGCAGCATCGCCAAGCGG 675

Qy        141 AsnProGluAlaIleThrGluValValGlnLeuProAsnHisPheSerAsnArgTyrTyr 160
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        676 AACCCTGAAGCCATCACTGAGGTCGTCCAGCTGCCCAATCACTTCTCCAACAGATACTAT 735

Qy        161 AsnArgLeuValArgSerLeuLeu 168
                ||||||||||||||||||||||||
Db        736 AACAGACTTGTCCGAAGCCTGCTG 759

RESULT 8
AL549427
LOCUS       AL549427                782 bp    mRNA    linear   EST 16-FEB-2001
DEFINITION  AL549427 LTI_NFL006_PL2 Homo sapiens cDNA clone CS0DI044YI18 5
            prime, mRNA sequence.
ACCESSION   AL549427
VERSION     AL549427.1  GI:12885398
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 782)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE     Full-length cDNA libraries and normalization
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Genoscope
            Genoscope - Centre National de Sequencage
            BP 191 91006 EVRY cedex - France
            Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
FEATURES             Location/Qualifiers
     source          1. .782
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="CS0DI044YI18"
                     /clone_lib="LTI_NFL006_PL2"
                     /tissue_type="placenta"
                     /note="Vector: pCMVSPORT 6; Site_1: NotI; 1st strand cDNA
                     was primed with a NotI-oligo(dT) primer.  Five prime end
                     enriched, double-stranded cDNA was digested with Not I and
                     cloned into the Not I and Eco RV sites of the pCMVSPORT 6
                     vector. Library was normalized. Library was constructed by
                     Life Technologies. Contact : Feng Liang Life Technologies,
                     a division of Invitrogen 9800 Medical Center Drive
                     Rockville, Maryland 20850, USA Fax : (1) 301 610 8371
                     Email : fliang@lifetech.com URL :
                     http://fulllength.invitrogen.com"
BASE COUNT      230 a    204 c    202 g    144 t      2 others
ORIGIN

Alignment Scores:
Pred. No.:              4.21e-146      Length:         782
Score:                  156.00         Matches:        156
Percent Similarity:     100.00%        Conservative:   0
Best Local Similarity:  100.00%        Mismatches:     0
Query Match:            63.16%         Indels:         0
DB:                     9              Gaps:           0

US-09-705-500A-3 (1-247) x AL549427 (1-782)

Qy         24 AsnAspSerValSerProArgLysSerArgValAlaAlaGlnAsnSerAlaGluValVal 43
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        313 AATGACTCTGTGAGCCCCAGGAAATCCCGAGTGGCGGCTCAAAACTCAGCTGAAGTGGTT 372

Qy         44 ArgCysLeuAsnSerAlaLeuGlnValGlyCysGlyAlaPheAlaCysLeuGluAsnSer 63
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        373 CGTTGCCTCAACAGTGCTCTACAGGTCGGCTGCGGGGCTTTTGCATGCCTGGAAAACTCC 432

Qy         64 ThrCysAspThrAspGlyMetTyrAspIleCysLysSerPheLeuTyrSerAlaAlaLys 83
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        433 ACCTGTGACACAGATGGGATGTATGACATCTGTAAATCCTTCTTGTACAGCGCTGCTAAA 492

Qy         84 PheAspThrGlnGlyLysAlaPheValLysGluSerLeuLysCysIleAlaAsnGlyVal 103
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        493 TTTGACACTCAGGGAAAAGCATTCGTCAAAGAGAGCTTAAAATGCATCGCCAACGGGGTC 552

Qy        104 ThrSerLysValPheLeuAlaIleArgArgCysSerThrPheGlnArgMetIleAlaGlu 123
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        553 ACCTCCAAGGTCTTCCTCGCCATTCGGAGGTGCTCCACTTTCCAAAGGATGATTGCTGAG 612

Qy        124 ValGlnGluGluCysTyrSerLysLeuAsnValCysSerIleAlaLysArgAsnProGlu 143
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        613 GTGCAGGAAGAGTGCTACAGCAAGCTGAATGTGTGCAGCATCGCCAAGCGGAACCCTGAA 672

Qy        144 AlaIleThrGluValValGlnLeuProAsnHisPheSerAsnArgTyrTyrAsnArgLeu 163
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        673 GCCATCACTGAGGTCGTCCAGCTGCCCAATCACTTCTCCAACAGATACTATAACAGACTT 732

Qy        164 ValArgSerLeuLeuGluCysAspGluAspThrValSerThrIleArg 179
                ||||||||||||||||||||||||||||||||||||||||||||||||
Db        733 GTCCGAAGCCTGCTGGAATGTGATGAAGACACAGTYAGCACAATCAGA 780

RESULT 9
BQ308414
LOCUS       BQ308414                577 bp    mRNA    linear   EST 16-MAY-2002
DEFINITION  MR0-BT4501-280601-103-c11 BT4501 Homo sapiens cDNA, mRNA sequence.
ACCESSION   BQ308414
VERSION     BQ308414.1  GI:20849730
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 577)
  AUTHORS   Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
            Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
            Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
            Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
            ,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
            Simpson,A.J.
  TITLE     Shotgun sequencing of the human transcriptome with ORF expressed
            sequence tags
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
  MEDLINE   20202663
COMMENT     Contact: Simpson A.J.G.
            Laboratory of Cancer Genetics
            Ludwig Institute for Cancer Research
            Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
            Brazil
            Tel: +55-11-2704922
            Fax: +55-11-2707001
            Email: asimpson@ludwig.org.br
            This sequence was derived from the FAPESP/LICR Human Cancer Genome
            Project. This entry can be seen in the following URL
            (http://www.ludwig.org.br/scripts/gethtml2.pl?t1=MR0&t2=MR0-BT4501-
            280601-103-c11&t3=2001-06-28&t4=1)
            Seq primer: puc 18 forward
            High quality sequence stop: 576.
FEATURES             Location/Qualifiers
     source          1. .577
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone_lib="BT4501"
                     /dev_stage="Adult"
                     /note="Organ: breast; Vector: puc18; Site_1: SmaI; Site_2:
                     SmaI; A mini-library was made by cloning products derived
                     from  ORESTES PCR (U.S. Letters Patent application No. 196
                     ,716 -  Ludwig Institute for Cancer Research) profiles
                     into the pUC 18 vector. Reverse transcription of tissue
                     mRNA and cDNA amplification were performed under low
                     stringency conditions."
```

```
BASE COUNT      161 a    159 c    140 g    117 t
ORIGIN

Alignment Scores:
Pred. No.:              3.55e-125       Length:         577
Score:                  135.00          Matches:        148
Percent Similarity:     99.33%          Conservative:   0
Best Local Similarity:  99.33%          Mismatches:     0
Query Match:            54.66%          Indels:         1
DB:                     14              Gaps:           0

US-09-705-500A-3 (1-247) x BQ308414 (1-577)

Qy         68 AspGlyMetTyrAspIleCysLysSerPheLeuTyrSerAlaAlaLysPheAspThrGln 87
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         89 GATGGGATGTATGACATCTGTAAATCCTTCTTGTACAGCGCTGCTAAATTTGACACTCAG 148

Qy         88 GlyLysAlaPheValLysGluSerLeuLysCysIleAlaAsnGlyValThrSerLysVal 107
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        149 GGAAAAGCATTCGTCAAAGAGAGCTTAAAATGCATCGCCAACGGGGTCACCTCCAAGGTC 208

Qy        108 PheLeuAlaIleArgArgCysSerThrPheGlnArgMetIleAlaGluValGlnGluGlu 127
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        209 TTCCTCGCCATTCGGAGGTGCTCCACTTTCCAAAGGATGATTGCTGAGGTGCAGGAAGAG 268

Qy        128 CysTyrSerLysLeuAsnValCysSerIleAlaLysArgAsnProGluAlaIleThrGlu 147
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        269 TGCTACAGCAAGCTGAATGTGTGCAGCATCGCCAAGCGGAACCCTGAAGCCATCACTGAG 328

Qy        148 ValValGlnLeuProAsnHisPheSerAsnArgTyrTyrAsnArgLeuValArgSerLeu 167
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        329 GTCGTCCAGCTGCCCAATCACTTCTCCAACAGATACTATAACAGACTTGTCCGAAGCCTG 388

Qy        168 LeuGluCysAspGluAspThrValSerThrIleArgAspSerLeuMetGluLysIleGly 187
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        389 CTGGAATGTGATGAAGACACAGTCAGCACAATCAGAGACAGCCTGATGGAGAAAATTGGG 448

Qy        188 Pro-AsnMetAlaSerLeuPheHisIleLeuGlnThrAspHisCysAlaGlnThrHisPr 207
              ||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        449 CCTAAACATGGCCAGCCTCTTCCACATCCTGCAGACAGACCACTGTGCCCAAACACACCC 508

Qy        207 oArgAlaAspPheAsnArgArgArg 215
              |||||||||||||||||||||||||
Db        509 ACGAGCTGACTTCAACAGGAGACGC 533

RESULT 10
AU122680
LOCUS       AU122680                907 bp    mRNA    linear   EST 01-AUG-2002
DEFINITION  AU122680 MAMMA1 Homo sapiens cDNA clone MAMMA1002879 5', mRNA
            sequence.
ACCESSION   AU122680
VERSION     AU122680.1  GI:10947396
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 907)
  AUTHORS   Ota,T., Nishikawa,T., Suzuki,Y., Ishii,S., Saito,K., Kawai,Y.,
            Yamamoto,J., Wakamatsu,A., Nakamura,Y., Nagai,T., Sugano,S. and
            Isogai,T.
  TITLE     HRI human cDNA project
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Takao Isogai
            Genomics Laboratory
            Helix Research Institute
            1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
            Tel: 81-438-52-3975
            Fax: 81-438-52-3986
            Email: genomics@hri.co.jp
            HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix
            Research Institute; cDNA library construction: Department of
            Virology, Institute of Medical Science, University of Tokyo, and
            Helix Research Institute.
FEATURES             Location/Qualifiers
     source          1. .907
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="MAMMA1002879"
                     /clone_lib="MAMMA1"
                     /tissue_type="mammary gland"
                     /note="Vector: pME18SFL3"
BASE COUNT      264 a    230 c    229 g    178 t      6 others
ORIGIN

Alignment Scores:
Pred. No.:              6.72e-112       Length:         907
Score:                  122.00          Matches:        122
Percent Similarity:     100.00%         Conservative:   0
Best Local Similarity:  100.00%         Mismatches:     0
Query Match:            49.39%          Indels:         0
DB:                     9               Gaps:           0

US-09-705-500A-3 (1-247) x AU122680 (1-907)

Qy          1 MetLeuGlnAsnSerAlaValLeuLeuValLeuValIleSerAlaSerAlaThrHisGlu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        283 ATGCTCCAAAACTCAGCGGTGCTTCTGGTGCTGGTGATCAGTGCTTCTGCAACCCATGAG 342

Qy         21 AlaGluGlnAsnAspSerValSerProArgLysSerArgValAlaAlaGlnAsnSerAla 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        343 GCGGAGCAGAATGACTCTGTGAGCCCCAGGAAATCCCGAGTGGCGGCTCAAAACTCAGCT 402

Qy         41 GluValValArgCysLeuAsnSerAlaLeuGlnValGlyCysGlyAlaPheAlaCysLeu 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        403 GAAGTGGTTCGTTGCCTCAACAGTGCTCTACAGGTCGGCTGCGGGGCTTTTGCATGCCTG 462

Qy         61 GluAsnSerThrCysAspThrAspGlyMetTyrAspIleCysLysSerPheLeuTyrSer 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        463 GAAAACTCCACCTGTGACACAGATGGGATGTATGACATCTGTAAATCCTTCTTGTACAGC 522

Qy         81 AlaAlaLysPheAspThrGlnGlyLysAlaPheValLysGluSerLeuLysCysIleAla 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        523 GCTGCTAAATTTGACACTCAGGGAAAAGCATTCGTCAAAGAGAGCTTAAAATGCATCGCC 582

Qy        101 AsnGlyValThrSerLysValPheLeuAlaIleArgArgCysSerThrPheGlnArgMet 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        583 AACGGGGTCACCTCCAAGGTCTTCCTCGCCATTCGGAGGTGCTCCACTTTCCAAAGGATG 642

Qy        121 IleAla 122
              ||||||
Db        643 ATTGCT 648

RESULT 11
BM924595
LOCUS       BM924595                1010 bp    mRNA    linear   EST 12-MAR-2002
DEFINITION  AGENCOURT_6767843 NIH_MGC_116 Homo sapiens cDNA clone IMAGE:5760977
            5', mRNA sequence.
ACCESSION   BM924595
VERSION     BM924595.1  GI:19374974
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1010)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Life Technologies, Inc.
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Agencourt Bioscience Corporation
            Clone distribution: MGC clone distribution information can be
```

found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM12808 row: n column: 18
High quality sequence stop: 614.

```
FEATURES             Location/Qualifiers
     source          1. .1010
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:5760977"
                     /clone_lib="NIH_MGC_116"
                     /lab_host="DH10B"
                     /note="Organ: pooled colon, kidney, stomach; Vector:
                     pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA
                     source anonymous pool of 3 colons, age 26 yo male, 49 yo
                     female, 71 yo male colon; 46 yo male kidney, and pool of 2
                     stomachs, 62 yo male and 70 yo female. Library is
                     oligo-dT primed and directionally cloned (EcoRV site is
                     destroyed upon cloning). Average insert size 1.4 kb,
                     insert size range 1-3 kb. Library is normalized and
                     enriched for full-length clones and was constructed by C.
                     Gruber (Invitrogen). Research Genetics tracking code
                     023. Note: this is a NIH_MGC Library."
BASE COUNT      305 a    285 c    251 g    169 t
ORIGIN

Alignment Scores:
Pred. No.:              7.88e-108      Length:         1010
Score:                  118.00         Matches:        118
Percent Similarity:     100.00%        Conservative:   0
Best Local Similarity:  100.00%        Mismatches:     0
Query Match:            47.77%         Indels:         0
DB:                     14             Gaps:           0

US-09-705-500A-3 (1-247) x BM924595 (1-1010)

Qy          1 MetLeuGlnAsnSerAlaValLeuLeuValLeuValIleSerAlaSerAlaThrHisGlu 20
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        263 ATGCTCCAAAACTCAGCAGTGCTTCTGGTGCTGGTGATCAGTGCTTCTGCAACCCATGAG 322

Qy         21 AlaGluGlnAsnAspSerValSerProArgLysSerArgValAlaAlaGlnAsnSerAla 40
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        323 GCGGAGCAGAATGACTCTGTGAGCCCCAGGAAATCCCGAGTGGCGGCTCAAAACTCAGCT 382

Qy         41 GluValValArgCysLeuAsnSerAlaLeuGlnValGlyCysGlyAlaPheAlaCysLeu 60
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        383 GAAGTGGTTCGTTGCCTCAACAGTGCTCTACAGGTCGGCTGCGGGGCTTTTGCATGCCTG 442

Qy         61 GluAsnSerThrCysAspThrAspGlyMetTyrAspIleCysLysSerPheLeuTyrSer 80
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        443 GAAAACTCCACCTGTGACACAGATGGGATGTATGACATCTGTAAATCCTTCTTGTACAGC 502

Qy         81 AlaAlaLysPheAspThrGlnGlyLysAlaPheValLysGluSerLeuLysCysIleAla 100
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        503 GCTGCTAAATTTGACACTCAGGGAAAAGCATTCGTCAAAGAGAGCTTAAAATGCATCGCC 562

Qy        101 AsnGlyValThrSerLysValPheLeuAlaIleArgArgCysSerThrPheGln 118
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        563 AACGGGGTCACCTCCAAGGTCTTCCTCGCCATTCGGAGGTGCTCCACTTTCCAA 616

RESULT 12
BI010260
LOCUS       BI010260                619 bp    mRNA    linear   EST 13-JUN-2001
DEFINITION  MR2-EN0094-050101-005-e11 EN0094 Homo sapiens cDNA, mRNA sequence.
ACCESSION   BI010260
VERSION     BI010260.1  GI:14414331
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 619)
  AUTHORS   Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
            Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
            Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
            Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
            ,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
            Simpson,A.J.
  TITLE     Shotgun sequencing of the human transcriptome with ORF expressed
            sequence tags
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
  MEDLINE   20202663
COMMENT     Contact: Simpson A.J.G.
            Laboratory of Cancer Genetics
            Ludwig Institute for Cancer Research
            Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
            Brazil
            Tel: +55-11-2704922
            Fax: +55-11-2707001
            Email: asimpson@ludwig.org.br
            This sequence was derived from the FAPESP/LICR Human Cancer Genome
            Project. This entry can be seen in the following URL
            (http://www.ludwig.org.br/scripts/gethtml2.pl?t1=MR2&t2=MR2-EN0094-
            050101-005-e11&t3=2001-01-05&t4=1)
            Seq primer: puc 18 forward
            High quality sequence stop: 579.
FEATURES             Location/Qualifiers
     source          1. .619
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone_lib="EN0094"
                     /dev_stage="Adult"
                     /note="Organ: lung_normal; Vector: puc18; Site_1: SmaI;
                     Site_2: SmaI; A mini-library was made by cloning products
                     derived from ORESTES PCR (U.S. Letters Patent application
                     No. 196,716 - Ludwig Institute for Cancer Research)
                     profiles into the pUC 18 vector. Reverse transcription of
                     tissue mRNA and cDNA amplification were performed under
                     low stringency conditions."
BASE COUNT      177 a    178 c    115 g    146 t      3 others
ORIGIN

Alignment Scores:
Pred. No.:              4.99e-95       Length:         619
Score:                  105.00         Matches:        105
Percent Similarity:     100.00%        Conservative:   0
Best Local Similarity:  100.00%        Mismatches:     0
Query Match:            42.51%         Indels:         0
DB:                     13             Gaps:           0

US-09-705-500A-3 (1-247) x BI010260 (1-619)

Qy        143 GluAlaIleThrGluValValGlnLeuProAsnHisPheSerAsnArgTyrTyrAsnArg 162
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          3 GAAGCCATCACTGAGGTCGTCCAGCTGCCCAATCACTTCTCCAACAGATACTATAACAGA 62

Qy        163 LeuValArgSerLeuLeuGluCysAspGluAspThrValSerThrIleArgAspSerLeu 182
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         63 CTTGTCCGAAGCCTGCTGGAATGTGATGAAGACACAGTCAGCACAATCAGAGACAGCCTG 122

Qy        183 MetGluLysIleGlyProAsnMetAlaSerLeuPheHisIleLeuGlnThrAspHisCys 202
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        123 ATGGAGAAAATTGGGCCTAACATGGCCAGCCTCTTCCACATCCTGCAGACAGACCACTGT 182

Qy        203 AlaGlnThrHisProArgAlaAspPheAsnArgArgArgThrAsnGluProGlnLysLeu 222
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        183 GCCCAAACACACCCACGAGCTGACTTCAACAGGAGACGCACCAATGAGCCGCAGAAGCTG 242

Qy        223 LysValLeuLeuArgAsnLeuArgGlyGluGluAspSerProSerHisIleLysArgThr 242
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        243 AAAGTCCTCCTCAGGAACCTCCGAGGTGAGGAGGACTCTCCCTCCCACATCAAACGCACA 302

Qy        243 SerHisGluSerAla 247
              ||||||||||||||||
Db        303 TCCCATGAGAGTGCA 317

RESULT 13
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```
BI010412
LOCUS       BI010412                605 bp    mRNA    linear   EST 13-JUN-2001
DEFINITION  MR2-EN0094-050101-007-d02 EN0094 Homo sapiens cDNA, mRNA sequence.
ACCESSION   BI010412
VERSION     BI010412.1  GI:14414483
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 605)
  AUTHORS   Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
            Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
            Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
            Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
            ,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
            Simpson,A.J.
  TITLE     Shotgun sequencing of the human transcriptome with ORF expressed
            sequence tags
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
  MEDLINE   20202663
COMMENT     Contact: Simpson A.J.G.
            Laboratory of Cancer Genetics
            Ludwig Institute for Cancer Research
            Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
            Brazil
            Tel: +55-11-2704922
            Fax: +55-11-2707001
            Email: asimpson@ludwig.org.br
            This sequence was derived from the FAPESP/LICR Human Cancer Genome
            Project. This entry can be seen in the following URL
            (http://www.ludwig.org.br/scripts/gethtml2.pl?t1=MR2&t2=MR2-EN0094-
            050101-007-d02&t3=2001-01-05&t4=1)
            Seq primer: puc 18 forward
            High quality sequence stop: 605.
FEATURES             Location/Qualifiers
     source          1. .605
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone_lib="EN0094"
                     /dev_stage="Adult"
                     /note="Organ: lung_normal; Vector: puc18; Site_1: SmaI;
                     Site_2: SmaI; A mini-library was made by cloning products
                     derived from  ORESTES PCR (U.S. Letters Patent application
                     No. 196,716 -  Ludwig Institute for Cancer Research)
                     profiles into  the pUC 18 vector. Reverse transcription of
                     tissue mRNA and cDNA amplification were performed under
                     low stringency conditions."
BASE COUNT      173 a    174 c    117 g    140 t      1 others
ORIGIN

Alignment Scores:
Pred. No.:              4.94e-93        Length:         605
Score:                  103.00          Matches:        103
Percent Similarity:     100.00%         Conservative:   0
Best Local Similarity:  100.00%         Mismatches:     0
Query Match:            41.70%          Indels:         0
DB:                     13              Gaps:           0

US-09-705-500A-3 (1-247) x BI010412 (1-605)

Qy        145 IleThrGluValValGlnLeuProAsnHisPheSerAsnArgTyrTyrAsnArgLeuVal 164
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         24 ATCACTGAGGTCGTCCAGCTGCCCAATCACTTCTCCAACAGATACTATAACAGACTTGTC 83

Qy        165 ArgSerLeuLeuGluCysAspGluAspThrValSerThrIleArgAspSerLeuMetGlu 184
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         84 CGAAGCCTGCTGGAATGTGATGAAGACACAGTCAGCACAATCAGAGACAGCCTGATGGAG 143

Qy        185 LysIleGlyProAsnMetAlaSerLeuPheHisIleLeuGlnThrAspHisCysAlaGln 204
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        144 AAAATTGGGCCTAACATGGCCAGCCTCTTCCACATCCTGCAGACAGACCACTGTGCCCAA 203

Qy        205 ThrHisProArgAlaAspPheAsnArgArgArgThrAsnGluProGlnLysLeuLysVal 224
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        204 ACACACCCACGAGCTGACTTCAACAGGAGACGCACCAATGAGCCGCAGAAGCTGAAAGTC 263

Qy        225 LeuLeuArgAsnLeuArgGlyGluGluAspSerProSerHisIleLysArgThrSerHis 244
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        264 CTCCTCAGGAACCTCCGAGGTGAGGAGGACTCTCCCTCCCACATCAAACGCACATCCCAT 323

Qy        245 GluSerAla 247
              ||||||||
Db        324 GAGAGTGCA 332

RESULT 14
R72337
LOCUS       R72337                  483 bp    mRNA    linear   EST 02-JUN-1995
DEFINITION  yj89d08.r1 Soares breast 2NbHBst Homo sapiens cDNA clone
            IMAGE:155919 5' similar to SP:CSTP_ANGAU P18301 CORPUSCLES OF
            STANNIUS PROTEIN PRECURSOR ;, mRNA sequence.
ACCESSION   R72337
VERSION     R72337.1  GI:846369
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 483)
  AUTHORS   Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman
            ,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J.,
            Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston
            ,R., Williamson,A., Wohldmann,P. and Wilson,R.
  TITLE     The WashU-Merck EST Project
  JOURNAL   Unpublished (1995)
COMMENT     Contact: Wilson RK
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            Insert Size: 1711
            High quality sequence stops: 355
            Source: IMAGE Consortium, LLNL
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Insert Length: 1711   Std Error: 0.00
            Seq primer: M13RP1
            High quality sequence stop: 355.
FEATURES             Location/Qualifiers
     source          1. .483
                     /organism="Homo sapiens"
                     /db_xref="GDB:573869"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:155919"
                     /clone_lib="Soares breast 2NbHBst"
                     /sex="Female"
                     /dev_stage="adult"
                     /lab_host="DH10B (ampicillin resistant)"
                     /note="Organ: breast; Vector: pT7T3D (Pharmacia) with a
                     modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
                     strand cDNA was primed with a Not I - oligo(dT) primer [5'
                     TGTTACCAATCTGAAGTGGGAGCGGCCGCCCTTTTTTTTTTTTTTTTT 3'],
                     double-stranded cDNA was ligated to Eco RI adaptors
                     (Pharmacia), digested with Not I and cloned into the Not I
                     and Eco RI sites of a modified pT7T3 vector (Pharmacia).
                     Library went through one round of normalization to a Cot =
                     230. Library constructed by Bento Soares and M.Fatima
                     Bonaldo."
BASE COUNT      135 a    127 c    119 g     97 t      5 others
ORIGIN

Alignment Scores:
Pred. No.:              3.94e-89        Length:         483
Score:                  99.00           Matches:        125
Percent Similarity:     98.43%          Conservative:   0
```

```
Best Local Similarity:  98.43%        Mismatches:    0
Query Match:            40.08%        Indels:        2
DB:                     14            Gaps:          0

US-09-705-500A-3 (1-247) x R72337 (1-483)

Qy         89 LysAlaPheValLysGluSerLeuLysCysIleAlaAsnGlyValThrSerLysValPhe 108
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          3 AAAGCATTCGTCAAAGAGAGCTTAAAATGCATCGCCAACGGGGTCACCTCCAAGGTCTTC 62

Qy        109 LeuAlaIleArgArgCysSerThrPheGlnArgMetIleAlaGluValGlnGluGluCys 128
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         63 CTCGCCATTCGGAGGTGCTCCACTTTCCAAAGGATGATTGCTGAGGTGCAGGAAGAGTGC 122

Qy        129 TyrSerLysLeuAsnValCysSerIleAlaLysArgAsnProGluAlaIleThrGluVal 148
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        123 TACAGCAAGCTGAATGTGTGCAGCATCGCCAAGCGGAACCCTGAAGCCATCACTGAGGTC 182

Qy        149 ValGlnLeuProAsnHisPheSerAsnArgTyrTyrAsnArgLeuValArgSerLeuLeu 168
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        183 GTCCAGCTGCCCAATCACTTCTCCAACAGATACTATAACAGACTTGTCCGAAGCCTGCTG 242

Qy        169 GluCysAspGluAspThrValSerThrIleArgAspSerLeuMet-GluLysIle-GlyP 188
              |||||||||||||||||||||||||||||||||||||||||||| ||||||||| ||||
Db        243 GAATGTGATGAAGACACAGTCAGCACAATCAGAGACAGCCTGATGGGAGAAAATTGGGGC 302

Qy        188 roAsnMetAlaSerLeuPheHisIleLeuGlnThrAspHisCysAlaGlnThrHisProA 208
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        303 CTAACATGGCCAGCCTCTTCCACATCCTGCAGACAGACCACTGTGCCCAAACACACCCAC 362

Qy        208 rgAlaAspPheAsnArg 213
              |||||||||||||||||
Db        363 GAGCTGACTTCAACAGG 379

RESULT 15
AW996662/c
LOCUS       AW996662                437 bp    mRNA    linear   EST 05-JUN-2000
DEFINITION  QV3-BN0046-150400-151-b06 BN0046 Homo sapiens cDNA, mRNA sequence.
ACCESSION   AW996662
VERSION     AW996662.1  GI:8256896
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 437)
  AUTHORS   Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
            Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
            Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
            Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
            ,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
            Simpson,A.J.
  TITLE     Shotgun sequencing of the human transcriptome with ORF expressed
            sequence tags
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
  MEDLINE   20202663
COMMENT     Contact: Simpson A.J.G.
            Laboratory of Cancer Genetics
            Ludwig Institute for Cancer Research
            Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
            Brazil
            Tel: +55-11-2704922
            Fax: +55-11-2707001
            Email: asimpson@ludwig.org.br
            This sequence was derived from the FAPESP/LICR Human Cancer Genome
            Project. This entry can be seen in the following URL
            (http://www.ludwig.org.br/scripts/gethtml2.pl?t1=&t2=QV3-BN0046-150
            400-151-b06&t3=2000-04-15&t4=1)
            Seq primer: puc 18 forward
            High quality sequence start: 41
            High quality sequence stop: 437.
FEATURES             Location/Qualifiers
     source          1. .437
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone_lib="BN0046"
                     /dev_stage="Adult"
                     /note="Organ: breast_normal; Vector: puc18; Site_1: SmaI;
                     Site_2: SmaI; A mini-library was made by cloning products
                     derived from  ORESTES PCR (U.S. Letters Patent application
                     No. 196,716 -  Ludwig Institute for Cancer Research)
                     profiles into  the pUC 18 vector. Reverse transcription of
                     tissue mRNA and cDNA amplification were performed under
                     low stringency conditions."
BASE COUNT       75 a    102 c    130 g    130 t
ORIGIN

Alignment Scores:
Pred. No.:              3.63e-85        Length:         437
Score:                  95.00           Matches:        130
Percent Similarity:     98.48%          Conservative:   0
Best Local Similarity:  98.48%          Mismatches:     1
Query Match:            38.46%          Indels:         2
DB:                     10              Gaps:           0

US-09-705-500A-3 (1-247) x AW996662 (1-437)

Qy        116 ThrPheGlnArgMetIleAlaGluValGlnGluGluCysTyrSerLysLeuAsnValCys 135
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        435 ACTTTCCAAAGGATGATTGCTGAGGTGCAGGAAGAGTGCTACAGCAAGCTGAATGTGTGC 376

Qy        136 SerIleAlaLysArgAsnProGluAlaIleThrGluValValGlnLeuProAsnHisPhe 155
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        375 AGCATCGCCAAGCGGAACCCTGAAGCCATCACTGAGGTCGTCCAGCTGCCCAATCACTTC 316

Qy        156 SerAsnArgTyrTyrAsnArgLeuValArgSerLeuLeuGluCysAspGluAspThrVal 175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        315 TCCAACAGATACTATAACAGACTTGTCCGAAGCCTGCTGGAATGTGATGAAGACACAGTC 256

Qy        176 SerThrIleArgAspSerLeuMetGluLysIleGlyProAsnMetAlaSerLeuPheHis 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        255 AGCACAATCAGAGACAGCCTGATGGAGAAAATTGGGCCTAACATGGCCAGCCTCTTCCAC 196

Qy        196 IleLeuGlnThrAspHisCysAlaGlnThrHisProArgAlaAspPhe-AsnArgArgAr 215
              ||||||||||||||||||||||||||||||||||||||||||||    |||||||||||
Db        195 ATCCTGCAGACAGACCACTGTGCCCAAACACACCCACGAGCTGACGT-CAACAGGAGACG 137

Qy        215 gThrAsnGluProGlnLysLeuLysValLeuLeuArgAsnLeuArgGlyGluGluAspSe 235
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        136 CACCAATGAGCCGCAGAAGCTGAAAGTCCTCCTCAGGAACCTCCGAGGTGAGGAGGACTC 77

Qy        235 rProSerHisIleLysArgThrSerHisGluSer 246
              |||||||||||||||||||||||||||||||||
Db         76 TCCCTCCCACATCAAACGCACATCCCATGAGAGT 43


Search completed: June 12, 2003, 23:07:38
Job time : 1487 secs
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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: June 12, 2003, 16:06:38 ; Search time 203 Seconds
(without alignments)
5683.340 Million cell updates/sec

Title: US-09-705-500A-2
Perfect score: 3762
Sequence: 1 ggtggcagcagcagcatcac.....tgttacgttttattggtttc 3762

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 441362 seqs, 153338381 residues

Word size : 0

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : Issued_Patents_NA:*
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2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
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6: /cgn2_6/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	720	19.1	771	2	US-08-208-005C-1	Sequence 1, Appli
	2	720	19.1	771	2	US-09-038-597A-1	Sequence 1, Appli
	3	720	19.1	771	2	US-08-431-117A-1	Sequence 1, Appli
	4	41	1.1	36651	4	US-09-738-894A-3	Sequence 3, Appli
	5	40	1.1	99	4	US-08-679-493A-18	Sequence 18, Appl
c	6	40	1.1	62804	4	US-09-800-960-3	Sequence 3, Appli
c	7	39	1.0	62	2	US-08-659-453B-4	Sequence 4, Appli
c	8	39	1.0	62	3	US-09-089-853A-4	Sequence 4, Appli
c	9	39	1.0	62	4	US-09-131-009A-4	Sequence 4, Appli
c	10	39	1.0	62	4	US-09-092-226A-4	Sequence 4, Appli
c	11	39	1.0	62	4	US-09-130-862A-4	Sequence 4, Appli
c	12	39	1.0	62	4	US-09-090-809A-4	Sequence 4, Appli
c	13	39	1.0	62	4	US-09-053-116A-4	Sequence 4, Appli
c	14	39	1.0	66	2	US-08-659-453B-1	Sequence 1, Appli
c	15	39	1.0	66	3	US-09-089-853A-1	Sequence 1, Appli
c	16	39	1.0	66	4	US-09-131-009A-1	Sequence 1, Appli
c	17	39	1.0	66	4	US-09-092-226A-1	Sequence 1, Appli
c	18	39	1.0	66	4	US-09-130-862A-1	Sequence 1, Appli
c	19	39	1.0	66	4	US-09-090-809A-1	Sequence 1, Appli
c	20	39	1.0	66	4	US-09-053-116A-1	Sequence 1, Appli
	21	39	1.0	72	2	US-07-829-461A-6	Sequence 6, Appli
	22	39	1.0	72	4	US-09-197-649-5	Sequence 5, Appli
	23	39	1.0	139	4	US-08-679-493A-60	Sequence 60, Appl
	24	39	1.0	150	2	US-08-139-176D-1	Sequence 1, Appli
	25	39	1.0	150	3	US-09-041-841-1	Sequence 1, Appli
c	26	39	1.0	426	2	US-08-822-028-65	Sequence 65, Appl
c	27	39	1.0	426	4	US-08-479-285-65	Sequence 65, Appl
c	28	39	1.0	750	4	US-08-821-994-40	Sequence 40, Appl
c	29	39	1.0	763	4	US-09-484-970B-166	Sequence 166, App
	30	39	1.0	1094	4	US-09-280-116-243	Sequence 243, App
	31	39	1.0	1233	4	US-09-276-531-7	Sequence 7, Appli
c	32	39	1.0	1651	4	US-09-484-970B-17	Sequence 17, Appl
	33	39	1.0	2475	4	US-09-624-693A-20	Sequence 20, Appl
	34	39	1.0	3083	4	US-08-956-657-1	Sequence 1, Appli
c	35	39	1.0	3720	1	US-08-074-967-1	Sequence 1, Appli
c	36	39	1.0	3720	2	US-08-553-541B-1	Sequence 1, Appli
c	37	39	1.0	3720	4	US-09-268-202-1	Sequence 1, Appli
c	38	39	1.0	3720	5	PCT-US94-06669-1	Sequence 1, Appli
c	39	39	1.0	3952	2	US-08-381-691-16	Sequence 16, Appl
	40	39	1.0	4874	4	US-09-484-970B-36	Sequence 36, Appl
	41	39	1.0	17138	4	US-09-813-819-3	Sequence 3, Appli
c	42	39	1.0	17138	4	US-09-813-819-3	Sequence 3, Appli
	43	39	1.0	17138	4	US-09-920-048-3	Sequence 3, Appli
c	44	39	1.0	17138	4	US-09-920-048-3	Sequence 3, Appli
	45	39	1.0	36159	4	US-09-749-588-3	Sequence 3, Appli
	46	39	1.0	38564	4	US-09-734-673-3	Sequence 3, Appli
c	47	38	1.0	61	4	US-09-275-850-291	Sequence 291, App
c	48	38	1.0	76	4	US-09-287-936-1	Sequence 1, Appli
	49	38	1.0	80	1	US-08-435-809-3	Sequence 3, Appli
	50	38	1.0	80	1	US-08-349-316A-2	Sequence 2, Appli
c	51	38	1.0	82	4	US-08-679-493A-14	Sequence 14, Appl
	52	38	1.0	87	1	US-08-199-507B-54	Sequence 54, Appl
c	53	38	1.0	87	1	US-08-199-507B-54	Sequence 54, Appl
	54	38	1.0	87	1	US-08-243-870-2	Sequence 2, Appli
c	55	38	1.0	87	1	US-08-243-870-2	Sequence 2, Appli
	56	38	1.0	87	1	US-08-477-530-1	Sequence 1, Appli
c	57	38	1.0	87	1	US-08-477-530-1	Sequence 1, Appli
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c	59	38	1.0	87	1	US-08-477-530-1	Sequence 1, Appli
	60	38	1.0	87	1	US-08-409-439A-2	Sequence 2, Appli
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c	63	38	1.0	87	1	US-08-477-830-1	Sequence 1, Appli
	64	38	1.0	87	1	US-08-433-126A-40	Sequence 40, Appl
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c	67	38	1.0	87	1	US-08-309-245-2	Sequence 2, Appli
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	70	38	1.0	87	1	US-08-458-423A-49	Sequence 49, Appl
c	71	38	1.0	87	1	US-08-458-423A-49	Sequence 49, Appl
	72	38	1.0	87	1	US-08-458-423A-52	Sequence 52, Appl
c	73	38	1.0	87	1	US-08-458-423A-52	Sequence 52, Appl
	74	38	1.0	87	1	US-08-458-424B-49	Sequence 49, Appl
c	75	38	1.0	87	1	US-08-458-424B-49	Sequence 49, Appl
	76	38	1.0	87	1	US-08-458-424B-52	Sequence 52, Appl
c	77	38	1.0	87	1	US-08-458-424B-52	Sequence 52, Appl
	78	38	1.0	87	1	US-08-441-828-54	Sequence 54, Appl
c	79	38	1.0	87	1	US-08-441-828-54	Sequence 54, Appl
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c	81	38	1.0	87	1	US-08-433-124A-40	Sequence 40, Appl
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c	83	38	1.0	87	1	US-08-463-101-2	Sequence 2, Appli
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c	87	38	1.0	87	2	US-08-488-402A-64	Sequence 64, Appl
	88	38	1.0	87	2	US-08-488-402A-79	Sequence 79, Appl
c	89	38	1.0	87	2	US-08-488-402A-79	Sequence 79, Appl
	90	38	1.0	87	2	US-08-484-552A-64	Sequence 64, Appl
c	91	38	1.0	87	2	US-08-484-552A-64	Sequence 64, Appl
	92	38	1.0	87	2	US-08-484-552A-79	Sequence 79, Appl
c	93	38	1.0	87	2	US-08-484-552A-79	Sequence 79, Appl
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	96	38	1.0	87	2	US-08-799-949-2	Sequence 2, Appli
c	97	38	1.0	87	2	US-08-799-949-2	Sequence 2, Appli
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	100	38	1.0	87	2	US-08-477-527A-186	Sequence 186, App

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c 103	38	1.0	87	3	US-08-481-710-74	Sequence 74, Appl
104	38	1.0	87	3	US-08-481-710-186	Sequence 186, App
c 105	38	1.0	87	3	US-08-481-710-186	Sequence 186, App
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c 109	38	1.0	87	3	US-08-793-398-4	Sequence 4, Appli
c 110	38	1.0	87	3	US-08-973-965-13	Sequence 13, Appl
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c 114	38	1.0	87	3	US-08-976-413A-40	Sequence 40, Appl
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c 116	38	1.0	87	4	US-08-973-124-49	Sequence 49, Appl
117	38	1.0	87	4	US-08-973-124-52	Sequence 52, Appl
c 118	38	1.0	87	4	US-08-973-124-52	Sequence 52, Appl
119	38	1.0	87	4	US-09-335-012-44	Sequence 44, Appl
c 120	38	1.0	87	4	US-09-335-012-44	Sequence 44, Appl
121	38	1.0	87	4	US-09-364-539-192	Sequence 192, App
c 122	38	1.0	87	4	US-09-364-539-192	Sequence 192, App
123	38	1.0	87	4	US-09-941-964-44	Sequence 44, Appl
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c 128	38	1.0	87	5	PCT-US95-11982A-2	Sequence 2, Appli
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c 130	38	1.0	87	5	PCT-US95-11982A-4	Sequence 4, Appli
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c 132	38	1.0	87	5	PCT-US96-06059-40	Sequence 40, Appl
133	38	1.0	87	5	PCT-US96-08014-49	Sequence 49, Appl
c 134	38	1.0	87	5	PCT-US96-08014-49	Sequence 49, Appl
135	38	1.0	87	5	PCT-US96-08014-52	Sequence 52, Appl
c 136	38	1.0	87	5	PCT-US96-08014-52	Sequence 52, Appl
137	38	1.0	87	5	PCT-US96-09472-64	Sequence 64, Appl
c 138	38	1.0	87	5	PCT-US96-09472-64	Sequence 64, Appl
139	38	1.0	87	5	PCT-US96-09472-79	Sequence 79, Appl
c 140	38	1.0	87	5	PCT-US96-09472-79	Sequence 79, Appl
141	38	1.0	87	5	PCT-US96-09537-74	Sequence 74, Appl
c 142	38	1.0	87	5	PCT-US96-09537-74	Sequence 74, Appl
143	38	1.0	87	5	PCT-US96-09537-186	Sequence 186, App
c 144	38	1.0	87	5	PCT-US96-09537-186	Sequence 186, App
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c 149	38	1.0	92	5	PCT-US96-11473A-1	Sequence 1, Appli
c 150	38	1.0	93	1	US-08-370-567-27	Sequence 27, Appl
c 151	38	1.0	93	1	US-08-438-759-27	Sequence 27, Appl
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c 153	38	1.0	93	1	US-08-117-361C-15	Sequence 15, Appl
c 154	38	1.0	93	5	PCT-US94-05591-2	Sequence 2, Appli
c 155	38	1.0	93	5	PCT-US94-05684-27	Sequence 27, Appl
156	38	1.0	94	2	US-08-771-201-6	Sequence 6, Appli
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c 158	38	1.0	96	1	US-08-479-783A-36	Sequence 36, Appl
159	38	1.0	96	1	US-08-479-725-36	Sequence 36, Appl
c 160	38	1.0	96	1	US-08-479-725-36	Sequence 36, Appl
161	38	1.0	96	1	US-08-618-693-36	Sequence 36, Appl
c 162	38	1.0	96	1	US-08-618-693-36	Sequence 36, Appl
163	38	1.0	96	4	US-08-973-124-125	Sequence 125, App
c 164	38	1.0	96	4	US-08-973-124-125	Sequence 125, App
165	38	1.0	96	4	US-08-991-743C-36	Sequence 36, Appl
c 166	38	1.0	96	4	US-08-991-743C-36	Sequence 36, Appl
167	38	1.0	96	5	PCT-US96-08014-125	Sequence 125, App
c 168	38	1.0	96	5	PCT-US96-08014-125	Sequence 125, App
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c 172	38	1.0	97	1	US-08-447-172A-4	Sequence 4, Appli
173	38	1.0	97	4	US-08-952-793-248	Sequence 248, App
c 174	38	1.0	97	4	US-08-952-793-248	Sequence 248, App
175	38	1.0	97	4	US-08-952-793-390	Sequence 390, App
c 176	38	1.0	97	4	US-08-952-793-390	Sequence 390, App
177	38	1.0	97	5	PCT-US96-09455A-248	Sequence 248, App
c 178	38	1.0	97	5	PCT-US96-09455A-248	Sequence 248, App
179	38	1.0	97	5	PCT-US96-09455A-390	Sequence 390, App
c 180	38	1.0	97	5	PCT-US96-09455A-390	Sequence 390, App
181	38	1.0	104	1	US-08-591-989-11	Sequence 11, Appl
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c 184	38	1.0	104	2	US-08-139-176D-3	Sequence 3, Appli
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c 186	38	1.0	104	2	US-08-799-949-1	Sequence 1, Appli
c 187	38	1.0	104	3	US-09-041-841-2	Sequence 2, Appli
c 188	38	1.0	104	3	US-09-041-841-3	Sequence 3, Appli
189	38	1.0	104	4	US-09-364-543-1	Sequence 1, Appli
c 190	38	1.0	104	4	US-09-364-543-1	Sequence 1, Appli
191	38	1.0	104	4	US-09-364-539-191	Sequence 191, App
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195	38	1.0	107	1	US-08-441-591-4	Sequence 4, Appli
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199	38	1.0	107	1	US-08-303-362A-4	Sequence 4, Appli
c 200	38	1.0	107	1	US-08-303-362A-4	Sequence 4, Appli
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c 203	38	1.0	107	5	PCT-US95-05600-18	Sequence 18, Appl
204	38	1.0	107	5	PCT-US95-05600-21	Sequence 21, Appl
c 205	38	1.0	107	5	PCT-US95-05600-21	Sequence 21, Appl
206	38	1.0	147	2	US-08-618-700-6	Sequence 6, Appli
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208	38	1.0	147	2	US-08-618-700-7	Sequence 7, Appli
c 209	38	1.0	147	2	US-08-618-700-7	Sequence 7, Appli
210	38	1.0	147	3	US-09-157-601-6	Sequence 6, Appli
c 211	38	1.0	147	3	US-09-157-601-6	Sequence 6, Appli
212	38	1.0	147	3	US-09-157-601-7	Sequence 7, Appli
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c 215	38	1.0	150	3	US-09-041-841-1	Sequence 1, Appli
c 216	38	1.0	223	4	US-09-535-754-7	Sequence 7, Appli
c 217	38	1.0	231	4	US-08-679-493A-13	Sequence 13, Appl
c 218	38	1.0	313	4	US-09-094-381C-1	Sequence 1, Appli
c 219	38	1.0	313	4	US-09-094-381C-2	Sequence 2, Appli
c 220	38	1.0	313	4	US-09-094-381C-3	Sequence 3, Appli
c 221	38	1.0	313	4	US-09-094-381C-4	Sequence 4, Appli
c 222	38	1.0	313	4	US-09-094-381C-5	Sequence 5, Appli
c 223	38	1.0	321	4	US-09-094-381C-25	Sequence 25, Appl
c 224	38	1.0	321	4	US-09-094-381C-26	Sequence 26, Appl
c 225	38	1.0	321	4	US-09-094-381C-27	Sequence 27, Appl
c 226	38	1.0	321	4	US-09-094-381C-28	Sequence 28, Appl
c 227	38	1.0	321	4	US-09-094-381C-29	Sequence 29, Appl
228	38	1.0	563	4	US-09-276-531-38	Sequence 38, Appl
c 229	38	1.0	608	1	US-08-386-495-11	Sequence 11, Appl
c 230	38	1.0	608	5	PCT-US96-02331-11	Sequence 11, Appl
231	38	1.0	750	4	US-08-821-994-40	Sequence 40, Appl
c 232	38	1.0	959	4	US-09-724-510-1	Sequence 1, Appli
c 233	38	1.0	959	4	US-09-723-216-1	Sequence 1, Appli
c 234	38	1.0	959	4	US-09-675-227-1	Sequence 1, Appli
c 235	38	1.0	1070	4	US-09-718-841-3	Sequence 3, Appli
c 236	38	1.0	1070	4	US-09-718-810-3	Sequence 3, Appli
c 237	38	1.0	1252	4	US-09-276-531-92	Sequence 92, Appl
c 238	38	1.0	1280	4	US-09-276-531-52	Sequence 52, Appl
c 239	38	1.0	1689	4	US-09-718-841-1	Sequence 1, Appli
c 240	38	1.0	1689	4	US-09-718-810-1	Sequence 1, Appli
c 241	38	1.0	1738	3	US-09-120-365-89	Sequence 89, Appl
c 242	38	1.0	1738	4	US-09-515-039-89	Sequence 89, Appl
c 243	38	1.0	2409	4	US-09-293-322C-8	Sequence 8, Appli
244	38	1.0	4997	1	US-08-232-463-1	Sequence 1, Appli
c 245	38	1.0	8285	4	US-09-732-025-3	Sequence 3, Appli
246	38	1.0	8313	1	US-08-232-463-2	Sequence 2, Appli

	247	38	1.0	8775	1	US-08-232-463-5	Sequence 5, Appli
	248	38	1.0	9454	1	US-08-232-463-3	Sequence 3, Appli
	249	38	1.0	9454	1	US-08-232-463-4	Sequence 4, Appli
	250	38	1.0	11528	3	US-08-444-644-18	Sequence 18, Appl
	251	38	1.0	11528	4	US-08-232-246A-18	Sequence 18, Appl
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c	253	38	1.0	19806	4	US-09-740-028A-3	Sequence 3, Appli
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	255	38	1.0	65042	4	US-09-784-316-3	Sequence 3, Appli
c	256	38	1.0	65042	4	US-09-784-316-3	Sequence 3, Appli
	257	38	1.0	112132	4	US-09-741-150-3	Sequence 3, Appli
c	258	37	1.0	39	2	US-08-659-453B-2	Sequence 2, Appli
c	259	37	1.0	39	3	US-09-089-853A-2	Sequence 2, Appli
c	260	37	1.0	39	4	US-09-131-009A-2	Sequence 2, Appli
c	261	37	1.0	39	4	US-09-092-226A-2	Sequence 2, Appli
c	262	37	1.0	39	4	US-09-130-862A-2	Sequence 2, Appli
c	263	37	1.0	39	4	US-09-090-809A-2	Sequence 2, Appli
c	264	37	1.0	39	4	US-09-053-116A-2	Sequence 2, Appli
	265	37	1.0	44	2	US-08-659-453B-22	Sequence 22, Appl
	266	37	1.0	44	3	US-09-089-853A-22	Sequence 22, Appl
	267	37	1.0	44	4	US-09-131-009A-22	Sequence 22, Appl
	268	37	1.0	44	4	US-09-092-226A-22	Sequence 22, Appl
	269	37	1.0	44	4	US-09-130-862A-22	Sequence 22, Appl
	270	37	1.0	44	4	US-09-090-809A-22	Sequence 22, Appl
	271	37	1.0	44	4	US-09-053-116A-22	Sequence 22, Appl
	272	37	1.0	61	4	US-09-275-850-291	Sequence 291, App
	273	37	1.0	62	2	US-08-659-453B-4	Sequence 4, Appli
	274	37	1.0	62	3	US-09-089-853A-4	Sequence 4, Appli
	275	37	1.0	62	4	US-09-131-009A-4	Sequence 4, Appli
	276	37	1.0	62	4	US-09-092-226A-4	Sequence 4, Appli
	277	37	1.0	62	4	US-09-130-862A-4	Sequence 4, Appli
	278	37	1.0	62	4	US-09-090-809A-4	Sequence 4, Appli
	279	37	1.0	62	4	US-09-053-116A-4	Sequence 4, Appli
	280	37	1.0	66	2	US-08-659-453B-1	Sequence 1, Appli
	281	37	1.0	66	3	US-09-089-853A-1	Sequence 1, Appli
	282	37	1.0	66	4	US-09-131-009A-1	Sequence 1, Appli
	283	37	1.0	66	4	US-09-092-226A-1	Sequence 1, Appli
	284	37	1.0	66	4	US-09-130-862A-1	Sequence 1, Appli
	285	37	1.0	66	4	US-09-090-809A-1	Sequence 1, Appli
	286	37	1.0	66	4	US-09-053-116A-1	Sequence 1, Appli
c	287	37	1.0	67	1	US-08-260-582-3	Sequence 3, Appli
	288	37	1.0	67	3	US-07-876-288-14	Sequence 14, Appl
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	290	37	1.0	68	2	US-08-659-453B-9	Sequence 9, Appli
	291	37	1.0	68	3	US-09-089-853A-9	Sequence 9, Appli
	292	37	1.0	68	4	US-09-131-009A-9	Sequence 9, Appli
	293	37	1.0	68	4	US-09-092-226A-9	Sequence 9, Appli
	294	37	1.0	68	4	US-09-130-862A-9	Sequence 9, Appli
	295	37	1.0	68	4	US-09-090-809A-9	Sequence 9, Appli
	296	37	1.0	68	4	US-09-053-116A-9	Sequence 9, Appli
	297	37	1.0	71	1	US-08-317-403A-1	Sequence 1, Appli
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c	300	37	1.0	71	1	US-08-471-985A-1	Sequence 1, Appli
	301	37	1.0	71	1	US-08-400-440A-38	Sequence 38, Appl
c	302	37	1.0	71	1	US-08-400-440A-38	Sequence 38, Appl
	303	37	1.0	71	1	US-08-458-423A-43	Sequence 43, Appl
c	304	37	1.0	71	1	US-08-458-423A-43	Sequence 43, Appl
	305	37	1.0	71	1	US-08-458-423A-46	Sequence 46, Appl
c	306	37	1.0	71	1	US-08-458-423A-46	Sequence 46, Appl
	307	37	1.0	71	1	US-08-458-424B-43	Sequence 43, Appl
c	308	37	1.0	71	1	US-08-458-424B-43	Sequence 43, Appl
	309	37	1.0	71	1	US-08-458-424B-46	Sequence 46, Appl
c	310	37	1.0	71	1	US-08-458-424B-46	Sequence 46, Appl
	311	37	1.0	71	1	US-08-463-093A-38	Sequence 38, Appl
c	312	37	1.0	71	1	US-08-463-093A-38	Sequence 38, Appl
	313	37	1.0	71	1	US-08-472-255A-64	Sequence 64, Appl
c	314	37	1.0	71	1	US-08-472-255A-64	Sequence 64, Appl
	315	37	1.0	71	1	US-08-479-724A-64	Sequence 64, Appl
c	316	37	1.0	71	1	US-08-479-724A-64	Sequence 64, Appl
	317	37	1.0	71	1	US-08-591-989-6	Sequence 6, Appli
c	318	37	1.0	71	1	US-08-591-989-6	Sequence 6, Appli
	319	37	1.0	71	2	US-08-488-402A-33	Sequence 33, Appl
c	320	37	1.0	71	2	US-08-488-402A-33	Sequence 33, Appl
	321	37	1.0	71	2	US-08-465-591A-1	Sequence 1, Appli
c	322	37	1.0	71	2	US-08-465-591A-1	Sequence 1, Appli
	323	37	1.0	71	2	US-08-465-594A-1	Sequence 1, Appli
c	324	37	1.0	71	2	US-08-465-594A-1	Sequence 1, Appli
	325	37	1.0	71	2	US-08-484-552A-33	Sequence 33, Appl
c	326	37	1.0	71	2	US-08-484-552A-33	Sequence 33, Appl
	327	37	1.0	71	2	US-08-460-888A-38	Sequence 38, Appl
c	328	37	1.0	71	2	US-08-460-888A-38	Sequence 38, Appl
	329	37	1.0	71	2	US-08-477-527A-1	Sequence 1, Appli
c	330	37	1.0	71	2	US-08-477-527A-1	Sequence 1, Appli
	331	37	1.0	71	2	US-08-477-527A-256	Sequence 256, App
c	332	37	1.0	71	2	US-08-477-527A-256	Sequence 256, App
	333	37	1.0	71	2	US-08-894-578-38	Sequence 38, Appl
c	334	37	1.0	71	2	US-08-894-578-38	Sequence 38, Appl
	335	37	1.0	71	3	US-08-472-256B-64	Sequence 64, Appl
c	336	37	1.0	71	3	US-08-472-256B-64	Sequence 64, Appl
	337	37	1.0	71	3	US-08-481-710-1	Sequence 1, Appli
c	338	37	1.0	71	3	US-08-481-710-1	Sequence 1, Appli
	339	37	1.0	71	3	US-08-481-710-256	Sequence 256, App
c	340	37	1.0	71	3	US-08-481-710-256	Sequence 256, App
	341	37	1.0	71	3	US-09-046-247-1	Sequence 1, Appli
c	342	37	1.0	71	3	US-09-046-247-1	Sequence 1, Appli
	343	37	1.0	71	4	US-08-870-930-11	Sequence 11, Appl
c	344	37	1.0	71	4	US-08-870-930-11	Sequence 11, Appl
	345	37	1.0	71	4	US-08-973-124-43	Sequence 43, Appl
c	346	37	1.0	71	4	US-08-973-124-43	Sequence 43, Appl
	347	37	1.0	71	4	US-08-973-124-46	Sequence 46, Appl
c	348	37	1.0	71	4	US-08-973-124-46	Sequence 46, Appl
	349	37	1.0	71	4	US-08-973-124-186	Sequence 186, App
c	350	37	1.0	71	4	US-08-973-124-186	Sequence 186, App
	351	37	1.0	71	4	US-09-364-902-1	Sequence 1, Appli
c	352	37	1.0	71	4	US-09-364-902-1	Sequence 1, Appli
	353	37	1.0	71	4	US-09-275-850-38	Sequence 38, Appl
c	354	37	1.0	71	4	US-09-275-850-38	Sequence 38, Appl
	355	37	1.0	71	4	US-08-952-793-64	Sequence 64, Appl
c	356	37	1.0	71	4	US-08-952-793-64	Sequence 64, Appl
	357	37	1.0	71	4	US-08-952-793-389	Sequence 389, App
c	358	37	1.0	71	4	US-08-952-793-389	Sequence 389, App
	359	37	1.0	71	4	US-09-412-017-38	Sequence 38, Appl
c	360	37	1.0	71	4	US-09-412-017-38	Sequence 38, Appl
	361	37	1.0	71	4	US-09-364-539-190	Sequence 190, App
c	362	37	1.0	71	4	US-09-364-539-190	Sequence 190, App
	363	37	1.0	71	4	US-09-363-939A-1	Sequence 1, Appli
c	364	37	1.0	71	4	US-09-363-939A-1	Sequence 1, Appli
	365	37	1.0	71	4	US-09-363-939A-6	Sequence 6, Appli
c	366	37	1.0	71	4	US-09-363-939A-6	Sequence 6, Appli
	367	37	1.0	71	4	US-09-254-968-139	Sequence 139, App
c	368	37	1.0	71	4	US-09-254-968-139	Sequence 139, App
	369	37	1.0	71	5	PCT-US95-12401A-1	Sequence 1, Appli
c	370	37	1.0	71	5	PCT-US95-12401A-1	Sequence 1, Appli
	371	37	1.0	71	5	PCT-US96-08014-43	Sequence 43, Appl
c	372	37	1.0	71	5	PCT-US96-08014-43	Sequence 43, Appl
	373	37	1.0	71	5	PCT-US96-08014-46	Sequence 46, Appl
c	374	37	1.0	71	5	PCT-US96-08014-46	Sequence 46, Appl
	375	37	1.0	71	5	PCT-US96-08014-186	Sequence 186, App
c	376	37	1.0	71	5	PCT-US96-08014-186	Sequence 186, App
	377	37	1.0	71	5	PCT-US96-09455A-64	Sequence 64, Appl
c	378	37	1.0	71	5	PCT-US96-09455A-64	Sequence 64, Appl
	379	37	1.0	71	5	PCT-US96-09455A-389	Sequence 389, App
c	380	37	1.0	71	5	PCT-US96-09455A-389	Sequence 389, App
	381	37	1.0	71	5	PCT-US96-09472-33	Sequence 33, Appl
c	382	37	1.0	71	5	PCT-US96-09472-33	Sequence 33, Appl
	383	37	1.0	71	5	PCT-US96-09537-1	Sequence 1, Appli
c	384	37	1.0	71	5	PCT-US96-09537-1	Sequence 1, Appli
	385	37	1.0	71	5	PCT-US96-09537-256	Sequence 256, App
c	386	37	1.0	71	5	PCT-US96-09537-256	Sequence 256, App
	387	37	1.0	72	1	US-08-433-126A-1	Sequence 1, Appli
c	388	37	1.0	72	1	US-08-433-126A-1	Sequence 1, Appli
	389	37	1.0	72	1	US-08-433-124A-1	Sequence 1, Appli
c	390	37	1.0	72	1	US-08-433-124A-1	Sequence 1, Appli
	391	37	1.0	72	2	US-08-488-402A-1	Sequence 1, Appli
c	392	37	1.0	72	2	US-08-488-402A-1	Sequence 1, Appli

393	37	1.0	72	2	US-08-484-552A-1	Sequence 1, Appli
c 394	37	1.0	72	2	US-08-484-552A-1	Sequence 1, Appli
395	37	1.0	72	3	US-08-976-413A-1	Sequence 1, Appli
c 396	37	1.0	72	3	US-08-976-413A-1	Sequence 1, Appli
397	37	1.0	72	5	PCT-US96-06059-1	Sequence 1, Appli
c 398	37	1.0	72	5	PCT-US96-06059-1	Sequence 1, Appli
399	37	1.0	72	5	PCT-US96-09472-1	Sequence 1, Appli
c 400	37	1.0	72	5	PCT-US96-09472-1	Sequence 1, Appli
401	37	1.0	74	4	US-09-193-068-15	Sequence 15, Appl
402	37	1.0	75	1	US-08-437-815-10	Sequence 10, Appl
403	37	1.0	75	1	US-08-897-040-10	Sequence 10, Appl
404	37	1.0	76	5	PCT-US95-05600-1	Sequence 1, Appli
405	37	1.0	78	4	US-09-193-068-17	Sequence 17, Appl
c 406	37	1.0	80	1	US-08-435-809-3	Sequence 3, Appli
c 407	37	1.0	80	1	US-08-349-316A-2	Sequence 2, Appli
c 408	37	1.0	80	1	US-08-472-194A-4	Sequence 4, Appli
c 409	37	1.0	80	4	US-09-193-068-23	Sequence 23, Appl
c 410	37	1.0	80	4	US-08-849-567A-4	Sequence 4, Appli
411	37	1.0	81	1	US-08-399-412A-4	Sequence 4, Appli
c 412	37	1.0	81	1	US-08-399-412A-4	Sequence 4, Appli
413	37	1.0	81	1	US-08-384-708A-98	Sequence 98, Appl
c 414	37	1.0	81	1	US-08-384-708A-98	Sequence 98, Appl
415	37	1.0	81	1	US-08-447-169A-60	Sequence 60, Appl
c 416	37	1.0	81	1	US-08-447-169A-60	Sequence 60, Appl
417	37	1.0	81	2	US-08-233-012C-60	Sequence 60, Appl
c 418	37	1.0	81	2	US-08-233-012C-60	Sequence 60, Appl
419	37	1.0	81	3	US-09-023-228B-2	Sequence 2, Appli
c 420	37	1.0	81	3	US-09-023-228B-2	Sequence 2, Appli
421	37	1.0	81	4	US-08-687-421-98	Sequence 98, Appl
c 422	37	1.0	81	4	US-08-687-421-98	Sequence 98, Appl
423	37	1.0	81	4	US-09-193-068-19	Sequence 19, Appl
424	37	1.0	81	4	US-09-163-025B-157	Sequence 157, App
c 425	37	1.0	81	4	US-09-163-025B-157	Sequence 157, App
c 426	37	1.0	83	4	US-08-687-421-325	Sequence 325, App
427	37	1.0	86	1	US-07-964-624D-43	Sequence 43, Appl
428	37	1.0	86	1	US-08-442-062-43	Sequence 43, Appl
429	37	1.0	86	1	US-08-748-697A-43	Sequence 43, Appl
430	37	1.0	86	4	US-09-165-616-43	Sequence 43, Appl
431	37	1.0	88	4	US-08-870-930-2	Sequence 2, Appli
c 432	37	1.0	88	4	US-08-870-930-2	Sequence 2, Appli
433	37	1.0	88	4	US-09-364-539-15	Sequence 15, Appl
c 434	37	1.0	88	4	US-09-364-539-15	Sequence 15, Appl
435	37	1.0	88	4	US-09-363-939A-4	Sequence 4, Appli
c 436	37	1.0	88	4	US-09-363-939A-4	Sequence 4, Appli
437	37	1.0	88	4	US-09-254-968-134	Sequence 134, App
c 438	37	1.0	88	4	US-09-254-968-134	Sequence 134, App
439	37	1.0	90	4	US-08-679-493A-17	Sequence 17, Appl
440	37	1.0	91	1	US-08-317-403A-2	Sequence 2, Appli
c 441	37	1.0	91	1	US-08-317-403A-2	Sequence 2, Appli
442	37	1.0	91	1	US-08-471-985A-2	Sequence 2, Appli
c 443	37	1.0	91	1	US-08-471-985A-2	Sequence 2, Appli
444	37	1.0	91	5	PCT-US95-12401A-2	Sequence 2, Appli
c 445	37	1.0	91	5	PCT-US95-12401A-2	Sequence 2, Appli
446	37	1.0	96	1	US-08-234-613-1	Sequence 1, Appli
447	37	1.0	96	1	US-08-753-054-19	Sequence 19, Appl
448	37	1.0	96	2	US-08-237-973-1	Sequence 1, Appli
c 449	37	1.0	98	1	US-08-234-613-4	Sequence 4, Appli
450	37	1.0	98	1	US-08-399-412A-7	Sequence 7, Appli
451	37	1.0	98	1	US-08-447-172A-28	Sequence 28, Appl
452	37	1.0	98	1	US-08-447-172A-31	Sequence 31, Appl
453	37	1.0	98	1	US-08-472-255A-1	Sequence 1, Appli
454	37	1.0	98	1	US-08-479-724A-1	Sequence 1, Appli
c 455	37	1.0	98	2	US-08-237-973-4	Sequence 4, Appli
456	37	1.0	98	3	US-08-472-256B-1	Sequence 1, Appli
457	37	1.0	98	3	US-09-023-228B-1	Sequence 1, Appli
c 458	37	1.0	98	3	US-09-023-228B-1	Sequence 1, Appli
459	37	1.0	98	4	US-08-952-793-1	Sequence 1, Appli
460	37	1.0	98	4	US-08-849-567A-50	Sequence 50, Appl
461	37	1.0	98	4	US-09-163-025B-156	Sequence 156, App
c 462	37	1.0	98	4	US-09-163-025B-156	Sequence 156, App
463	37	1.0	98	5	PCT-US96-09455A-1	Sequence 1, Appli
c 464	37	1.0	99	4	US-08-679-493A-18	Sequence 18, Appl
465	37	1.0	99	4	US-08-849-567A-51	Sequence 51, Appl
466	37	1.0	101	1	US-07-843-125-6	Sequence 6, Appli
c 467	37	1.0	107	4	US-09-193-068-21	Sequence 21, Appl
468	37	1.0	110	1	US-08-299-498A-3	Sequence 3, Appli
469	37	1.0	110	5	PCT-US95-10813-3	Sequence 3, Appli
470	37	1.0	112	1	US-08-299-498A-32	Sequence 32, Appl
471	37	1.0	112	5	PCT-US95-10813-32	Sequence 32, Appl
c 472	37	1.0	120	1	US-07-843-125-4	Sequence 4, Appli
473	37	1.0	120	2	US-08-787-042-1	Sequence 1, Appli
c 474	37	1.0	120	2	US-08-787-042-1	Sequence 1, Appli
c 475	37	1.0	121	4	US-09-535-754-10	Sequence 10, Appl
c 476	37	1.0	123	4	US-09-535-754-9	Sequence 9, Appli
477	37	1.0	134	1	US-08-299-498A-5	Sequence 5, Appli
478	37	1.0	134	5	PCT-US95-10813-5	Sequence 5, Appli
c 479	37	1.0	154	2	US-08-721-684C-7	Sequence 7, Appli
c 480	37	1.0	154	2	US-09-005-970-7	Sequence 7, Appli
c 481	37	1.0	154	4	US-09-407-715-7	Sequence 7, Appli
c 482	37	1.0	195	4	US-09-186-276B-64	Sequence 64, Appl
c 483	37	1.0	195	4	US-08-842-445-64	Sequence 64, Appl
c 484	37	1.0	195	4	US-09-186-188B-64	Sequence 64, Appl
c 485	37	1.0	207	2	US-08-039-198B-6	Sequence 6, Appli
486	37	1.0	212	4	US-09-574-141A-86	Sequence 86, Appl
c 487	37	1.0	215	4	US-09-535-754-8	Sequence 8, Appli
488	37	1.0	231	4	US-08-679-493A-13	Sequence 13, Appl
489	37	1.0	313	4	US-09-094-381C-1	Sequence 1, Appli
490	37	1.0	313	4	US-09-094-381C-2	Sequence 2, Appli
491	37	1.0	313	4	US-09-094-381C-3	Sequence 3, Appli
492	37	1.0	313	4	US-09-094-381C-4	Sequence 4, Appli
493	37	1.0	313	4	US-09-094-381C-5	Sequence 5, Appli
494	37	1.0	321	4	US-09-094-381C-25	Sequence 25, Appl
495	37	1.0	321	4	US-09-094-381C-26	Sequence 26, Appl
496	37	1.0	321	4	US-09-094-381C-27	Sequence 27, Appl
497	37	1.0	321	4	US-09-094-381C-28	Sequence 28, Appl
498	37	1.0	321	4	US-09-094-381C-29	Sequence 29, Appl
c 499	37	1.0	324	2	US-08-378-939-21	Sequence 21, Appl
500	37	1.0	324	2	US-08-378-939-27	Sequence 27, Appl
501	37	1.0	345	4	US-09-025-203-16	Sequence 16, Appl
502	37	1.0	495	2	US-08-465-380-31	Sequence 31, Appl
503	37	1.0	495	2	US-08-486-397-31	Sequence 31, Appl
504	37	1.0	495	2	US-08-486-399-31	Sequence 31, Appl
505	37	1.0	495	2	US-08-461-965-31	Sequence 31, Appl
c 506	37	1.0	551	2	US-08-647-368A-4	Sequence 4, Appli
507	37	1.0	605	3	US-09-109-204-19	Sequence 19, Appl
c 508	37	1.0	605	3	US-09-109-204-19	Sequence 19, Appl
509	37	1.0	633	4	US-09-812-484-25	Sequence 25, Appl
510	37	1.0	738	1	US-07-843-125-2	Sequence 2, Appli
c 511	37	1.0	738	1	US-07-843-125-2	Sequence 2, Appli
c 512	37	1.0	759	3	US-09-109-205-11	Sequence 11, Appl
513	37	1.0	759	4	US-09-276-531-71	Sequence 71, Appl
514	37	1.0	763	4	US-09-484-970B-166	Sequence 166, App
c 515	37	1.0	804	4	US-09-276-531-54	Sequence 54, Appl
c 516	37	1.0	808	4	US-08-791-115B-12	Sequence 12, Appl
517	37	1.0	902	4	US-08-906-156A-38	Sequence 38, Appl
c 518	37	1.0	902	4	US-08-906-156A-38	Sequence 38, Appl
519	37	1.0	960	1	US-08-624-125-13	Sequence 13, Appl
c 520	37	1.0	960	1	US-08-624-125-13	Sequence 13, Appl
521	37	1.0	1143	4	US-09-276-531-103	Sequence 103, App
c 522	37	1.0	1183	2	US-08-731-722-8	Sequence 8, Appli
523	37	1.0	1285	2	US-08-039-198B-7	Sequence 7, Appli
524	37	1.0	1457	2	US-08-039-198B-1	Sequence 1, Appli
c 525	37	1.0	1457	2	US-08-039-198B-1	Sequence 1, Appli
526	37	1.0	1471	2	US-08-039-198B-8	Sequence 8, Appli
c 527	37	1.0	1471	2	US-08-039-198B-8	Sequence 8, Appli
528	37	1.0	1576	5	PCT-US95-11405-34	Sequence 34, Appl
529	37	1.0	1596	4	US-09-484-970B-148	Sequence 148, App
c 530	37	1.0	1596	4	US-09-484-970B-148	Sequence 148, App
c 531	37	1.0	1713	4	US-08-759-436-1	Sequence 1, Appli
c 532	37	1.0	1750	3	US-09-120-365-90	Sequence 90, Appl
c 533	37	1.0	1750	4	US-09-515-039-90	Sequence 90, Appl
534	37	1.0	1769	4	US-09-484-970B-46	Sequence 46, Appl
c 535	37	1.0	1769	4	US-09-484-970B-46	Sequence 46, Appl
c 536	37	1.0	1782	1	US-08-374-155A-13	Sequence 13, Appl
c 537	37	1.0	1782	2	US-08-785-396-13	Sequence 13, Appl
538	37	1.0	2030	4	US-09-484-970B-152	Sequence 152, App

c 539	37	1.0	2038	4	US-09-276-531-37	Sequence 37, Appl
540	37	1.0	2087	4	US-09-484-970B-153	Sequence 153, App
c 541	37	1.0	2116	2	US-08-663-566A-18	Sequence 18, Appl
c 542	37	1.0	2116	2	US-08-023-610-18	Sequence 18, Appl
c 543	37	1.0	2116	2	US-08-288-065A-18	Sequence 18, Appl
c 544	37	1.0	2116	2	US-08-362-240A-18	Sequence 18, Appl
c 545	37	1.0	2116	5	PCT-US95-10245-18	Sequence 18, Appl
546	37	1.0	2215	3	US-08-891-789B-7	Sequence 7, Appli
c 547	37	1.0	2215	3	US-08-891-789B-7	Sequence 7, Appli
c 548	37	1.0	2428	2	US-08-849-536A-3	Sequence 3, Appli
549	37	1.0	2793	1	US-08-209-747-1	Sequence 1, Appli
550	37	1.0	2793	1	US-08-458-298-1	Sequence 1, Appli
c 551	37	1.0	2847	4	US-09-484-970B-22	Sequence 22, Appl
552	37	1.0	3141	2	US-08-956-242-1	Sequence 1, Appli
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554	37	1.0	3141	3	US-09-351-215-1	Sequence 1, Appli
c 555	37	1.0	3141	3	US-09-351-215-1	Sequence 1, Appli
556	37	1.0	3846	2	US-08-845-161A-5	Sequence 5, Appli
c 557	37	1.0	3846	2	US-08-845-161A-5	Sequence 5, Appli
558	37	1.0	3846	4	US-09-270-751-5	Sequence 5, Appli
c 559	37	1.0	3846	4	US-09-270-751-5	Sequence 5, Appli
560	37	1.0	3846	4	US-09-168-218B-3	Sequence 3, Appli
c 561	37	1.0	3846	4	US-09-168-218B-3	Sequence 3, Appli
562	37	1.0	4339	4	US-09-484-970B-164	Sequence 164, App
563	37	1.0	4701	3	US-08-651-472-64	Sequence 64, Appl
564	37	1.0	4701	4	US-08-358-928-64	Sequence 64, Appl
565	37	1.0	4772	4	US-09-484-970B-133	Sequence 133, App
566	37	1.0	4858	4	US-09-392-184-1	Sequence 1, Appli
c 567	37	1.0	6775	4	US-09-402-929-4	Sequence 4, Appli
568	37	1.0	8285	4	US-09-732-025-3	Sequence 3, Appli
569	37	1.0	8299	1	US-08-462-014-2	Sequence 2, Appli
570	37	1.0	8299	3	US-08-923-137-3	Sequence 3, Appli
571	37	1.0	8299	4	US-08-973-334-5	Sequence 5, Appli
572	37	1.0	8299	4	US-09-563-869A-5	Sequence 5, Appli
573	37	1.0	10785	3	US-08-444-644-27	Sequence 27, Appl
c 574	37	1.0	10785	3	US-08-444-644-27	Sequence 27, Appl
575	37	1.0	10785	4	US-08-232-246A-27	Sequence 27, Appl
c 576	37	1.0	10785	4	US-08-232-246A-27	Sequence 27, Appl
577	37	1.0	10844	3	US-08-444-644-41	Sequence 41, Appl
c 578	37	1.0	10844	3	US-08-444-644-41	Sequence 41, Appl
579	37	1.0	10844	4	US-08-232-246A-41	Sequence 41, Appl
c 580	37	1.0	10844	4	US-08-232-246A-41	Sequence 41, Appl
581	37	1.0	11827	4	US-09-739-455-3	Sequence 3, Appli
582	37	1.0	12127	3	US-08-444-644-32	Sequence 32, Appl
c 583	37	1.0	12127	3	US-08-444-644-32	Sequence 32, Appl
584	37	1.0	12127	4	US-08-232-246A-32	Sequence 32, Appl
c 585	37	1.0	12127	4	US-08-232-246A-32	Sequence 32, Appl
586	37	1.0	12412	1	US-08-390-878-18	Sequence 18, Appl
587	37	1.0	13977	4	US-09-484-970B-60	Sequence 60, Appl
588	37	1.0	13999	3	US-08-444-644-24	Sequence 24, Appl
589	37	1.0	13999	4	US-08-232-246A-24	Sequence 24, Appl
c 590	37	1.0	14753	4	US-09-821-736-3	Sequence 3, Appli
591	37	1.0	19806	4	US-09-740-028A-3	Sequence 3, Appli
592	37	1.0	28001	4	US-09-819-993-3	Sequence 3, Appli
c 593	37	1.0	36651	4	US-09-738-894A-3	Sequence 3, Appli
594	37	1.0	84495	4	US-09-797-906-3	Sequence 3, Appli
c 595	37	1.0	84495	4	US-09-797-906-3	Sequence 3, Appli
c 596	37	1.0	111282	4	US-09-754-250-3	Sequence 3, Appli
c 597	37	1.0	112132	4	US-09-741-150-3	Sequence 3, Appli
598	36	1.0	37	1	US-08-162-590A-5	Sequence 5, Appli
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600	36	1.0	37	1	US-08-162-590A-6	Sequence 6, Appli
c 601	36	1.0	37	1	US-08-162-590A-6	Sequence 6, Appli
602	36	1.0	37	1	US-08-162-590A-7	Sequence 7, Appli
c 603	36	1.0	37	1	US-08-162-590A-7	Sequence 7, Appli
604	36	1.0	37	1	US-08-162-590A-8	Sequence 8, Appli
c 605	36	1.0	37	1	US-08-162-590A-8	Sequence 8, Appli
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608	36	1.0	39	4	US-09-131-009A-2	Sequence 2, Appli
609	36	1.0	39	4	US-09-092-226A-2	Sequence 2, Appli
610	36	1.0	39	4	US-09-130-862A-2	Sequence 2, Appli
611	36	1.0	39	4	US-09-275-850-340	Sequence 340, App
612	36	1.0	39	4	US-09-090-809A-2	Sequence 2, Appli
613	36	1.0	39	4	US-09-053-116A-2	Sequence 2, Appli
614	36	1.0	40	3	US-09-028-128A-1	Sequence 1, Appli
c 615	36	1.0	40	3	US-09-028-128A-1	Sequence 1, Appli
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c 617	36	1.0	42	2	US-08-659-453B-14	Sequence 14, Appl
618	36	1.0	42	3	US-09-089-853A-14	Sequence 14, Appl
c 619	36	1.0	42	3	US-09-089-853A-14	Sequence 14, Appl
620	36	1.0	42	4	US-09-131-009A-14	Sequence 14, Appl
c 621	36	1.0	42	4	US-09-131-009A-14	Sequence 14, Appl
622	36	1.0	42	4	US-09-092-226A-14	Sequence 14, Appl
c 623	36	1.0	42	4	US-09-092-226A-14	Sequence 14, Appl
624	36	1.0	42	4	US-09-130-862A-14	Sequence 14, Appl
c 625	36	1.0	42	4	US-09-130-862A-14	Sequence 14, Appl
626	36	1.0	42	4	US-09-090-809A-14	Sequence 14, Appl
c 627	36	1.0	42	4	US-09-090-809A-14	Sequence 14, Appl
628	36	1.0	42	4	US-09-053-116A-14	Sequence 14, Appl
c 629	36	1.0	42	4	US-09-053-116A-14	Sequence 14, Appl
c 630	36	1.0	44	2	US-08-659-453B-22	Sequence 22, Appl
c 631	36	1.0	44	3	US-09-089-853A-22	Sequence 22, Appl
c 632	36	1.0	44	4	US-09-131-009A-22	Sequence 22, Appl
c 633	36	1.0	44	4	US-09-092-226A-22	Sequence 22, Appl
c 634	36	1.0	44	4	US-09-130-862A-22	Sequence 22, Appl
c 635	36	1.0	44	4	US-09-090-809A-22	Sequence 22, Appl
c 636	36	1.0	44	4	US-09-053-116A-22	Sequence 22, Appl
637	36	1.0	57	2	US-08-136-214-8	Sequence 8, Appli
c 638	36	1.0	57	2	US-08-136-214-8	Sequence 8, Appli
639	36	1.0	66	1	US-08-748-697A-13	Sequence 13, Appl
c 640	36	1.0	66	1	US-08-748-697A-13	Sequence 13, Appl
641	36	1.0	66	4	US-08-952-793-292	Sequence 292, App
c 642	36	1.0	66	4	US-08-952-793-292	Sequence 292, App
643	36	1.0	66	4	US-09-165-616-13	Sequence 13, Appl
c 644	36	1.0	66	4	US-09-165-616-13	Sequence 13, Appl
645	36	1.0	66	5	PCT-US96-09455A-292	Sequence 292, App
c 646	36	1.0	66	5	PCT-US96-09455A-292	Sequence 292, App
647	36	1.0	67	1	US-08-260-582-3	Sequence 3, Appli
c 648	36	1.0	67	3	US-07-876-288-14	Sequence 14, Appl
649	36	1.0	67	5	PCT-US95-05471-3	Sequence 3, Appli
c 650	36	1.0	68	2	US-08-659-453B-9	Sequence 9, Appli
c 651	36	1.0	68	3	US-09-089-853A-9	Sequence 9, Appli
c 652	36	1.0	68	4	US-09-131-009A-9	Sequence 9, Appli
c 653	36	1.0	68	4	US-09-092-226A-9	Sequence 9, Appli
c 654	36	1.0	68	4	US-09-130-862A-9	Sequence 9, Appli
c 655	36	1.0	68	4	US-09-090-809A-9	Sequence 9, Appli
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c 660	36	1.0	71	1	US-08-458-424B-5	Sequence 5, Appli
661	36	1.0	71	4	US-08-973-124-5	Sequence 5, Appli
c 662	36	1.0	71	4	US-08-973-124-5	Sequence 5, Appli
663	36	1.0	71	5	PCT-US96-08014-5	Sequence 5, Appli
c 664	36	1.0	71	5	PCT-US96-08014-5	Sequence 5, Appli
c 665	36	1.0	72	2	US-07-829-461A-6	Sequence 6, Appli
c 666	36	1.0	72	4	US-09-197-649-5	Sequence 5, Appli
c 667	36	1.0	74	4	US-09-193-068-15	Sequence 15, Appl
c 668	36	1.0	75	1	US-08-437-815-10	Sequence 10, Appl
c 669	36	1.0	75	1	US-08-897-040-10	Sequence 10, Appl
670	36	1.0	76	4	US-09-287-936-1	Sequence 1, Appli
c 671	36	1.0	76	5	PCT-US95-05600-1	Sequence 1, Appli
c 672	36	1.0	78	4	US-09-193-068-17	Sequence 17, Appl
673	36	1.0	80	1	US-08-471-985A-112	Sequence 112, App
c 674	36	1.0	80	1	US-08-471-985A-112	Sequence 112, App
675	36	1.0	80	1	US-08-472-255A-126	Sequence 126, App
c 676	36	1.0	80	1	US-08-472-255A-126	Sequence 126, App
677	36	1.0	80	1	US-08-479-724A-126	Sequence 126, App
c 678	36	1.0	80	1	US-08-479-724A-126	Sequence 126, App
679	36	1.0	80	1	US-08-472-194A-4	Sequence 4, Appli
680	36	1.0	80	1	US-08-418-859-47	Sequence 47, Appl
c 681	36	1.0	80	1	US-08-418-859-47	Sequence 47, Appl
682	36	1.0	80	2	US-08-643-181-47	Sequence 47, Appl
c 683	36	1.0	80	2	US-08-643-181-47	Sequence 47, Appl
684	36	1.0	80	3	US-08-472-256B-126	Sequence 126, App

c 685	36	1.0	80	3	US-08-472-256B-126	Sequence 126, App
686	36	1.0	80	4	US-09-193-068-23	Sequence 23, Appl
687	36	1.0	80	4	US-08-952-793-126	Sequence 126, App
c 688	36	1.0	80	4	US-08-952-793-126	Sequence 126, App
689	36	1.0	80	4	US-08-849-567A-4	Sequence 4, Appli
690	36	1.0	80	5	PCT-US95-12401A-112	Sequence 112, App
c 691	36	1.0	80	5	PCT-US95-12401A-112	Sequence 112, App
692	36	1.0	80	5	PCT-US96-09455A-126	Sequence 126, App
c 693	36	1.0	80	5	PCT-US96-09455A-126	Sequence 126, App
694	36	1.0	81	1	US-08-447-169A-240	Sequence 240, App
c 695	36	1.0	81	1	US-08-447-169A-240	Sequence 240, App
c 696	36	1.0	81	4	US-09-193-068-19	Sequence 19, Appl
697	36	1.0	82	4	US-08-679-493A-14	Sequence 14, Appl
698	36	1.0	83	4	US-08-687-421-325	Sequence 325, App
699	36	1.0	85	4	US-09-275-850-338	Sequence 338, App
c 700	36	1.0	85	4	US-09-275-850-339	Sequence 339, App
c 701	36	1.0	86	1	US-07-964-624D-43	Sequence 43, Appl
c 702	36	1.0	86	1	US-08-442-062-43	Sequence 43, Appl
703	36	1.0	86	1	US-08-479-783A-1	Sequence 1, Appli
c 704	36	1.0	86	1	US-08-479-783A-1	Sequence 1, Appli
705	36	1.0	86	1	US-08-479-725-1	Sequence 1, Appli
c 706	36	1.0	86	1	US-08-479-725-1	Sequence 1, Appli
707	36	1.0	86	1	US-08-618-693-1	Sequence 1, Appli
c 708	36	1.0	86	1	US-08-618-693-1	Sequence 1, Appli
709	36	1.0	86	1	US-08-447-169A-237	Sequence 237, App
c 710	36	1.0	86	1	US-08-447-169A-237	Sequence 237, App
c 711	36	1.0	86	1	US-08-748-697A-43	Sequence 43, Appl
712	36	1.0	86	4	US-08-687-421-322	Sequence 322, App
c 713	36	1.0	86	4	US-08-687-421-322	Sequence 322, App
714	36	1.0	86	4	US-08-973-124-90	Sequence 90, Appl
c 715	36	1.0	86	4	US-08-973-124-90	Sequence 90, Appl
716	36	1.0	86	4	US-08-991-743C-1	Sequence 1, Appli
c 717	36	1.0	86	4	US-08-991-743C-1	Sequence 1, Appli
c 718	36	1.0	86	4	US-09-165-616-43	Sequence 43, Appl
719	36	1.0	86	5	PCT-US96-08014-90	Sequence 90, Appl
c 720	36	1.0	86	5	PCT-US96-08014-90	Sequence 90, Appl
721	36	1.0	87	1	US-08-199-507B-57	Sequence 57, Appl
c 722	36	1.0	87	1	US-08-199-507B-57	Sequence 57, Appl
723	36	1.0	87	1	US-08-441-828-57	Sequence 57, Appl
c 724	36	1.0	87	1	US-08-441-828-57	Sequence 57, Appl
725	36	1.0	87	3	US-08-973-965-13	Sequence 13, Appl
726	36	1.0	88	4	US-09-363-939A-5	Sequence 5, Appli
c 727	36	1.0	88	4	US-09-363-939A-5	Sequence 5, Appli
728	36	1.0	90	1	US-08-358-995-28	Sequence 28, Appl
c 729	36	1.0	90	4	US-08-679-493A-17	Sequence 17, Appl
730	36	1.0	93	1	US-08-370-567-27	Sequence 27, Appl
731	36	1.0	93	1	US-08-438-759-27	Sequence 27, Appl
732	36	1.0	93	1	US-08-458-423A-2	Sequence 2, Appli
c 733	36	1.0	93	1	US-08-458-423A-2	Sequence 2, Appli
734	36	1.0	93	1	US-08-458-424B-2	Sequence 2, Appli
c 735	36	1.0	93	1	US-08-458-424B-2	Sequence 2, Appli
736	36	1.0	93	1	US-08-538-911-2	Sequence 2, Appli
737	36	1.0	93	1	US-08-117-361C-15	Sequence 15, Appl
738	36	1.0	93	4	US-08-973-124-2	Sequence 2, Appli
c 739	36	1.0	93	4	US-08-973-124-2	Sequence 2, Appli
740	36	1.0	93	5	PCT-US94-05591-2	Sequence 2, Appli
741	36	1.0	93	5	PCT-US94-05684-27	Sequence 27, Appl
742	36	1.0	93	5	PCT-US96-08014-2	Sequence 2, Appli
c 743	36	1.0	93	5	PCT-US96-08014-2	Sequence 2, Appli
c 744	36	1.0	94	2	US-08-771-201-6	Sequence 6, Appli
745	36	1.0	95	1	US-08-458-423A-4	Sequence 4, Appli
c 746	36	1.0	95	1	US-08-458-423A-4	Sequence 4, Appli
747	36	1.0	95	1	US-08-458-424B-4	Sequence 4, Appli
c 748	36	1.0	95	1	US-08-458-424B-4	Sequence 4, Appli
749	36	1.0	95	4	US-08-973-124-4	Sequence 4, Appli
c 750	36	1.0	95	4	US-08-973-124-4	Sequence 4, Appli
751	36	1.0	95	5	PCT-US96-08014-4	Sequence 4, Appli
c 752	36	1.0	95	5	PCT-US96-08014-4	Sequence 4, Appli
c 753	36	1.0	96	1	US-08-234-613-1	Sequence 1, Appli
c 754	36	1.0	96	1	US-08-753-054-19	Sequence 19, Appl
c 755	36	1.0	96	2	US-08-237-973-1	Sequence 1, Appli
756	36	1.0	98	1	US-08-234-613-4	Sequence 4, Appli
c 757	36	1.0	98	1	US-08-399-412A-7	Sequence 7, Appli
c 758	36	1.0	98	1	US-08-447-172A-28	Sequence 28, Appl
c 759	36	1.0	98	1	US-08-447-172A-31	Sequence 31, Appl
c 760	36	1.0	98	1	US-08-472-255A-1	Sequence 1, Appli
c 761	36	1.0	98	1	US-08-479-724A-1	Sequence 1, Appli
762	36	1.0	98	2	US-08-237-973-4	Sequence 4, Appli
c 763	36	1.0	98	3	US-08-472-256B-1	Sequence 1, Appli
c 764	36	1.0	98	4	US-08-952-793-1	Sequence 1, Appli
c 765	36	1.0	98	4	US-08-849-567A-50	Sequence 50, Appl
c 766	36	1.0	98	5	PCT-US96-09455A-1	Sequence 1, Appli
c 767	36	1.0	99	4	US-08-849-567A-51	Sequence 51, Appl
c 768	36	1.0	101	1	US-07-843-125-6	Sequence 6, Appli
769	36	1.0	104	2	US-08-139-176D-2	Sequence 2, Appli
770	36	1.0	104	2	US-08-139-176D-3	Sequence 3, Appli
771	36	1.0	104	3	US-09-041-841-2	Sequence 2, Appli
772	36	1.0	104	3	US-09-041-841-3	Sequence 3, Appli
773	36	1.0	105	1	US-08-219-012-52	Sequence 52, Appl
c 774	36	1.0	105	1	US-08-219-012-52	Sequence 52, Appl
775	36	1.0	105	4	US-08-687-421-240	Sequence 240, App
c 776	36	1.0	105	4	US-08-687-421-240	Sequence 240, App
777	36	1.0	107	1	US-08-472-194A-23	Sequence 23, Appl
c 778	36	1.0	107	1	US-08-472-194A-23	Sequence 23, Appl
779	36	1.0	107	4	US-08-849-567A-23	Sequence 23, Appl
c 780	36	1.0	107	4	US-08-849-567A-23	Sequence 23, Appl
781	36	1.0	108	4	US-09-296-328A-15	Sequence 15, Appl
c 782	36	1.0	108	4	US-09-296-328A-15	Sequence 15, Appl
c 783	36	1.0	110	1	US-08-299-498A-3	Sequence 3, Appli
c 784	36	1.0	110	5	PCT-US95-10813-3	Sequence 3, Appli
c 785	36	1.0	112	1	US-08-299-498A-32	Sequence 32, Appl
c 786	36	1.0	112	5	PCT-US95-10813-32	Sequence 32, Appl
787	36	1.0	117	1	US-08-458-423A-1	Sequence 1, Appli
c 788	36	1.0	117	1	US-08-458-423A-1	Sequence 1, Appli
789	36	1.0	117	1	US-08-458-424B-1	Sequence 1, Appli
c 790	36	1.0	117	1	US-08-458-424B-1	Sequence 1, Appli
791	36	1.0	117	4	US-08-973-124-1	Sequence 1, Appli
c 792	36	1.0	117	4	US-08-973-124-1	Sequence 1, Appli
793	36	1.0	117	5	PCT-US96-08014-1	Sequence 1, Appli
c 794	36	1.0	117	5	PCT-US96-08014-1	Sequence 1, Appli
795	36	1.0	119	4	US-08-679-493A-15	Sequence 15, Appl
c 796	36	1.0	119	4	US-08-679-493A-15	Sequence 15, Appl
797	36	1.0	120	1	US-07-843-125-4	Sequence 4, Appli
798	36	1.0	121	4	US-09-535-754-10	Sequence 10, Appl
799	36	1.0	122	4	US-09-193-068-16	Sequence 16, Appl
c 800	36	1.0	122	4	US-09-193-068-16	Sequence 16, Appl
801	36	1.0	123	4	US-09-535-754-9	Sequence 9, Appli
802	36	1.0	132	2	US-08-771-201-7	Sequence 7, Appli
c 803	36	1.0	132	2	US-08-771-201-7	Sequence 7, Appli
c 804	36	1.0	134	1	US-08-299-498A-5	Sequence 5, Appli
c 805	36	1.0	134	5	PCT-US95-10813-5	Sequence 5, Appli
c 806	36	1.0	139	4	US-08-679-493A-60	Sequence 60, Appl
807	36	1.0	141	1	US-08-375-116A-131	Sequence 131, App
c 808	36	1.0	141	1	US-08-375-116A-131	Sequence 131, App
809	36	1.0	142	1	US-08-375-116A-130	Sequence 130, App
c 810	36	1.0	142	1	US-08-375-116A-130	Sequence 130, App
811	36	1.0	149	3	US-08-903-139B-31	Sequence 31, Appl
c 812	36	1.0	149	3	US-08-903-139B-31	Sequence 31, Appl
813	36	1.0	152	2	US-08-771-201-8	Sequence 8, Appli
c 814	36	1.0	152	2	US-08-771-201-8	Sequence 8, Appli
815	36	1.0	154	2	US-08-721-684C-7	Sequence 7, Appli
816	36	1.0	154	2	US-09-005-970-7	Sequence 7, Appli
817	36	1.0	154	4	US-09-407-715-7	Sequence 7, Appli
818	36	1.0	155	3	US-08-903-139B-15	Sequence 15, Appl
c 819	36	1.0	155	3	US-08-903-139B-15	Sequence 15, Appl
820	36	1.0	195	4	US-09-186-276B-64	Sequence 64, Appl
821	36	1.0	195	4	US-08-842-445-64	Sequence 64, Appl
822	36	1.0	195	4	US-09-186-188B-64	Sequence 64, Appl
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c 825	36	1.0	208	1	US-08-375-116A-132	Sequence 132, App
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827	36	1.0	215	4	US-09-535-754-8	Sequence 8, Appli
828	36	1.0	223	4	US-09-535-754-7	Sequence 7, Appli
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c 835	36	1.0	345	4	US-09-025-203-16	Sequence 16, Appl
836	36	1.0	348	4	US-09-672-609-18	Sequence 18, Appl
c 837	36	1.0	348	4	US-09-672-609-18	Sequence 18, Appl
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840	36	1.0	398	4	US-09-574-141A-89	Sequence 89, Appl
c 841	36	1.0	398	4	US-09-574-141A-89	Sequence 89, Appl
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c 843	36	1.0	423	2	US-08-822-028-62	Sequence 62, Appl
844	36	1.0	423	4	US-08-479-285-62	Sequence 62, Appl
c 845	36	1.0	423	4	US-08-479-285-62	Sequence 62, Appl
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847	36	1.0	426	4	US-08-479-285-65	Sequence 65, Appl
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c 849	36	1.0	479	4	US-09-254-352B-39	Sequence 39, Appl
c 850	36	1.0	495	2	US-08-465-380-31	Sequence 31, Appl
c 851	36	1.0	495	2	US-08-486-397-31	Sequence 31, Appl
c 852	36	1.0	495	2	US-08-486-399-31	Sequence 31, Appl
c 853	36	1.0	495	2	US-08-461-965-31	Sequence 31, Appl
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855	36	1.0	595	4	US-09-276-531-63	Sequence 63, Appl
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864	36	1.0	699	4	US-09-276-531-91	Sequence 91, Appl
c 865	36	1.0	699	4	US-09-276-531-91	Sequence 91, Appl
866	36	1.0	759	3	US-09-109-205-11	Sequence 11, Appl
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868	36	1.0	804	4	US-09-276-531-54	Sequence 54, Appl
869	36	1.0	808	4	US-08-791-115B-12	Sequence 12, Appl
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877	36	1.0	959	4	US-09-723-216-1	Sequence 1, Appli
878	36	1.0	959	4	US-09-675-227-1	Sequence 1, Appli
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880	36	1.0	1070	4	US-09-718-810-3	Sequence 3, Appli
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883	36	1.0	1076	4	US-08-837-199A-46	Sequence 46, Appl
c 884	36	1.0	1076	4	US-08-837-199A-46	Sequence 46, Appl
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c 888	36	1.0	1143	4	US-09-276-531-103	Sequence 103, App
889	36	1.0	1183	2	US-08-731-722-8	Sequence 8, Appli
c 890	36	1.0	1233	4	US-09-276-531-7	Sequence 7, Appli
891	36	1.0	1252	4	US-09-276-531-92	Sequence 92, Appl
892	36	1.0	1280	4	US-09-276-531-52	Sequence 52, Appl
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910	36	1.0	1610	4	US-09-276-531-56	Sequence 56, Appl
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912	36	1.0	1651	4	US-09-484-970B-17	Sequence 17, Appl
913	36	1.0	1689	4	US-09-718-841-1	Sequence 1, Appli
914	36	1.0	1689	4	US-09-718-810-1	Sequence 1, Appli
915	36	1.0	1713	4	US-08-759-436-1	Sequence 1, Appli
916	36	1.0	1738	3	US-09-120-365-89	Sequence 89, Appl
917	36	1.0	1738	4	US-09-515-039-89	Sequence 89, Appl
918	36	1.0	1750	3	US-09-120-365-90	Sequence 90, Appl
919	36	1.0	1750	4	US-09-515-039-90	Sequence 90, Appl
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925	36	1.0	2038	4	US-09-276-531-37	Sequence 37, Appl
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928	36	1.0	2116	2	US-08-023-610-18	Sequence 18, Appl
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930	36	1.0	2116	2	US-08-362-240A-18	Sequence 18, Appl
931	36	1.0	2116	5	PCT-US95-10245-18	Sequence 18, Appl
932	36	1.0	2157	4	US-08-837-199A-15	Sequence 15, Appl
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953	36	1.0	2847	4	US-09-484-970B-22	Sequence 22, Appl
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964	36	1.0	3720	5	PCT-US94-06669-1	Sequence 1, Appli
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969	36	1.0	3837	4	US-09-723-096-1	Sequence 1, Appli
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971	36	1.0	3915	2	US-08-485-139-6	Sequence 6, Appli
c 972	36	1.0	3915	2	US-08-485-139-6	Sequence 6, Appli
973	36	1.0	3915	3	US-08-750-357-6	Sequence 6, Appli
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979	36	1.0	4533	3	US-08-863-790-27	Sequence 27, Appl
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981	36	1.0	4533	3	US-08-296-749-27	Sequence 27, Appl
c 982	36	1.0	4533	3	US-08-296-749-27	Sequence 27, Appl
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c 993	36	1.0	8299	4	US-09-563-869A-5	Sequence 5, Appli
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ALIGNMENTS

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RESULT 1
US-08-208-005C-1
; Sequence 1, Application US/08208005C
; Patent No. 5837498
;  GENERAL INFORMATION:
;    APPLICANT:  OLSEN, ET AL.
;    TITLE OF INVENTION:  Corpuscles of Stannius Protein, Stanniocalcin
;    NUMBER OF SEQUENCES:  5
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  CARELLA, BYRNE, BAIN, GILFILLAN,
;      ADDRESSEE:  CECCHI, STEWART & OLSTEIN
;      STREET:  6 BECKER FARM ROAD
;      CITY:  ROSELAND
;      STATE:  NEW JERSEY
;      COUNTRY:  USA
;      ZIP:  07068
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5 INCH DISKETTE
;      COMPUTER:  IBM PS/2
;      OPERATING SYSTEM:  MS-DOS
;      SOFTWARE:  WORD PERFECT 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/208,005C
;      FILING DATE:  8 MARCH 1994
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  FERRARO, GREGORY D.
;      REGISTRATION NUMBER:  36,134
;      REFERENCE/DOCKET NUMBER:  325800-78
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  201-994-1700
;      TELEFAX:  201-994-1744
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  771 BASE PAIRS
;      TYPE:  NUCLEIC ACID
;      STRANDEDNESS:  SINGLE
;      TOPOLOGY:  LINEAR
;    MOLECULE TYPE:  cDNA
US-08-208-005C-1
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  Query Match           19.1%;  Score 720;  DB 2;  Length 771;
  Best Local Similarity   99.9%;  Pred. No. 2.4e-313;
  Matches  770;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        159 GAAACTTCTCAGAGAATGCTCCAAAACTCAGCAGTGCTTCTGGTGCTGGTGATCAGTGCT 218
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Db          1 GAAACTTCTCAGAGAATGCTCCAAAACTCAGCAGTGCTTCTGGTGCTGGTGATCAGTGCT 60

Qy        219 TCTGCAACCCATGAGGCGGAGCAGAATGACTCTGTGAGCCCCAGGAAATCCCGAGTGGCG 278
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Db         61 TCTGCAACCCATGAGGCGGAGCAGAATGACTCTGTGAGCCCCAGGAAATCCCGAGTGGCG 120

Qy        279 GCTCAAAACTCAGCTGAAGTGGTTCGTTGCCTCAACAGTGCTCTACAGGTCGGCTGCGGG 338
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Qy        519 ACTTTCCAAAGGATGATTGCTGAGGTGCAGGAAGAGTGCTACAGCAAGCTGAATGTGTGC 578
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Qy        579 AGCATCGCCAAGCGGAACCCTGAAGCCATCACTGAGGTCGTCCAGCTGCCCAATCACTTC 638
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Qy        639 TCCAACAGATACTATAACAGACTTGTCCGAAGCCTGCTGGAATGTGATGAAGACACAGTC 698
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Db        481 TCCAACAGATACTATAACAGACTTGTCCGAAGCCTGCTGGAATGTGATGAAGACACAGTC 540

Qy        699 AGCACAATCAGAGACAGCCTGATGGAGAAAATTGGGCCTAACATGGCCAGCCTCTTCCAC 758
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 AGCACAATCAGAGACAGCCTGATGGAGAAAATTGGGCCTAACATGGCCAGCCTCTTCCAC 600

Qy        759 ATCCTGCAGACAGACCACTGTGCCCAAACACACCCACGAGCTGACTTCAACAGGAGACGC 818
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 ATCCTGCAGACAGACCACTGTGCCCAAACACACCCACGAGCTGACTTCAACAGGAGACGC 660

Qy        819 ACCAATGAGCCGCAGAAGCTGAAAGTCCTCCTCAGGAACCTCCGAGGTGAGGAGGACTCT 878
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 ACCAATGAGCCGCAGAAGCTGAAAGTCCTCCTCAGGAACCTCCGAGGTGAGGAGGACTCT 720

Qy        879 CCCTCCCACATCAAACGCACATCCCATGAGAGTGCATAACCAGGGAGAGGT 929
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 CCCTCCCACATCAAACGCACATCCCATGAGAGTGCATAACCAGGGAGAGGT 771
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RESULT 2
US-09-038-597A-1
; Sequence 1, Application US/09038597A
; Patent No. 5877290
;  GENERAL INFORMATION:
;    APPLICANT:  OLSEN, ET AL.
;    TITLE OF INVENTION:  Corpuscles of Stannius Protein,
;    TITLE OF INVENTION:  Stanniocalcin
;    NUMBER OF SEQUENCES:  5
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  CARELLA, BYRNE, BAIN, GILFILLAN,
;      ADDRESSEE:  CECCHI, STEWART & OLSTEIN
;      STREET:  6 BECKER FARM ROAD
;      CITY:  ROSELAND
;      STATE:  NEW JERSEY
;      COUNTRY:  USA
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;      ZIP:  07068
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5 INCH DISKETTE
;      COMPUTER:  IBM PS/2
;      OPERATING SYSTEM:  MS-DOS
;      SOFTWARE:  WORD PERFECT 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/038,597A
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/208,005
;      FILING DATE:  8-MARCH-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  FERRARO, GREGORY D.
;      REGISTRATION NUMBER:  36,134
;      REFERENCE/DOCKET NUMBER:  325800-78
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  201-994-1700
;      TELEFAX:  201-994-1744
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  771 BASE PAIRS
;      TYPE:  NUCLEIC ACID
;      STRANDEDNESS:  SINGLE
;      TOPOLOGY:  LINEAR
;    MOLECULE TYPE:  cDNA
US-09-038-597A-1

  Query Match           19.1%;  Score 720;  DB 2;  Length 771;
  Best Local Similarity   99.9%;  Pred. No. 2.4e-313;
  Matches  770;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        159 GAAACTTCTCAGAGAATGCTCCAAAACTCAGCAGTGCTTCTGGTGCTGGTGATCAGTGCT 218
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GAAACTTCTCAGAGAATGCTCCAAAACTCAGCAGTGCTTCTGGTGCTGGTGATCAGTGCT 60

Qy        219 TCTGCAACCCATGAGGCGGAGCAGAATGACTCTGTGAGCCCCAGGAAATCCCGAGTGGCG 278
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TCTGCAACCCATGAGGCGGAGCAGAATGACTCTGTGAGCCCCAGGAAATCCCGAGTGGCG 120

Qy        279 GCTCAAAACTCAGCTGAAGTGGTTCGTTGCCTCAACAGTGCTCTACAGGTCGGCTGCGGG 338
              || ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GCCCAAAACTCAGCTGAAGTGGTTCGTTGCCTCAACAGTGCTCTACAGGTCGGCTGCGGG 180

Qy        339 GCTTTTGCATGCCTGGAAAACTCCACCTGTGACACAGATGGGATGTATGACATCTGTAAA 398
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GCTTTTGCATGCCTGGAAAACTCCACCTGTGACACAGATGGGATGTATGACATCTGTAAA 240

Qy        399 TCCTTCTTGTACAGCGCTGCTAAATTTGACACTCAGGGAAAAGCATTCGTCAAAGAGAGC 458
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TCCTTCTTGTACAGCGCTGCTAAATTTGACACTCAGGGAAAAGCATTCGTCAAAGAGAGC 300

Qy        459 TTAAAATGCATCGCCAACGGGGTCACCTCCAAGGTCTTCCTCGCCATTCGGAGGTGCTCC 518
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TTAAAATGCATCGCCAACGGGGTCACCTCCAAGGTCTTCCTCGCCATTCGGAGGTGCTCC 360

Qy        519 ACTTTCCAAAGGATGATTGCTGAGGTGCAGGAAGAGTGCTACAGCAAGCTGAATGTGTGC 578
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 ACTTTCCAAAGGATGATTGCTGAGGTGCAGGAAGAGTGCTACAGCAAGCTGAATGTGTGC 420

Qy        579 AGCATCGCCAAGCGGAACCCTGAAGCCATCACTGAGGTCGTCCAGCTGCCCAATCACTTC 638
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 AGCATCGCCAAGCGGAACCCTGAAGCCATCACTGAGGTCGTCCAGCTGCCCAATCACTTC 480

Qy        639 TCCAACAGATACTATAACAGACTTGTCCGAAGCCTGCTGGAATGTGATGAAGACACAGTC 698
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 TCCAACAGATACTATAACAGACTTGTCCGAAGCCTGCTGGAATGTGATGAAGACACAGTC 540

Qy        699 AGCACAATCAGAGACAGCCTGATGGAGAAAATTGGGCCTAACATGGCCAGCCTCTTCCAC 758
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 AGCACAATCAGAGACAGCCTGATGGAGAAAATTGGGCCTAACATGGCCAGCCTCTTCCAC 600

Qy        759 ATCCTGCAGACAGACCACTGTGCCCAAACACACCCACGAGCTGACTTCAACAGGAGACGC 818
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 ATCCTGCAGACAGACCACTGTGCCCAAACACACCCACGAGCTGACTTCAACAGGAGACGC 660

Qy        819 ACCAATGAGCCGCAGAAGCTGAAAGTCCTCCTCAGGAACCTCCGAGGTGAGGAGGACTCT 878
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 ACCAATGAGCCGCAGAAGCTGAAAGTCCTCCTCAGGAACCTCCGAGGTGAGGAGGACTCT 720

Qy        879 CCCTCCCACATCAAACGCACATCCCATGAGAGTGCATAACCAGGGAGAGGT 929
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 CCCTCCCACATCAAACGCACATCCCATGAGAGTGCATAACCAGGGAGAGGT 771


RESULT 3
US-08-431-117A-1
; Sequence 1, Application US/08431117A
; Patent No. 5994301
;  GENERAL INFORMATION:
;    APPLICANT:  OLSEN, ET AL.
;    TITLE OF INVENTION:  Corpuscles of Stannius Protein, Stanniocalcin
;    NUMBER OF SEQUENCES:  8
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  CARELLA, BYRNE, BAIN, GILFILLAN,
;      ADDRESSEE:  CECCHI, STEWART & OLSTEIN
;      STREET:  6 BECKER FARM ROAD
;      CITY:  ROSELAND
;      STATE:  NEW JERSEY
;      COUNTRY:  USA
;      ZIP:  07068
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5 INCH DISKETTE
;      COMPUTER:  IBM PS/2
;      OPERATING SYSTEM:  MS-DOS
;      SOFTWARE:  WORD PERFECT 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/431,117A
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/208,005
;      FILING DATE:  8 MARCH 1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  FERRARO, GREGORY D.
;      REGISTRATION NUMBER:  36,134
;      REFERENCE/DOCKET NUMBER:  325800-296
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  201-994-1700
;      TELEFAX:  201-994-1744
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  771 BASE PAIRS
;      TYPE:  NUCLEIC ACID
;      STRANDEDNESS:  SINGLE
;      TOPOLOGY:  LINEAR
;    MOLECULE TYPE:  cDNA
US-08-431-117A-1

  Query Match           19.1%;  Score 720;  DB 2;  Length 771;
  Best Local Similarity   99.9%;  Pred. No. 2.4e-313;
  Matches  770;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        159 GAAACTTCTCAGAGAATGCTCCAAAACTCAGCAGTGCTTCTGGTGCTGGTGATCAGTGCT 218
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GAAACTTCTCAGAGAATGCTCCAAAACTCAGCAGTGCTTCTGGTGCTGGTGATCAGTGCT 60

Qy        219 TCTGCAACCCATGAGGCGGAGCAGAATGACTCTGTGAGCCCCAGGAAATCCCGAGTGGCG 278
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TCTGCAACCCATGAGGCGGAGCAGAATGACTCTGTGAGCCCCAGGAAATCCCGAGTGGCG 120

Qy        279 GCTCAAAACTCAGCTGAAGTGGTTCGTTGCCTCAACAGTGCTCTACAGGTCGGCTGCGGG 338
              || ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GCCCAAAACTCAGCTGAAGTGGTTCGTTGCCTCAACAGTGCTCTACAGGTCGGCTGCGGG 180
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Qy        339 GCTTTTGCATGCCTGGAAAACTCCACCTGTGACACAGATGGGATGTATGACATCTGTAAA 398
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GCTTTTGCATGCCTGGAAAACTCCACCTGTGACACAGATGGGATGTATGACATCTGTAAA 240

Qy        399 TCCTTCTTGTACAGCGCTGCTAAATTTGACACTCAGGGAAAAGCATTCGTCAAAGAGAGC 458
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TCCTTCTTGTACAGCGCTGCTAAATTTGACACTCAGGGAAAAGCATTCGTCAAAGAGAGC 300

Qy        459 TTAAAATGCATCGCCAACGGGGTCACCTCCAAGGTCTTCCTCGCCATTCGGAGGTGCTCC 518
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TTAAAATGCATCGCCAACGGGGTCACCTCCAAGGTCTTCCTCGCCATTCGGAGGTGCTCC 360

Qy        519 ACTTTCCAAAGGATGATTGCTGAGGTGCAGGAAGAGTGCTACAGCAAGCTGAATGTGTGC 578
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 ACTTTCCAAAGGATGATTGCTGAGGTGCAGGAAGAGTGCTACAGCAAGCTGAATGTGTGC 420

Qy        579 AGCATCGCCAAGCGGAACCCTGAAGCCATCACTGAGGTCGTCCAGCTGCCCAATCACTTC 638
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 AGCATCGCCAAGCGGAACCCTGAAGCCATCACTGAGGTCGTCCAGCTGCCCAATCACTTC 480

Qy        639 TCCAACAGATACTATAACAGACTTGTCCGAAGCCTGCTGGAATGTGATGAAGACACAGTC 698
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 TCCAACAGATACTATAACAGACTTGTCCGAAGCCTGCTGGAATGTGATGAAGACACAGTC 540

Qy        699 AGCACAATCAGAGACAGCCTGATGGAGAAAATTGGGCCTAACATGGCCAGCCTCTTCCAC 758
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 AGCACAATCAGAGACAGCCTGATGGAGAAAATTGGGCCTAACATGGCCAGCCTCTTCCAC 600

Qy        759 ATCCTGCAGACAGACCACTGTGCCCAAACACACCCACGAGCTGACTTCAACAGGAGACGC 818
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 ATCCTGCAGACAGACCACTGTGCCCAAACACACCCACGAGCTGACTTCAACAGGAGACGC 660

Qy        819 ACCAATGAGCCGCAGAAGCTGAAAGTCCTCCTCAGGAACCTCCGAGGTGAGGAGGACTCT 878
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 ACCAATGAGCCGCAGAAGCTGAAAGTCCTCCTCAGGAACCTCCGAGGTGAGGAGGACTCT 720

Qy        879 CCCTCCCACATCAAACGCACATCCCATGAGAGTGCATAACCAGGGAGAGGT 929
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 CCCTCCCACATCAAACGCACATCCCATGAGAGTGCATAACCAGGGAGAGGT 771
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RESULT 4
US-09-738-894A-3
; Sequence 3, Application US/09738894A
; Patent No. 6331423
; GENERAL INFORMATION:
; APPLICANT: GUEGLER, Karl et al
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL000636
; CURRENT APPLICATION NUMBER: US/09/738,894A
; CURRENT FILING DATE: 2000-12-18
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 36651
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(36651)
; OTHER INFORMATION: n = A,T,C or G
US-09-738-894A-3

Query Match 1.1%; Score 41; DB 4; Length 36651;
Best Local Similarity 100.0%; Pred. No. 4.5e-09;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy       2365 AGAAANNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 2405
              |||||||||||||||||||||||||||||||||||||||||||||
Db      24831 AGAAANNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 24871
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RESULT 5
US-08-679-493A-18
; Sequence 18, Application US/08679493A
; Patent No. 6303295
; GENERAL INFORMATION:
; APPLICANT: Taylor, Ethan W.
; TITLE OF INVENTION: SELENOPROTEINS, CODING SEQUENCES AND METHODS
; FILE REFERENCE: 55-95
; CURRENT APPLICATION NUMBER: US/08/679,493A
; CURRENT FILING DATE: 1996-07-12
; PRIOR APPLICATION NUMBER: 60/001203
; PRIOR FILING DATE: 1995-07-14
; PRIOR APPLICATION NUMBER: 60/003,112
; PRIOR FILING DATE: 1995-09-01
; NUMBER OF SEQ ID NOS: 216
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 18
; LENGTH: 99
; TYPE: RNA
; ORGANISM: Visna virus
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(99)
; OTHER INFORMATION: N is A, U, G or C.
US-08-679-493A-18

Query Match 1.1%; Score 40; DB 4; Length 99;
Best Local Similarity 100.0%; Pred. No. 1.9e-08;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy       2366 GAAANNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 2405
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Db         27 GAAANNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 66
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RESULT 6
US-09-800-960-3/c
; Sequence 3, Application US/09800960
; Patent No. 6387677
; GENERAL INFORMATION:
; APPLICANT: YE, Jane et al.
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL001158
; CURRENT APPLICATION NUMBER: US/09/800,960
; CURRENT FILING DATE: 2001-03-08
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 62804
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(62804)
; OTHER INFORMATION: n = A,T,C or G
US-09-800-960-3

Query Match 1.1%; Score 40; DB 4; Length 62804;
Best Local Similarity 100.0%; Pred. No. 1.2e-08;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy       2370 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNCTGG 2409
              ||||||||||||||||||||||||||||||||||||||||
Db        393 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNCTGG 354
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RESULT 7
US-08-659-453B-4/c
; Sequence 4, Application US/08659453B
; Patent No. 5846719

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;  GENERAL INFORMATION:
;    APPLICANT:  Sydney Brenner, Glenn Albrecht, Stephen C. Macevicz
;    TITLE OF INVENTION:  Oligonucleotide Tags for Sorting and Identification
;    NUMBER OF SEQUENCES:  27
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Stephen C. Macevicz, Spectragen, Inc.
;      STREET:  3832 Bay Center Place
;      CITY:  Hayward
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94545
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5 inch diskette
;      COMPUTER:  IBM compatible
;      OPERATING SYSTEM:  Windows 95
;      SOFTWARE:  Microsoft Word 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/659,453B
;      FILING DATE:  06-JUN-96
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US95/12791
;      FILING DATE:  12-OCT-95
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/478,238
;      FILING DATE:  07-JUN-95
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/485,105
;      FILING DATE:  07-JUN-95
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US95/12791
;      FILING DATE:  12-OCT-95
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Stephen C. Macevicz
;      REGISTRATION NUMBER:  30,285
;      REFERENCE/DOCKET NUMBER:  cbd4wo
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (510) 670-9365
;      TELEFAX:  (510) 670-9302
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  62 nucleotides
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
US-08-659-453B-4

  Query Match             1.0%;  Score 39;  DB 2;  Length 62;
  Best Local Similarity   100.0%;  Pred. No. 5.6e-08;
  Matches   39;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2367 AAANNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 2405
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Db         46 AAANNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 8


RESULT 8
US-09-089-853A-4/c
; Sequence 4, Application US/09089853A
; Patent No. 6138077
;  GENERAL INFORMATION:
;    APPLICANT:  Sydney Brenner, Stephen C. Macevicz
;    TITLE OF INVENTION:  A Method, Apparatus and Computer Program Product for Determini
;    NUMBER OF SEQUENCES:  27
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Stephen C. Macevicz, Lynx Therapeutics, Inc.
;      STREET:  25861 Industrial Blvd.
;      CITY:  Hayward
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94545
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5 inch diskette
;      COMPUTER:  IBM compatible
;      OPERATING SYSTEM:  Windows 98
;      SOFTWARE:  Microsoft Word2000
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/089,853A
;      FILING DATE:  03-JUN-98
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/659,453
;      FILING DATE:  06-JUN-96
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/358,810
;      FILING DATE:  19-DEC-94
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/322,348
;      FILING DATE:  13-OCT-94
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Stephen C. Macevicz
;      REGISTRATION NUMBER:  30,285
;      REFERENCE/DOCKET NUMBER:  802-11
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (510) 670-9365
;      TELEFAX:  (510) 670-9302
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  62 nucleotides
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
US-09-089-853A-4

  Query Match             1.0%;  Score 39;  DB 3;  Length 62;
  Best Local Similarity   100.0%;  Pred. No. 5.6e-08;
  Matches   39;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2367 AAANNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 2405
             |||||||||||||||||||||||||||||||||||||||
Db         46 AAANNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 8


RESULT 9
US-09-131-009A-4/c
; Sequence 4, Application US/09131009A
; Patent No. 6172214
; Patent No. 6172214 6171856
;  GENERAL INFORMATION:
;    APPLICANT:  Sydney Brenner, Glenn Albrecht, Stephen C. Macevicz
;    TITLE OF INVENTION:  Oligonucleotide Tags for Sorting and Identification
;    NUMBER OF SEQUENCES:  27
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Stephen C. Macevicz, Lynx Therapeutics, Inc.
;      STREET:  25861 Industrial Blvd.
;      CITY:  Hayward
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94545
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5 inch diskette
;      COMPUTER:  IBM compatible
;      OPERATING SYSTEM:  Windows 98
;      SOFTWARE:  Microsoft Word2000
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/131,009A
;      FILING DATE:  06-AUG-98
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/659,453
;      FILING DATE:  06-JUN-96
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/358,810
;      FILING DATE:  19-DEC-94
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/322,348
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;      FILING DATE:  13-OCT-94
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Stephen C. Macevicz
;      REGISTRATION NUMBER:  30,285
;      REFERENCE/DOCKET NUMBER:  802-10
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (510) 670-9365
;      TELEFAX:  (510) 670-9302
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  62 nucleotides
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
US-09-131-009A-4

  Query Match             1.0%;  Score 39;  DB 4;  Length 62;
  Best Local Similarity   100.0%;  Pred. No. 5.6e-08;
  Matches   39;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2367 AAANNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 2405
              |||||||||||||||||||||||||||||||||||||||
Db         46 AAANNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 8


RESULT 10
US-09-092-226A-4/c
; Sequence 4, Application US/09092226A
; Patent No. 6172218
;  GENERAL INFORMATION:
;    APPLICANT:  Sydney Brenner
;    TITLE OF INVENTION:  Oligonucleotide Tags for Sorting and Identification
;    NUMBER OF SEQUENCES:  27
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Stephen C. Macevicz, Lynx Therapeutics, Inc.
;      STREET:  25861 Industrial Blvd.
;      CITY:  Hayward
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94545
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5 inch diskette
;      COMPUTER:  IBM compatible
;      OPERATING SYSTEM:  Windows 98
;      SOFTWARE:  Microsoft Word2000
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/092,226A
;      FILING DATE:  05-JUN-98
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/659,453
;      FILING DATE:  06-JUN-96
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/358,810
;      FILING DATE:  19-DEC-94
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/322,348
;      FILING DATE:  13-OCT-94
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Stephen C. Macevicz
;      REGISTRATION NUMBER:  30,285
;      REFERENCE/DOCKET NUMBER:  802-09
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (510) 670-9365
;      TELEFAX:  (510) 670-9302
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  62 nucleotides
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
US-09-092-226A-4

  Query Match             1.0%;  Score 39;  DB 4;  Length 62;
  Best Local Similarity   100.0%;  Pred. No. 5.6e-08;
  Matches   39;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Db         46 AAANNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 8


RESULT 11
US-09-130-862A-4/c
; Sequence 4, Application US/09130862A
; Patent No. 6235475
;  GENERAL INFORMATION:
;    APPLICANT:  Sydney Brenner
;    TITLE OF INVENTION:  Oligonucleotide Tags for Sorting and Identification
;    NUMBER OF SEQUENCES:  27
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Stephen C. Macevicz, Lynx Therapeutics, Inc.
;      STREET:  25861 Industrial Blvd.
;      CITY:  Hayward
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94545
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5 inch diskette
;      COMPUTER:  IBM compatible
;      OPERATING SYSTEM:  Windows 98
;      SOFTWARE:  Microsoft Word2000
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/130,862A
;      FILING DATE:  06-AUG-98
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/659,453
;      FILING DATE:  06-JUN-96
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/358,810
;      FILING DATE:  19-DEC-94
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/322,348
;      FILING DATE:  13-OCT-94
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Stephen C. Macevicz
;      REGISTRATION NUMBER:  30,285
;      REFERENCE/DOCKET NUMBER:  802-12
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (510) 670-9365
;      TELEFAX:  (510) 670-9302
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  62 nucleotides
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
US-09-130-862A-4

  Query Match             1.0%;  Score 39;  DB 4;  Length 62;
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Db         46 AAANNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 8


RESULT 12
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; Sequence 4, Application US/09090809A
; Patent No. 6280935
;  GENERAL INFORMATION:
;    APPLICANT:  Stephen C. Macevicz
;    TITLE OF INVENTION:  Method of Detecting the Presence or Absence of a Plurality of 1
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;    NUMBER OF SEQUENCES:  27
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Stephen C. Macevicz, Lynx Therapeutics, Inc.
;      STREET:  25861 Industrial Blvd.
;      CITY:  Hayward
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94545
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5 inch diskette
;      COMPUTER:  IBM compatible
;      OPERATING SYSTEM:  Windows 98
;      SOFTWARE:  Microsoft Word2000
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/090,809A
;      FILING DATE:  04-JUN-98
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/659,453
;      FILING DATE:  06-JUN-96
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/358,810
;      FILING DATE:  19-DEC-94
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/322,348
;      FILING DATE:  13-OCT-94
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Stephen C. Macevicz
;      REGISTRATION NUMBER:  30,285
;      REFERENCE/DOCKET NUMBER:  802-08
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (510) 670-9365
;      TELEFAX:  (510) 670-9302
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  62 nucleotides
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
US-09-090-809A-4

  Query Match             1.0%;  Score 39;  DB 4;  Length 62;
  Best Local Similarity   100.0%;  Pred. No. 5.6e-08;
  Matches   39;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2367 AAANNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 2405
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Db         46 AAANNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 8


RESULT 13
US-09-053-116A-4/c
; Sequence 4, Application US/09053116A
; Patent No. 6352828
;   GENERAL INFORMATION:
;        APPLICANT: Sydney Brenner, Glenn Albrecht, Stephen C. Macevicz
;        TITLE OF INVENTION: Oligonucleotide Tags for Sorting and Identification
;        NUMBER OF SEQUENCES: 27
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Stephen C. Macevicz, Spectragen, Inc.
;             STREET: 3832 Bay Center Place
;             CITY: Hayward
;             STATE: California
;             COUNTRY: USA
;             ZIP: 94545
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: 3.5 inch diskette
;             COMPUTER: IBM compatible
;             OPERATING SYSTEM: Windows 95
;             SOFTWARE: Microsoft Word 5.1
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/053,116A
;             FILING DATE: 01-Apr-1998
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 08/659,453
;             FILING DATE: <Unknown>
;             APPLICATION NUMBER: 08/478,238
;             FILING DATE: 07-JUN-95
;             APPLICATION NUMBER: 08/485,105
;             FILING DATE: 07-JUN-95
;             APPLICATION NUMBER: PCT/US95/12791
;             FILING DATE: 12-OCT-95
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Stephen C. Macevicz
;             REGISTRATION NUMBER: 30,285
;             REFERENCE/DOCKET NUMBER: cbd4wo
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (510) 670-9365
;             TELEFAX: (510) 670-9302
;   INFORMATION FOR SEQ ID NO: 4:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 62 nucleotides
;             TYPE: nucleic acid
;             STRANDEDNESS: double
;             TOPOLOGY: linear
;        SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-053-116A-4

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Db         46 AAANNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 8


RESULT 14
US-08-659-453B-1/c
; Sequence 1, Application US/08659453B
; Patent No. 5846719
;  GENERAL INFORMATION:
;    APPLICANT:  Sydney Brenner, Glenn Albrecht, Stephen C. Macevicz
;    TITLE OF INVENTION:  Oligonucleotide Tags for Sorting and Identification
;    NUMBER OF SEQUENCES:  27
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Stephen C. Macevicz, Spectragen, Inc.
;      STREET:  3832 Bay Center Place
;      CITY:  Hayward
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94545
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5 inch diskette
;      COMPUTER:  IBM compatible
;      OPERATING SYSTEM:  Windows 95
;      SOFTWARE:  Microsoft Word 5.1
;    CURRENT APPLICATION DATA:
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;      FILING DATE:  06-JUN-96
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US95/12791
;      FILING DATE:  12-OCT-95
;    PRIOR APPLICATION DATA:
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;      FILING DATE:  07-JUN-95
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/485,105
;      FILING DATE:  07-JUN-95
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US95/12791
;      FILING DATE:  12-OCT-95
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Stephen C. Macevicz
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;       REGISTRATION NUMBER:  30,285
;       REFERENCE/DOCKET NUMBER:  cbd4wo
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (510) 670-9365
;       TELEFAX:  (510) 670-9302
;   INFORMATION FOR SEQ ID NO:  1:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  66 nucleotides
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
US-08-659-453B-1

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RESULT 15
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; Sequence 1, Application US/09089853A
; Patent No. 6138077
;  GENERAL INFORMATION:
;    APPLICANT:  Sydney Brenner, Stephen C. Macevicz
;    TITLE OF INVENTION:  A Method, Apparatus and Computer Program Product for Determini
;    NUMBER OF SEQUENCES:  27
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Stephen C. Macevicz, Lynx Therapeutics, Inc.
;      STREET:  25861 Industrial Blvd.
;      CITY:  Hayward
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94545
;    COMPUTER READABLE FORM:
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;      COMPUTER:  IBM compatible
;      OPERATING SYSTEM:  Windows 98
;      SOFTWARE:  Microsoft Word2000
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/089,853A
;      FILING DATE:  03-JUN-98
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/659,453
;      FILING DATE:  06-JUN-96
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/358,810
;      FILING DATE:  19-DEC-94
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/322,348
;      FILING DATE:  13-OCT-94
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Stephen C. Macevicz
;      REGISTRATION NUMBER:  30,285
;      REFERENCE/DOCKET NUMBER:  802-11
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (510) 670-9365
;      TELEFAX:  (510) 670-9302
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  66 nucleotides
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-09-089-853A-1

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  Best Local Similarity   100.0%;  Pred. No. 5.6e-08;
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Title: US-09-705-500A-2
Perfect score: 3762
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Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 870385 seqs, 699768693 residues

Word size : 0

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Minimum DB seq length: 0
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Database : Published_Applications_NA:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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	1	2174	57.8	3897	9	US-10-198-846-13651	Sequence 13651, A
	2	2129	56.6	3765	12	US-10-044-090-638	Sequence 638, App
	3	1831	48.7	2572	10	US-09-925-300-486	Sequence 486, App
	4	814	21.6	1283	10	US-09-840-989A-1	Sequence 1, Appli
	5	720	19.1	771	12	US-10-116-051-1	Sequence 1, Appli
	6	494	13.1	585	10	US-09-778-320-149	Sequence 149, App
	7	494	13.1	585	10	US-09-910-689-149	Sequence 149, App
	8	494	13.1	585	12	US-10-010-742-149	Sequence 149, App
c	9	462	12.3	473	9	US-10-060-036-2677	Sequence 2677, Ap
	10	436	11.6	436	9	US-09-918-995-33032	Sequence 33032, A
c	11	405	10.8	510	9	US-09-736-457-4	Sequence 4, Appli
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c	13	405	10.8	510	9	US-09-849-626-4	Sequence 4, Appli
c	14	405	10.8	510	9	US-10-017-754-4	Sequence 4, Appli
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	17	122	3.2	420	10	US-09-778-320-141	Sequence 141, App
	18	122	3.2	420	10	US-09-910-689-141	Sequence 141, App
	19	122	3.2	420	12	US-10-010-742-141	Sequence 141, App
c	20	120	3.2	362	10	US-09-864-761-4563	Sequence 4563, Ap
c	21	116	3.1	1074	9	US-10-198-846-7201	Sequence 7201, Ap
	22	55	1.5	401	10	US-09-960-352-4108	Sequence 4108, Ap
c	23	43	1.1	2572	10	US-09-925-300-486	Sequence 486, App
	24	41	1.1	359	9	US-10-011-585A-77	Sequence 77, Appl
	25	41	1.1	573	9	US-09-989-919-45	Sequence 45, Appl
	26	41	1.1	30676	10	US-09-927-091-8	Sequence 8, Appli
	27	41	1.1	36651	10	US-09-964-469-3	Sequence 3, Appli
c	28	41	1.1	254366	9	US-09-822-871-3	Sequence 3, Appli
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	30	40	1.1	933	9	US-10-198-846-9242	Sequence 9242, Ap
	31	40	1.1	1581	9	US-10-198-846-13973	Sequence 13973, A
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	36	40	1.1	46718	9	US-10-274-873-3	Sequence 3, Appli
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	39	40	1.1	64467	9	US-10-274-409-3	Sequence 3, Appli
	40	40	1.1	74586	10	US-09-781-558-3	Sequence 3, Appli
c	41	40	1.1	78785	9	US-09-978-167-3	Sequence 3, Appli
	42	40	1.1	88191	10	US-09-799-799-3	Sequence 3, Appli
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	49	39	1.0	462	9	US-09-918-995-19257	Sequence 19257, A
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	51	39	1.0	487	9	US-10-034-934-30	Sequence 30, Appl
	52	39	1.0	488	9	US-09-918-995-20849	Sequence 20849, A
	53	39	1.0	490	9	US-09-918-995-24758	Sequence 24758, A
	54	39	1.0	492	9	US-10-198-846-10882	Sequence 10882, A
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	57	39	1.0	496	9	US-09-918-995-20853	Sequence 20853, A
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	61	39	1.0	546	9	US-09-918-995-32404	Sequence 32404, A
	62	39	1.0	551	9	US-09-918-995-26125	Sequence 26125, A
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	64	39	1.0	559	9	US-10-001-883-14	Sequence 14, Appl
	65	39	1.0	564	9	US-09-918-995-16187	Sequence 16187, A
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	73	39	1.0	650	10	US-09-955-866-15	Sequence 15, Appl
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	75	39	1.0	658	9	US-10-198-846-9362	Sequence 9362, Ap
	76	39	1.0	662	9	US-10-198-846-8045	Sequence 8045, Ap
	77	39	1.0	667	12	US-10-001-870-92	Sequence 92, Appl
	78	39	1.0	692	12	US-10-001-870-30	Sequence 30, Appl
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	86	39	1.0	895	9	US-10-198-846-7094	Sequence 7094, Ap
	87	39	1.0	910	9	US-10-198-846-5574	Sequence 5574, Ap
	88	39	1.0	917	9	US-10-198-846-7095	Sequence 7095, Ap
c	89	39	1.0	976	9	US-10-198-846-3576	Sequence 3576, Ap
	90	39	1.0	1024	9	US-10-202-193-44	Sequence 44, Appl
c	91	39	1.0	1061	9	US-10-011-445-40	Sequence 40, Appl
c	92	39	1.0	1146	9	US-10-177-900-9	Sequence 9, Appli

	93	39	1.0	1155	10	US-09-833-381-1293 Sequence 1293, Ap
	94	39	1.0	1203	9	US-10-011-585A-42 Sequence 42, Appl
	95	39	1.0	1222	9	US-10-011-585A-43 Sequence 43, Appl
	96	39	1.0	1302	9	US-10-245-103-69 Sequence 69, Appl
	97	39	1.0	1302	9	US-10-245-107-69 Sequence 69, Appl
	98	39	1.0	1302	9	US-10-245-143-69 Sequence 69, Appl
	99	39	1.0	1302	9	US-10-245-771-69 Sequence 69, Appl
	100	39	1.0	1302	9	US-10-245-851-69 Sequence 69, Appl
	101	39	1.0	1302	9	US-10-245-883-69 Sequence 69, Appl
	102	39	1.0	1302	9	US-10-237-535-69 Sequence 69, Appl
	103	39	1.0	1302	9	US-10-238-183-69 Sequence 69, Appl
	104	39	1.0	1302	9	US-10-238-283-69 Sequence 69, Appl
	105	39	1.0	1302	9	US-10-238-370-69 Sequence 69, Appl
	106	39	1.0	1302	9	US-10-245-055-69 Sequence 69, Appl
	107	39	1.0	1302	9	US-10-245-147-69 Sequence 69, Appl
	108	39	1.0	1302	9	US-10-245-730-69 Sequence 69, Appl
	109	39	1.0	1302	9	US-10-245-739-69 Sequence 69, Appl
	110	39	1.0	1302	9	US-10-246-210-69 Sequence 69, Appl
	111	39	1.0	1302	9	US-10-239-196-69 Sequence 69, Appl
	112	39	1.0	1302	9	US-10-243-024-69 Sequence 69, Appl
	113	39	1.0	1302	9	US-10-243-409-69 Sequence 69, Appl
	114	39	1.0	1302	9	US-10-245-033-69 Sequence 69, Appl
	115	39	1.0	1302	9	US-10-245-621-69 Sequence 69, Appl
	116	39	1.0	1302	9	US-10-245-880-69 Sequence 69, Appl
	117	39	1.0	1302	9	US-10-243-095-69 Sequence 69, Appl
	118	39	1.0	1302	9	US-10-245-185-69 Sequence 69, Appl
	119	39	1.0	1302	9	US-10-245-427-69 Sequence 69, Appl
	120	39	1.0	1302	9	US-10-245-473-69 Sequence 69, Appl
	121	39	1.0	1302	9	US-10-245-770-69 Sequence 69, Appl
	122	39	1.0	1302	9	US-10-245-877-69 Sequence 69, Appl
	123	39	1.0	1302	9	US-10-246-976-69 Sequence 69, Appl
	124	39	1.0	1302	9	US-10-243-320-69 Sequence 69, Appl
	125	39	1.0	1302	9	US-10-242-743-69 Sequence 69, Appl
	126	39	1.0	1302	9	US-10-242-845-69 Sequence 69, Appl
	127	39	1.0	1504	10	US-09-833-381-1137 Sequence 1137, Ap
c	128	39	1.0	1647	10	US-09-833-381-862 Sequence 862, App
c	129	39	1.0	1814	10	US-09-955-866-17 Sequence 17, Appl
c	130	39	1.0	1901	9	US-10-002-344A-130 Sequence 130, App
	131	39	1.0	2002	10	US-09-778-844-66 Sequence 66, Appl
c	132	39	1.0	2209	10	US-09-726-397A-2 Sequence 2, Appli
	133	39	1.0	2366	10	US-09-726-397A-3 Sequence 3, Appli
	134	39	1.0	2475	10	US-09-939-408A-20 Sequence 20, Appl
	135	39	1.0	2591	9	US-10-198-846-13636 Sequence 13636, A
	136	39	1.0	3032	10	US-09-833-381-1482 Sequence 1482, Ap
	137	39	1.0	3032	10	US-09-833-381-1483 Sequence 1483, Ap
	138	39	1.0	3075	10	US-09-833-381-1947 Sequence 1947, Ap
	139	39	1.0	3083	10	US-09-780-114-1 Sequence 1, Appli
c	140	39	1.0	3110	9	US-10-198-846-9938 Sequence 9938, Ap
	141	39	1.0	3114	10	US-09-833-381-1372 Sequence 1372, Ap
c	142	39	1.0	3210	9	US-09-989-920-122 Sequence 122, App
c	143	39	1.0	3720	10	US-09-107-058-1 Sequence 1, Appli
c	144	39	1.0	3720	10	US-09-761-117-1 Sequence 1, Appli
	145	39	1.0	3811	9	US-10-198-846-12380 Sequence 12380, A
	146	39	1.0	3970	9	US-10-158-646-9 Sequence 9, Appli
	147	39	1.0	4158	10	US-09-349-015-34 Sequence 34, Appl
	148	39	1.0	4428	10	US-09-833-381-1364 Sequence 1364, Ap
	149	39	1.0	4733	9	US-10-198-846-11332 Sequence 11332, A
c	150	39	1.0	5866	12	US-10-044-090-215 Sequence 215, App
c	151	39	1.0	6426	9	US-09-316-622-3 Sequence 3, Appli
c	152	39	1.0	6500	9	US-09-316-622-4 Sequence 4, Appli
	153	39	1.0	6542	9	US-10-198-846-9801 Sequence 9801, Ap
c	154	39	1.0	6652	12	US-10-044-090-762 Sequence 762, App
c	155	39	1.0	6750	9	US-09-316-622-2 Sequence 2, Appli
c	156	39	1.0	7074	9	US-09-316-622-1 Sequence 1, Appli
	157	39	1.0	9000	9	US-09-949-427-3 Sequence 3, Appli
c	158	39	1.0	10100	9	US-09-316-622-5 Sequence 5, Appli
c	159	39	1.0	10166	9	US-09-316-622-8 Sequence 8, Appli
c	160	39	1.0	10240	9	US-09-316-622-6 Sequence 6, Appli
c	161	39	1.0	10272	9	US-09-316-622-7 Sequence 7, Appli
	162	39	1.0	13608	10	US-09-861-846-3 Sequence 3, Appli
c	163	39	1.0	13608	10	US-09-861-846-3 Sequence 3, Appli
c	164	39	1.0	15515	10	US-09-822-860-3 Sequence 3, Appli
	165	39	1.0	17138	12	US-10-014-501-3 Sequence 3, Appli
c	166	39	1.0	17138	12	US-10-014-501-3 Sequence 3, Appli
	167	39	1.0	19217	10	US-09-955-866-18 Sequence 18, Appl
c	168	39	1.0	19217	10	US-09-955-866-18 Sequence 18, Appl
	169	39	1.0	21222	10	US-09-734-676-3 Sequence 3, Appli
c	170	39	1.0	23668	9	US-10-254-577-3 Sequence 3, Appli
c	171	39	1.0	23668	10	US-09-741-148A-3 Sequence 3, Appli
c	172	39	1.0	26320	9	US-10-166-221-3 Sequence 3, Appli
c	173	39	1.0	30676	10	US-09-927-091-8 Sequence 8, Appli
	174	39	1.0	31129	9	US-10-298-192-3 Sequence 3, Appli
	175	39	1.0	31766	9	US-10-288-478-5 Sequence 5, Appli
	176	39	1.0	31766	10	US-09-765-344-5 Sequence 5, Appli
	177	39	1.0	36159	12	US-10-135-687-3 Sequence 3, Appli
	178	39	1.0	40090	10	US-09-820-004-3 Sequence 3, Appli
c	179	39	1.0	41104	10	US-09-816-685-3 Sequence 3, Appli
c	180	39	1.0	64467	9	US-10-274-409-3 Sequence 3, Appli
c	181	39	1.0	65464	9	US-09-859-888-3 Sequence 3, Appli
	182	39	1.0	78785	9	US-09-978-167-3 Sequence 3, Appli
	183	39	1.0	96649	9	US-09-956-712-10 Sequence 10, Appl
c	184	39	1.0	98829	9	US-10-017-724-3 Sequence 3, Appli
c	185	39	1.0	106323	9	US-10-300-827-3 Sequence 3, Appli
c	186	39	1.0	106323	10	US-09-803-661-3 Sequence 3, Appli
	187	39	1.0	147309	10	US-09-742-312-3 Sequence 3, Appli
c	188	39	1.0	147309	10	US-09-742-312-3 Sequence 3, Appli
c	189	39	1.0	170834	10	US-09-835-232-7 Sequence 7, Appli
c	190	39	1.0	172637	10	US-09-805-458A-3 Sequence 3, Appli
	191	39	1.0	180216	10	US-09-835-232-6 Sequence 6, Appli
	192	39	1.0	202001	9	US-10-274-990-3 Sequence 3, Appli
	193	39	1.0	202001	10	US-09-734-674-3 Sequence 3, Appli
	194	39	1.0	203654	10	US-09-820-905-3 Sequence 3, Appli
	195	39	1.0	254366	9	US-09-822-871-3 Sequence 3, Appli
c	196	39	1.0	378361	9	US-09-901-136-3 Sequence 3, Appli
c	197	39	1.0	397658	10	US-09-813-320-3 Sequence 3, Appli
c	198	38	1.0	61	9	US-09-907-111-291 Sequence 291, App
	199	38	1.0	75	10	US-09-833-381-884 Sequence 884, App
c	200	38	1.0	86	10	US-09-781-902-63 Sequence 63, Appl
	201	38	1.0	87	9	US-09-916-443A-2 Sequence 2, Appli
c	202	38	1.0	87	9	US-09-916-443A-2 Sequence 2, Appli
	203	38	1.0	87	12	US-10-096-830-44 Sequence 44, Appl
c	204	38	1.0	87	12	US-10-096-830-44 Sequence 44, Appl
	205	38	1.0	90	10	US-09-780-929-100 Sequence 100, App
	206	38	1.0	96	9	US-09-851-486-36 Sequence 36, Appl
c	207	38	1.0	96	9	US-09-851-486-36 Sequence 36, Appl
	208	38	1.0	97	9	US-10-066-960-248 Sequence 248, App
c	209	38	1.0	97	9	US-10-066-960-248 Sequence 248, App
	210	38	1.0	97	9	US-10-066-960-390 Sequence 390, App
c	211	38	1.0	97	9	US-10-066-960-390 Sequence 390, App
	212	38	1.0	97	9	US-09-849-928-248 Sequence 248, App
c	213	38	1.0	97	9	US-09-849-928-248 Sequence 248, App
	214	38	1.0	97	9	US-09-849-928-390 Sequence 390, App
c	215	38	1.0	97	9	US-09-849-928-390 Sequence 390, App
	216	38	1.0	97	10	US-09-780-929-102 Sequence 102, App
c	217	38	1.0	103	9	US-09-952-680A-4 Sequence 4, Appli
	218	38	1.0	104	12	US-10-024-997-1 Sequence 1, Appli
c	219	38	1.0	104	12	US-10-024-997-1 Sequence 1, Appli
c	220	38	1.0	123	10	US-09-781-902-55 Sequence 55, Appl
	221	38	1.0	128	9	US-09-952-680A-1 Sequence 1, Appli
	222	38	1.0	147	9	US-09-916-443A-6 Sequence 6, Appli
c	223	38	1.0	147	9	US-09-916-443A-6 Sequence 6, Appli
	224	38	1.0	147	9	US-09-916-443A-7 Sequence 7, Appli
c	225	38	1.0	147	9	US-09-916-443A-7 Sequence 7, Appli
	226	38	1.0	217	9	US-10-082-830-29 Sequence 29, Appl
c	227	38	1.0	223	9	US-10-108-077-7 Sequence 7, Appli
c	228	38	1.0	223	10	US-09-867-262-6 Sequence 6, Appli
c	229	38	1.0	223	10	US-09-885-551A-7 Sequence 7, Appli
c	230	38	1.0	223	12	US-10-087-426-7 Sequence 7, Appli
c	231	38	1.0	233	10	US-09-872-153-8 Sequence 8, Appli
c	232	38	1.0	258	12	US-10-006-773-7 Sequence 7, Appli
	233	38	1.0	275	10	US-09-294-093B-290 Sequence 290, App
c	234	38	1.0	281	9	US-10-011-585A-55 Sequence 55, Appl
	235	38	1.0	282	9	US-10-016-634A-30 Sequence 30, Appl
c	236	38	1.0	284	10	US-09-294-093B-2241 Sequence 2241, Ap
	237	38	1.0	290	10	US-09-294-093B-4960 Sequence 4960, Ap
	238	38	1.0	303	9	US-09-989-920-110 Sequence 110, App

239	38	1.0	390	9	US-10-016-157A-131	Sequence 131, App
c 240	38	1.0	397	9	US-10-198-846-10914	Sequence 10914, A
241	38	1.0	418	10	US-09-833-381-785	Sequence 785, App
c 242	38	1.0	427	10	US-09-886-241-3	Sequence 3, Appli
243	38	1.0	451	9	US-09-918-995-24108	Sequence 24108, A
c 244	38	1.0	480	10	US-09-771-209-35	Sequence 35, Appl
c 245	38	1.0	483	10	US-09-895-686-36	Sequence 36, Appl
246	38	1.0	488	9	US-09-918-995-15307	Sequence 15307, A
c 247	38	1.0	502	9	US-10-011-445-24	Sequence 24, Appl
248	38	1.0	502	9	US-09-918-995-1333	Sequence 1333, Ap
c 249	38	1.0	502	9	US-09-918-995-19713	Sequence 19713, A
250	38	1.0	509	9	US-09-918-995-23157	Sequence 23157, A
251	38	1.0	535	9	US-09-292-758-76	Sequence 76, Appl
252	38	1.0	557	9	US-09-918-995-29207	Sequence 29207, A
c 253	38	1.0	564	9	US-10-198-846-10780	Sequence 10780, A
254	38	1.0	570	9	US-10-158-646-8	Sequence 8, Appli
c 255	38	1.0	570	9	US-10-158-646-8	Sequence 8, Appli
256	38	1.0	594	10	US-09-812-102-77	Sequence 77, Appl
c 257	38	1.0	598	9	US-10-198-846-8956	Sequence 8956, Ap
258	38	1.0	607	9	US-10-198-846-8124	Sequence 8124, Ap
259	38	1.0	608	9	US-10-198-846-8643	Sequence 8643, Ap
c 260	38	1.0	612	9	US-10-198-846-8479	Sequence 8479, Ap
261	38	1.0	617	9	US-10-001-876-8	Sequence 8, Appli
c 262	38	1.0	625	9	US-10-198-846-8846	Sequence 8846, Ap
c 263	38	1.0	637	9	US-10-016-634A-83	Sequence 83, Appl
264	38	1.0	654	9	US-10-001-876-103	Sequence 103, App
265	38	1.0	664	9	US-10-198-846-8060	Sequence 8060, Ap
c 266	38	1.0	664	9	US-10-198-846-8060	Sequence 8060, Ap
267	38	1.0	665	9	US-10-198-846-1717	Sequence 1717, Ap
268	38	1.0	667	9	US-10-002-344A-103	Sequence 103, App
269	38	1.0	687	10	US-09-962-436-41	Sequence 41, Appl
270	38	1.0	708	10	US-09-833-381-1258	Sequence 1258, Ap
c 271	38	1.0	727	12	US-10-001-879-84	Sequence 84, Appl
272	38	1.0	734	10	US-09-995-494-13	Sequence 13, Appl
273	38	1.0	780	9	US-09-867-915-27	Sequence 27, Appl
c 274	38	1.0	780	9	US-09-867-915-27	Sequence 27, Appl
275	38	1.0	781	10	US-09-910-943-383	Sequence 383, App
c 276	38	1.0	790	9	US-10-198-846-12288	Sequence 12288, A
c 277	38	1.0	792	9	US-10-198-846-4417	Sequence 4417, Ap
c 278	38	1.0	800	12	US-10-001-879-64	Sequence 64, Appl
c 279	38	1.0	801	9	US-10-082-830-92	Sequence 92, Appl
c 280	38	1.0	805	9	US-09-989-920-41	Sequence 41, Appl
281	38	1.0	813	9	US-10-198-846-9643	Sequence 9643, Ap
c 282	38	1.0	825	9	US-10-198-846-9241	Sequence 9241, Ap
c 283	38	1.0	829	9	US-10-198-846-5328	Sequence 5328, Ap
284	38	1.0	830	9	US-10-198-846-3049	Sequence 3049, Ap
285	38	1.0	833	9	US-10-198-846-9070	Sequence 9070, Ap
286	38	1.0	847	9	US-10-198-846-3295	Sequence 3295, Ap
c 287	38	1.0	848	9	US-10-198-846-5016	Sequence 5016, Ap
288	38	1.0	855	9	US-10-198-846-13201	Sequence 13201, A
289	38	1.0	857	9	US-10-198-846-5325	Sequence 5325, Ap
c 290	38	1.0	858	9	US-10-198-846-3300	Sequence 3300, Ap
291	38	1.0	860	9	US-10-198-846-6112	Sequence 6112, Ap
292	38	1.0	869	9	US-10-198-846-6262	Sequence 6262, Ap
293	38	1.0	871	9	US-10-198-846-3735	Sequence 3735, Ap
294	38	1.0	875	9	US-10-198-846-4245	Sequence 4245, Ap
295	38	1.0	879	9	US-10-198-846-6634	Sequence 6634, Ap
c 296	38	1.0	883	9	US-10-198-846-6966	Sequence 6966, Ap
c 297	38	1.0	886	9	US-10-198-846-3058	Sequence 3058, Ap
c 298	38	1.0	899	9	US-10-198-846-12466	Sequence 12466, A
299	38	1.0	909	9	US-10-198-846-2884	Sequence 2884, Ap
300	38	1.0	909	9	US-10-198-846-13858	Sequence 13858, A
301	38	1.0	910	9	US-10-198-846-4726	Sequence 4726, Ap
c 302	38	1.0	959	10	US-09-723-276-1	Sequence 1, Appli
c 303	38	1.0	962	9	US-10-198-846-10845	Sequence 10845, A
304	38	1.0	999	9	US-10-103-200A-17	Sequence 17, Appl
305	38	1.0	1024	9	US-10-202-193-49	Sequence 49, Appl
c 306	38	1.0	1033	9	US-10-002-344A-53	Sequence 53, Appl
307	38	1.0	1035	9	US-10-002-344A-85	Sequence 85, Appl
c 308	38	1.0	1061	9	US-10-198-846-6965	Sequence 6965, Ap
309	38	1.0	1109	10	US-09-349-015-19	Sequence 19, Appl
310	38	1.0	1118	9	US-10-198-846-5504	Sequence 5504, Ap
311	38	1.0	1134	9	US-10-002-344A-42	Sequence 42, Appl
c 312	38	1.0	1307	10	US-09-995-494-66	Sequence 66, Appl
313	38	1.0	1339	10	US-09-778-844-73	Sequence 73, Appl
314	38	1.0	1433	9	US-10-198-846-4247	Sequence 4247, Ap
315	38	1.0	1435	9	US-10-016-157A-87	Sequence 87, Appl
316	38	1.0	1461	9	US-10-198-846-13947	Sequence 13947, A
317	38	1.0	1619	9	US-10-198-846-13876	Sequence 13876, A
318	38	1.0	1626	9	US-10-198-846-13819	Sequence 13819, A
c 319	38	1.0	1704	9	US-10-011-445-41	Sequence 41, Appl
320	38	1.0	1734	10	US-09-349-015-23	Sequence 23, Appl
c 321	38	1.0	1740	10	US-09-349-015-30	Sequence 30, Appl
322	38	1.0	1753	12	US-10-044-090-314	Sequence 314, App
323	38	1.0	1810	10	US-09-833-381-1056	Sequence 1056, Ap
324	38	1.0	1815	9	US-09-771-382-22	Sequence 22, Appl
c 325	38	1.0	1824	9	US-10-198-846-11256	Sequence 11256, A
326	38	1.0	1833	9	US-10-071-766-95	Sequence 95, Appl
c 327	38	1.0	2002	10	US-09-778-844-66	Sequence 66, Appl
328	38	1.0	2033	9	US-10-198-846-9925	Sequence 9925, Ap
c 329	38	1.0	2141	9	US-09-784-554B-5	Sequence 5, Appli
330	38	1.0	2146	9	US-10-071-766-83	Sequence 83, Appl
331	38	1.0	2202	9	US-10-198-846-13731	Sequence 13731, A
332	38	1.0	2220	9	US-10-117-846-13	Sequence 13, Appl
333	38	1.0	2288	9	US-10-198-846-10854	Sequence 10854, A
c 334	38	1.0	2292	9	US-10-198-846-10658	Sequence 10658, A
c 335	38	1.0	2409	10	US-09-839-497A-8	Sequence 8, Appli
336	38	1.0	2507	12	US-10-044-090-783	Sequence 783, App
337	38	1.0	2644	10	US-09-833-381-868	Sequence 868, App
338	38	1.0	2832	10	US-09-764-864-371	Sequence 371, App
c 339	38	1.0	3075	10	US-09-833-381-1947	Sequence 1947, Ap
340	38	1.0	3110	9	US-10-198-846-9938	Sequence 9938, Ap
341	38	1.0	3207	9	US-10-071-766-88	Sequence 88, Appl
c 342	38	1.0	3337	9	US-10-198-846-10985	Sequence 10985, A
c 343	38	1.0	3607	9	US-09-981-353-155	Sequence 155, App
c 344	38	1.0	4021	9	US-10-071-766-57	Sequence 57, Appl
c 345	38	1.0	4021	12	US-10-002-600-40	Sequence 40, Appl
c 346	38	1.0	4395	9	US-10-198-846-13574	Sequence 13574, A
c 347	38	1.0	4467	10	US-09-349-015-21	Sequence 21, Appl
c 348	38	1.0	4563	12	US-10-002-600-26	Sequence 26, Appl
349	38	1.0	4576	12	US-10-044-090-703	Sequence 703, App
c 350	38	1.0	4712	9	US-09-974-298-180	Sequence 180, App
c 351	38	1.0	5394	9	US-10-071-766-74	Sequence 74, Appl
352	38	1.0	5464	10	US-09-741-153-3	Sequence 3, Appli
c 353	38	1.0	5464	10	US-09-741-153-3	Sequence 3, Appli
c 354	38	1.0	6615	9	US-10-029-413A-9	Sequence 9, Appli
355	38	1.0	7819	10	US-09-955-866-14	Sequence 14, Appl
c 356	38	1.0	7819	10	US-09-955-866-14	Sequence 14, Appl
357	38	1.0	8674	12	US-10-044-090-814	Sequence 814, App
358	38	1.0	8925	9	US-09-802-640-27	Sequence 27, Appl
359	38	1.0	9179	10	US-09-955-866-16	Sequence 16, Appl
c 360	38	1.0	9179	10	US-09-955-866-16	Sequence 16, Appl
c 361	38	1.0	13182	10	US-09-817-199A-3	Sequence 3, Appli
362	38	1.0	17752	10	US-09-748-127-3	Sequence 3, Appli
c 363	38	1.0	19806	9	US-10-118-037-3	Sequence 3, Appli
c 364	38	1.0	21784	10	US-09-820-002-3	Sequence 3, Appli
c 365	38	1.0	21990	9	US-09-942-429A-9	Sequence 9, Appli
c 366	38	1.0	31766	9	US-10-288-478-5	Sequence 5, Appli
c 367	38	1.0	31766	10	US-09-765-344-5	Sequence 5, Appli
368	38	1.0	31814	10	US-09-817-182-3	Sequence 3, Appli
c 369	38	1.0	31814	10	US-09-817-182-3	Sequence 3, Appli
c 370	38	1.0	34337	10	US-09-741-149-3	Sequence 3, Appli
c 371	38	1.0	45862	9	US-10-216-355-3	Sequence 3, Appli
c 372	38	1.0	46050	10	US-09-820-003A-3	Sequence 3, Appli
373	38	1.0	48667	10	US-09-822-268A-3	Sequence 3, Appli
c 374	38	1.0	58985	9	US-09-901-152-3	Sequence 3, Appli
375	38	1.0	63588	9	US-10-243-735-3	Sequence 3, Appli
376	38	1.0	65042	9	US-10-229-124-3	Sequence 3, Appli
c 377	38	1.0	65042	9	US-10-229-124-3	Sequence 3, Appli
378	38	1.0	65464	9	US-09-859-888-3	Sequence 3, Appli
c 379	38	1.0	69327	10	US-09-777-921A-3	Sequence 3, Appli
c 380	38	1.0	74962	9	US-10-274-974-3	Sequence 3, Appli
381	38	1.0	83450	9	US-09-811-469-3	Sequence 3, Appli
382	38	1.0	148567	9	US-10-254-869-3	Sequence 3, Appli
383	38	1.0	148567	10	US-09-801-876B-3	Sequence 3, Appli
384	38	1.0	170834	10	US-09-835-232-7	Sequence 7, Appli

385	38	1.0	172637	10	US-09-805-458A-3	Sequence 3, Appli
386	38	1.0	174493	9	US-10-238-709-3	Sequence 3, Appli
c 387	38	1.0	174493	9	US-10-238-709-3	Sequence 3, Appli
388	38	1.0	174493	10	US-09-804-471A-3	Sequence 3, Appli
c 389	38	1.0	174493	10	US-09-804-471A-3	Sequence 3, Appli
c 390	38	1.0	180216	10	US-09-835-232-6	Sequence 6, Appli
391	38	1.0	186957	9	US-10-185-770-3	Sequence 3, Appli
392	38	1.0	197997	10	US-09-822-246-3	Sequence 3, Appli
c 393	38	1.0	197997	10	US-09-822-246-3	Sequence 3, Appli
c 394	38	1.0	202001	9	US-10-274-990-3	Sequence 3, Appli
c 395	38	1.0	202001	10	US-09-734-674-3	Sequence 3, Appli
396	38	1.0	326014	10	US-09-731-231A-3	Sequence 3, Appli
c 397	38	1.0	326014	10	US-09-731-231A-3	Sequence 3, Appli
c 398	38	1.0	402850	9	US-09-844-653-5	Sequence 5, Appli
c 399	38	1.0	1503841	9	US-09-946-807-1	Sequence 1, Appli
c 400	38	1.0	1503841	10	US-09-795-668-1	Sequence 1, Appli
c 401	38	1.0	1503841	10	US-09-795-686-1	Sequence 1, Appli
c 402	37	1.0	42	9	US-10-223-126-33	Sequence 33, Appl
c 403	37	1.0	43	9	US-10-223-126-34	Sequence 34, Appl
c 404	37	1.0	44	9	US-10-223-126-35	Sequence 35, Appl
c 405	37	1.0	45	9	US-10-223-126-36	Sequence 36, Appl
c 406	37	1.0	46	9	US-10-223-126-37	Sequence 37, Appl
c 407	37	1.0	47	9	US-10-223-126-38	Sequence 38, Appl
c 408	37	1.0	48	9	US-10-223-126-39	Sequence 39, Appl
c 409	37	1.0	49	9	US-10-223-126-40	Sequence 40, Appl
c 410	37	1.0	50	9	US-10-223-126-41	Sequence 41, Appl
c 411	37	1.0	51	9	US-10-223-126-42	Sequence 42, Appl
c 412	37	1.0	52	9	US-10-223-126-43	Sequence 43, Appl
c 413	37	1.0	53	9	US-10-223-126-44	Sequence 44, Appl
c 414	37	1.0	54	9	US-10-223-126-45	Sequence 45, Appl
c 415	37	1.0	55	9	US-10-223-126-46	Sequence 46, Appl
c 416	37	1.0	56	9	US-09-997-931-73	Sequence 73, Appl
c 417	37	1.0	56	9	US-10-223-126-47	Sequence 47, Appl
c 418	37	1.0	57	9	US-10-223-126-48	Sequence 48, Appl
c 419	37	1.0	58	9	US-10-223-126-49	Sequence 49, Appl
c 420	37	1.0	59	9	US-10-223-126-50	Sequence 50, Appl
c 421	37	1.0	60	9	US-09-997-931-90	Sequence 90, Appl
c 422	37	1.0	60	9	US-10-223-126-51	Sequence 51, Appl
423	37	1.0	61	9	US-09-907-111-291	Sequence 291, App
c 424	37	1.0	61	9	US-10-223-126-52	Sequence 52, Appl
c 425	37	1.0	62	9	US-10-223-126-53	Sequence 53, Appl
c 426	37	1.0	63	9	US-10-223-126-54	Sequence 54, Appl
c 427	37	1.0	64	9	US-10-223-126-55	Sequence 55, Appl
c 428	37	1.0	65	8	US-08-681-219-35	Sequence 35, Appl
c 429	37	1.0	65	9	US-10-223-126-56	Sequence 56, Appl
c 430	37	1.0	66	9	US-10-223-126-57	Sequence 57, Appl
c 431	37	1.0	67	9	US-10-223-126-58	Sequence 58, Appl
c 432	37	1.0	68	9	US-10-223-126-59	Sequence 59, Appl
c 433	37	1.0	69	9	US-10-223-126-60	Sequence 60, Appl
c 434	37	1.0	70	9	US-10-223-126-61	Sequence 61, Appl
435	37	1.0	71	9	US-09-907-111-38	Sequence 38, Appl
c 436	37	1.0	71	9	US-09-907-111-38	Sequence 38, Appl
437	37	1.0	71	9	US-10-066-960-64	Sequence 64, Appl
c 438	37	1.0	71	9	US-10-066-960-64	Sequence 64, Appl
439	37	1.0	71	9	US-10-066-960-389	Sequence 389, App
c 440	37	1.0	71	9	US-10-066-960-389	Sequence 389, App
441	37	1.0	71	9	US-09-849-928-64	Sequence 64, Appl
c 442	37	1.0	71	9	US-09-849-928-64	Sequence 64, Appl
443	37	1.0	71	9	US-09-849-928-389	Sequence 389, App
c 444	37	1.0	71	9	US-09-849-928-389	Sequence 389, App
c 445	37	1.0	71	9	US-10-223-126-62	Sequence 62, Appl
446	37	1.0	71	10	US-09-978-969-1	Sequence 1, Appli
c 447	37	1.0	71	10	US-09-978-969-1	Sequence 1, Appli
c 448	37	1.0	72	9	US-10-223-126-63	Sequence 63, Appl
c 449	37	1.0	73	9	US-10-223-126-64	Sequence 64, Appl
450	37	1.0	74	9	US-09-201-396-18	Sequence 18, Appl
c 451	37	1.0	74	9	US-10-223-126-65	Sequence 65, Appl
c 452	37	1.0	75	9	US-10-223-126-66	Sequence 66, Appl
c 453	37	1.0	76	9	US-10-223-126-67	Sequence 67, Appl
454	37	1.0	76	10	US-09-815-171A-6	Sequence 6, Appli
c 455	37	1.0	77	9	US-10-223-126-68	Sequence 68, Appl
c 456	37	1.0	78	9	US-10-223-126-69	Sequence 69, Appl
c 457	37	1.0	79	9	US-10-223-126-70	Sequence 70, Appl
458	37	1.0	80	9	US-10-172-620-8	Sequence 8, Appli
c 459	37	1.0	80	9	US-10-172-620-8	Sequence 8, Appli
c 460	37	1.0	80	9	US-10-223-126-71	Sequence 71, Appl
461	37	1.0	81	9	US-09-860-474-60	Sequence 60, Appl
c 462	37	1.0	81	9	US-09-860-474-60	Sequence 60, Appl
463	37	1.0	81	9	US-10-037-282-157	Sequence 157, App
c 464	37	1.0	81	9	US-10-037-282-157	Sequence 157, App
c 465	37	1.0	81	9	US-10-223-126-72	Sequence 72, Appl
c 466	37	1.0	82	9	US-10-223-126-73	Sequence 73, Appl
467	37	1.0	83	9	US-10-101-461-12	Sequence 12, Appl
c 468	37	1.0	83	9	US-10-223-126-74	Sequence 74, Appl
c 469	37	1.0	84	9	US-10-223-126-75	Sequence 75, Appl
470	37	1.0	85	9	US-09-201-396-26	Sequence 26, Appl
c 471	37	1.0	85	9	US-10-223-126-76	Sequence 76, Appl
472	37	1.0	86	9	US-10-040-497-43	Sequence 43, Appl
c 473	37	1.0	86	9	US-10-223-126-77	Sequence 77, Appl
c 474	37	1.0	87	9	US-10-223-126-78	Sequence 78, Appl
c 475	37	1.0	88	9	US-10-223-126-79	Sequence 79, Appl
c 476	37	1.0	89	9	US-10-223-126-80	Sequence 80, Appl
c 477	37	1.0	90	9	US-10-223-126-81	Sequence 81, Appl
478	37	1.0	90	10	US-09-822-698A-35	Sequence 35, Appl
c 479	37	1.0	90	10	US-09-780-929-100	Sequence 100, App
c 480	37	1.0	91	9	US-10-223-126-82	Sequence 82, Appl
c 481	37	1.0	92	9	US-10-223-126-83	Sequence 83, Appl
482	37	1.0	92	10	US-09-815-171A-7	Sequence 7, Appli
c 483	37	1.0	92	10	US-09-815-171A-8	Sequence 8, Appli
484	37	1.0	92	10	US-09-815-171A-9	Sequence 9, Appli
c 485	37	1.0	92	10	US-09-815-171A-9	Sequence 9, Appli
c 486	37	1.0	92	10	US-09-815-171A-10	Sequence 10, Appl
c 487	37	1.0	92	10	US-09-815-171A-11	Sequence 11, Appl
488	37	1.0	92	10	US-09-815-171A-13	Sequence 13, Appl
c 489	37	1.0	92	10	US-09-815-171A-13	Sequence 13, Appl
c 490	37	1.0	93	9	US-10-223-126-84	Sequence 84, Appl
c 491	37	1.0	94	9	US-10-223-126-85	Sequence 85, Appl
c 492	37	1.0	95	9	US-10-223-126-86	Sequence 86, Appl
c 493	37	1.0	96	9	US-10-223-126-87	Sequence 87, Appl
c 494	37	1.0	97	9	US-10-223-126-88	Sequence 88, Appl
c 495	37	1.0	97	10	US-09-780-929-102	Sequence 102, App
496	37	1.0	98	9	US-10-066-960-1	Sequence 1, Appli
497	37	1.0	98	9	US-09-849-928-1	Sequence 1, Appli
498	37	1.0	98	9	US-10-037-282-156	Sequence 156, App
c 499	37	1.0	98	9	US-10-037-282-156	Sequence 156, App
c 500	37	1.0	98	9	US-10-223-126-89	Sequence 89, Appl
c 501	37	1.0	99	9	US-10-223-126-90	Sequence 90, Appl
c 502	37	1.0	100	9	US-10-223-126-91	Sequence 91, Appl
503	37	1.0	101	9	US-09-821-160A-14	Sequence 14, Appl
c 504	37	1.0	101	9	US-09-821-160A-14	Sequence 14, Appl
c 505	37	1.0	101	9	US-10-223-126-92	Sequence 92, Appl
c 506	37	1.0	102	9	US-09-879-813-48	Sequence 48, Appl
c 507	37	1.0	102	9	US-10-223-126-93	Sequence 93, Appl
c 508	37	1.0	103	9	US-09-997-931-101	Sequence 101, App
c 509	37	1.0	103	9	US-10-223-126-94	Sequence 94, Appl
c 510	37	1.0	104	9	US-10-223-126-95	Sequence 95, Appl
c 511	37	1.0	105	9	US-10-223-126-96	Sequence 96, Appl
c 512	37	1.0	106	9	US-10-223-126-97	Sequence 97, Appl
c 513	37	1.0	107	9	US-10-223-126-98	Sequence 98, Appl
c 514	37	1.0	108	9	US-10-223-126-99	Sequence 99, Appl
c 515	37	1.0	109	9	US-10-223-126-100	Sequence 100, App
c 516	37	1.0	110	9	US-10-223-126-101	Sequence 101, App
c 517	37	1.0	111	9	US-10-223-126-102	Sequence 102, App
c 518	37	1.0	112	9	US-10-223-126-103	Sequence 103, App
c 519	37	1.0	113	9	US-10-223-126-104	Sequence 104, App
c 520	37	1.0	114	9	US-10-223-126-105	Sequence 105, App
c 521	37	1.0	115	9	US-10-223-126-106	Sequence 106, App
c 522	37	1.0	116	9	US-10-223-126-107	Sequence 107, App
c 523	37	1.0	117	9	US-10-223-126-108	Sequence 108, App
c 524	37	1.0	118	9	US-10-223-126-109	Sequence 109, App
c 525	37	1.0	119	9	US-10-223-126-110	Sequence 110, App
c 526	37	1.0	120	9	US-10-223-126-111	Sequence 111, App
c 527	37	1.0	121	9	US-10-108-077-10	Sequence 10, Appl
c 528	37	1.0	121	9	US-10-223-126-112	Sequence 112, App
c 529	37	1.0	121	10	US-09-867-262-9	Sequence 9, Appli
c 530	37	1.0	121	10	US-09-885-551A-10	Sequence 10, Appl

c 531	37	1.0	121	12	US-10-087-426-10	Sequence 10, Appl
c 532	37	1.0	122	9	US-10-223-126-113	Sequence 113, App
c 533	37	1.0	123	9	US-10-108-077-9	Sequence 9, Appli
c 534	37	1.0	123	9	US-10-223-126-114	Sequence 114, App
c 535	37	1.0	123	10	US-09-867-262-8	Sequence 8, Appli
c 536	37	1.0	123	10	US-09-885-551A-9	Sequence 9, Appli
c 537	37	1.0	123	12	US-10-087-426-9	Sequence 9, Appli
c 538	37	1.0	124	9	US-10-223-126-115	Sequence 115, App
c 539	37	1.0	125	9	US-10-223-126-116	Sequence 116, App
c 540	37	1.0	126	9	US-10-223-126-117	Sequence 117, App
c 541	37	1.0	127	9	US-10-223-126-118	Sequence 118, App
c 542	37	1.0	128	9	US-10-223-126-119	Sequence 119, App
c 543	37	1.0	129	9	US-10-223-126-120	Sequence 120, App
544	37	1.0	130	9	US-09-879-813-52	Sequence 52, Appl
c 545	37	1.0	130	9	US-09-879-813-52	Sequence 52, Appl
c 546	37	1.0	130	9	US-10-223-126-121	Sequence 121, App
c 547	37	1.0	131	9	US-10-223-126-122	Sequence 122, App
c 548	37	1.0	132	9	US-10-223-126-123	Sequence 123, App
c 549	37	1.0	133	9	US-10-223-126-124	Sequence 124, App
c 550	37	1.0	134	9	US-10-223-126-125	Sequence 125, App
c 551	37	1.0	135	9	US-10-223-126-126	Sequence 126, App
c 552	37	1.0	136	9	US-10-223-126-127	Sequence 127, App
c 553	37	1.0	137	9	US-10-223-126-128	Sequence 128, App
c 554	37	1.0	138	9	US-10-223-126-129	Sequence 129, App
c 555	37	1.0	139	9	US-10-223-126-130	Sequence 130, App
c 556	37	1.0	140	9	US-10-223-126-131	Sequence 131, App
c 557	37	1.0	141	9	US-10-223-126-132	Sequence 132, App
c 558	37	1.0	142	9	US-10-223-126-133	Sequence 133, App
c 559	37	1.0	143	9	US-10-223-126-134	Sequence 134, App
c 560	37	1.0	144	9	US-10-223-126-135	Sequence 135, App
c 561	37	1.0	145	9	US-10-223-126-136	Sequence 136, App
c 562	37	1.0	146	9	US-10-223-126-137	Sequence 137, App
c 563	37	1.0	147	9	US-10-223-126-138	Sequence 138, App
c 564	37	1.0	147	9	US-10-223-126-139	Sequence 139, App
c 565	37	1.0	149	9	US-10-223-126-140	Sequence 140, App
c 566	37	1.0	150	9	US-10-223-126-141	Sequence 141, App
c 567	37	1.0	151	9	US-10-223-126-142	Sequence 142, App
c 568	37	1.0	152	9	US-10-223-126-143	Sequence 143, App
c 569	37	1.0	153	9	US-10-223-126-144	Sequence 144, App
c 570	37	1.0	154	9	US-09-884-566-7	Sequence 7, Appli
c 571	37	1.0	154	9	US-10-223-126-145	Sequence 145, App
c 572	37	1.0	154	9	US-10-223-126-147	Sequence 147, App
c 573	37	1.0	155	9	US-10-223-126-146	Sequence 146, App
c 574	37	1.0	157	9	US-10-223-126-148	Sequence 148, App
c 575	37	1.0	158	9	US-10-223-126-149	Sequence 149, App
c 576	37	1.0	159	9	US-10-223-126-150	Sequence 150, App
c 577	37	1.0	160	9	US-10-223-126-151	Sequence 151, App
c 578	37	1.0	161	9	US-10-223-126-152	Sequence 152, App
c 579	37	1.0	162	9	US-10-223-126-153	Sequence 153, App
c 580	37	1.0	163	9	US-10-223-126-154	Sequence 154, App
c 581	37	1.0	166	9	US-09-879-813-31	Sequence 31, Appl
582	37	1.0	171	10	US-09-910-943-184	Sequence 184, App
c 583	37	1.0	171	10	US-09-910-943-184	Sequence 184, App
584	37	1.0	193	9	US-10-082-830-116	Sequence 116, App
c 585	37	1.0	193	9	US-10-082-830-116	Sequence 116, App
c 586	37	1.0	195	9	US-10-253-007-64	Sequence 64, Appl
c 587	37	1.0	215	9	US-10-108-077-8	Sequence 8, Appli
c 588	37	1.0	215	10	US-09-867-262-7	Sequence 7, Appli
c 589	37	1.0	215	10	US-09-885-551A-8	Sequence 8, Appli
c 590	37	1.0	215	12	US-10-087-426-8	Sequence 8, Appli
c 591	37	1.0	217	9	US-10-082-830-29	Sequence 29, Appl
592	37	1.0	229	10	US-09-923-876-2247	Sequence 2247, Ap
c 593	37	1.0	229	10	US-09-923-876-2247	Sequence 2247, Ap
594	37	1.0	252	9	US-10-198-846-9990	Sequence 9990, Ap
c 595	37	1.0	257	9	US-10-007-280A-25	Sequence 25, Appl
596	37	1.0	258	9	US-10-198-846-10304	Sequence 10304, A
597	37	1.0	258	12	US-10-006-773-7	Sequence 7, Appli
598	37	1.0	268	10	US-09-848-889-4	Sequence 4, Appli
c 599	37	1.0	268	10	US-09-848-889-4	Sequence 4, Appli
600	37	1.0	270	10	US-09-923-876-4507	Sequence 4507, Ap
601	37	1.0	289	10	US-09-294-093B-3157	Sequence 3157, Ap
c 602	37	1.0	289	10	US-09-294-093B-3157	Sequence 3157, Ap
603	37	1.0	291	10	US-09-833-381-140	Sequence 140, App
604	37	1.0	297	9	US-10-043-487-66	Sequence 66, Appl
c 605	37	1.0	299	9	US-10-043-487-94	Sequence 94, Appl
606	37	1.0	300	10	US-09-294-093B-5686	Sequence 5686, Ap
607	37	1.0	317	10	US-09-294-093B-5547	Sequence 5547, Ap
608	37	1.0	326	10	US-09-878-574-4464	Sequence 4464, Ap
c 609	37	1.0	326	10	US-09-878-574-4464	Sequence 4464, Ap
c 610	37	1.0	328	9	US-10-082-830-132	Sequence 132, App
c 611	37	1.0	344	9	US-10-001-857-10	Sequence 10, Appl
612	37	1.0	345	9	US-09-999-025-16	Sequence 16, Appl
613	37	1.0	345	9	US-09-999-040-16	Sequence 16, Appl
614	37	1.0	345	9	US-09-998-817-16	Sequence 16, Appl
615	37	1.0	345	9	US-09-999-021-16	Sequence 16, Appl
616	37	1.0	345	9	US-10-040-997-16	Sequence 16, Appl
c 617	37	1.0	345	9	US-09-918-995-29865	Sequence 29865, A
618	37	1.0	353	9	US-10-000-256A-80	Sequence 80, Appl
c 619	37	1.0	360	9	US-10-002-344A-55	Sequence 55, Appl
c 620	37	1.0	360	9	US-09-918-995-7501	Sequence 7501, Ap
621	37	1.0	373	9	US-10-016-157A-122	Sequence 122, App
c 622	37	1.0	374	9	US-09-918-995-33771	Sequence 33771, A
c 623	37	1.0	390	9	US-10-016-157A-131	Sequence 131, App
624	37	1.0	390	9	US-10-082-830-10	Sequence 10, Appl
c 625	37	1.0	390	10	US-09-872-153-7	Sequence 7, Appli
c 626	37	1.0	401	9	US-09-918-995-4092	Sequence 4092, Ap
627	37	1.0	403	9	US-10-198-846-6128	Sequence 6128, Ap
628	37	1.0	406	9	US-09-918-995-16807	Sequence 16807, A
c 629	37	1.0	407	9	US-09-918-995-14312	Sequence 14312, A
c 630	37	1.0	408	12	US-10-001-879-48	Sequence 48, Appl
631	37	1.0	416	9	US-10-198-846-9365	Sequence 9365, Ap
c 632	37	1.0	422	9	US-10-198-846-3252	Sequence 3252, Ap
633	37	1.0	422	10	US-09-833-381-239	Sequence 239, App
c 634	37	1.0	424	9	US-09-918-995-35911	Sequence 35911, A
635	37	1.0	430	9	US-10-016-634A-67	Sequence 67, Appl
c 636	37	1.0	430	9	US-10-016-634A-67	Sequence 67, Appl
c 637	37	1.0	440	9	US-10-000-256A-114	Sequence 114, App
c 638	37	1.0	441	9	US-10-198-846-4895	Sequence 4895, Ap
c 639	37	1.0	442	10	US-09-812-102-11	Sequence 11, Appl
c 640	37	1.0	444	9	US-09-918-995-31562	Sequence 31562, A
c 641	37	1.0	449	9	US-10-198-846-13613	Sequence 13613, A
c 642	37	1.0	453	9	US-10-198-846-12821	Sequence 12821, A
643	37	1.0	456	9	US-10-002-344A-106	Sequence 106, App
c 644	37	1.0	461	9	US-09-918-995-20879	Sequence 20879, A
645	37	1.0	464	9	US-10-198-846-12147	Sequence 12147, A
646	37	1.0	465	9	US-10-071-766-75	Sequence 75, Appl
c 647	37	1.0	466	9	US-10-198-846-9502	Sequence 9502, Ap
c 648	37	1.0	470	9	US-09-918-995-12497	Sequence 12497, A
649	37	1.0	471	9	US-09-918-995-15927	Sequence 15927, A
c 650	37	1.0	473	9	US-09-918-995-24807	Sequence 24807, A
c 651	37	1.0	475	9	US-09-918-995-32075	Sequence 32075, A
652	37	1.0	476	10	US-09-833-381-493	Sequence 493, App
653	37	1.0	477	9	US-09-918-995-13559	Sequence 13559, A
654	37	1.0	477	9	US-09-918-995-19447	Sequence 19447, A
655	37	1.0	480	10	US-09-771-209-35	Sequence 35, Appl
656	37	1.0	481	9	US-09-918-995-20978	Sequence 20978, A
657	37	1.0	488	9	US-10-078-090-45	Sequence 45, Appl
c 658	37	1.0	488	9	US-10-007-280A-84	Sequence 84, Appl
659	37	1.0	488	9	US-09-918-995-13632	Sequence 13632, A
c 660	37	1.0	489	9	US-10-001-883-30	Sequence 30, Appl
c 661	37	1.0	490	9	US-09-918-995-32519	Sequence 32519, A
662	37	1.0	491	9	US-09-918-995-22560	Sequence 22560, A
663	37	1.0	492	9	US-09-918-995-2286	Sequence 2286, Ap
664	37	1.0	492	9	US-09-918-995-9264	Sequence 9264, Ap
c 665	37	1.0	492	9	US-09-918-995-19293	Sequence 19293, A
c 666	37	1.0	492	9	US-09-918-995-19506	Sequence 19506, A
667	37	1.0	493	9	US-09-736-457-13	Sequence 13, Appl
668	37	1.0	493	9	US-09-902-941-13	Sequence 13, Appl
669	37	1.0	493	9	US-09-849-626-13	Sequence 13, Appl
670	37	1.0	493	9	US-10-017-754-13	Sequence 13, Appl
c 671	37	1.0	493	9	US-09-918-995-11006	Sequence 11006, A
c 672	37	1.0	493	9	US-09-918-995-15639	Sequence 15639, A
c 673	37	1.0	493	9	US-09-918-995-20998	Sequence 20998, A
c 674	37	1.0	493	9	US-10-198-846-9528	Sequence 9528, Ap
c 675	37	1.0	494	9	US-09-918-995-2820	Sequence 2820, Ap
676	37	1.0	497	12	US-10-001-879-97	Sequence 97, Appl

c 677	37	1.0	500	9	US-09-918-995-10695	Sequence 10695, A
678	37	1.0	506	9	US-09-918-995-12167	Sequence 12167, A
679	37	1.0	506	9	US-09-918-995-19851	Sequence 19851, A
680	37	1.0	507	9	US-09-918-995-20255	Sequence 20255, A
681	37	1.0	515	9	US-10-007-280A-42	Sequence 42, Appl
682	37	1.0	515	9	US-09-918-995-30655	Sequence 30655, A
c 683	37	1.0	515	9	US-09-918-995-30655	Sequence 30655, A
684	37	1.0	515	9	US-10-198-846-8481	Sequence 8481, Ap
685	37	1.0	515	9	US-10-198-846-9239	Sequence 9239, Ap
686	37	1.0	524	10	US-09-833-381-492	Sequence 492, App
c 687	37	1.0	526	10	US-09-954-456-1885	Sequence 1885, Ap
c 688	37	1.0	527	9	US-10-000-256A-52	Sequence 52, Appl
689	37	1.0	529	9	US-10-002-344A-79	Sequence 79, Appl
c 690	37	1.0	530	9	US-09-989-920-44	Sequence 44, Appl
691	37	1.0	530	9	US-10-007-280A-43	Sequence 43, Appl
c 692	37	1.0	531	9	US-10-198-846-9095	Sequence 9095, Ap
693	37	1.0	532	9	US-10-198-846-13798	Sequence 13798, A
c 694	37	1.0	535	9	US-09-292-758-76	Sequence 76, Appl
c 695	37	1.0	537	9	US-10-000-256A-55	Sequence 55, Appl
696	37	1.0	537	9	US-09-918-995-28028	Sequence 28028, A
c 697	37	1.0	544	10	US-09-757-781-45	Sequence 45, Appl
c 698	37	1.0	548	9	US-10-016-157A-28	Sequence 28, Appl
699	37	1.0	549	9	US-09-918-995-16128	Sequence 16128, A
700	37	1.0	550	9	US-10-198-846-13099	Sequence 13099, A
701	37	1.0	552	9	US-09-918-995-12506	Sequence 12506, A
c 702	37	1.0	554	9	US-10-074-475-60	Sequence 60, Appl
703	37	1.0	557	12	US-10-001-843-4	Sequence 4, Appli
704	37	1.0	562	9	US-10-011-585A-125	Sequence 125, App
705	37	1.0	562	9	US-09-918-995-12370	Sequence 12370, A
706	37	1.0	565	9	US-10-198-846-10923	Sequence 10923, A
707	37	1.0	566	9	US-10-198-846-12670	Sequence 12670, A
c 708	37	1.0	569	9	US-09-918-995-15940	Sequence 15940, A
c 709	37	1.0	572	9	US-10-007-280A-64	Sequence 64, Appl
710	37	1.0	573	10	US-09-833-381-677	Sequence 677, App
c 711	37	1.0	574	9	US-10-198-846-8326	Sequence 8326, Ap
712	37	1.0	575	9	US-09-918-995-26554	Sequence 26554, A
c 713	37	1.0	576	9	US-09-918-995-15389	Sequence 15389, A
c 714	37	1.0	576	9	US-10-198-846-9129	Sequence 9129, Ap
715	37	1.0	580	10	US-09-833-381-676	Sequence 676, App
c 716	37	1.0	585	9	US-10-082-830-38	Sequence 38, Appl
717	37	1.0	587	9	US-09-918-995-15078	Sequence 15078, A
718	37	1.0	590	10	US-09-880-107-3485	Sequence 3485, Ap
c 719	37	1.0	592	9	US-10-198-846-8360	Sequence 8360, Ap
c 720	37	1.0	592	9	US-10-198-846-8381	Sequence 8381, Ap
721	37	1.0	592	10	US-09-765-231A-9	Sequence 9, Appli
c 722	37	1.0	593	9	US-10-198-846-8741	Sequence 8741, Ap
c 723	37	1.0	597	9	US-10-198-846-9361	Sequence 9361, Ap
c 724	37	1.0	598	9	US-10-198-846-5370	Sequence 5370, Ap
c 725	37	1.0	598	10	US-09-812-102-31	Sequence 31, Appl
726	37	1.0	604	9	US-10-198-846-9019	Sequence 9019, Ap
c 727	37	1.0	604	9	US-10-198-846-9019	Sequence 9019, Ap
728	37	1.0	605	9	US-10-284-985-19	Sequence 19, Appl
c 729	37	1.0	605	9	US-10-284-985-19	Sequence 19, Appl
c 730	37	1.0	606	9	US-10-034-934-9	Sequence 9, Appli
731	37	1.0	611	9	US-10-198-846-8503	Sequence 8503, Ap
732	37	1.0	611	9	US-10-198-846-8565	Sequence 8565, Ap
733	37	1.0	612	9	US-10-002-344A-83	Sequence 83, Appl
c 734	37	1.0	613	9	US-10-198-846-8743	Sequence 8743, Ap
c 735	37	1.0	614	9	US-10-198-846-8324	Sequence 8324, Ap
c 736	37	1.0	614	9	US-10-198-846-8745	Sequence 8745, Ap
c 737	37	1.0	616	9	US-10-198-846-9541	Sequence 9541, Ap
738	37	1.0	617	9	US-10-011-445-35	Sequence 35, Appl
c 739	37	1.0	617	9	US-10-011-445-35	Sequence 35, Appl
740	37	1.0	618	9	US-10-198-846-9198	Sequence 9198, Ap
741	37	1.0	619	9	US-10-082-830-35	Sequence 35, Appl
c 742	37	1.0	620	9	US-10-198-846-7949	Sequence 7949, Ap
c 743	37	1.0	620	9	US-10-198-846-9548	Sequence 9548, Ap
744	37	1.0	622	9	US-10-198-846-5452	Sequence 5452, Ap
c 745	37	1.0	622	9	US-10-198-846-8454	Sequence 8454, Ap
746	37	1.0	622	9	US-10-198-846-12806	Sequence 12806, A
c 747	37	1.0	624	9	US-10-198-846-8333	Sequence 8333, Ap
748	37	1.0	630	9	US-10-198-846-7990	Sequence 7990, Ap
749	37	1.0	631	9	US-10-198-846-8328	Sequence 8328, Ap
c 750	37	1.0	632	9	US-10-198-846-4836	Sequence 4836, Ap
751	37	1.0	634	9	US-10-198-846-8831	Sequence 8831, Ap
c 752	37	1.0	634	9	US-10-198-846-8831	Sequence 8831, Ap
c 753	37	1.0	635	9	US-10-198-846-8868	Sequence 8868, Ap
754	37	1.0	635	9	US-10-198-846-9655	Sequence 9655, Ap
c 755	37	1.0	635	9	US-10-198-846-9655	Sequence 9655, Ap
756	37	1.0	637	9	US-10-016-634A-83	Sequence 83, Appl
c 757	37	1.0	639	9	US-10-198-846-9050	Sequence 9050, Ap
758	37	1.0	639	10	US-09-880-107-3484	Sequence 3484, Ap
759	37	1.0	641	9	US-10-198-846-6063	Sequence 6063, Ap
c 760	37	1.0	641	9	US-10-198-846-6063	Sequence 6063, Ap
c 761	37	1.0	641	9	US-10-198-846-8541	Sequence 8541, Ap
c 762	37	1.0	641	9	US-10-198-846-8991	Sequence 8991, Ap
c 763	37	1.0	642	9	US-10-198-846-8266	Sequence 8266, Ap
c 764	37	1.0	643	9	US-10-198-846-6061	Sequence 6061, Ap
765	37	1.0	646	10	US-09-771-209-23	Sequence 23, Appl
c 766	37	1.0	646	10	US-09-771-209-23	Sequence 23, Appl
767	37	1.0	646	10	US-09-771-209-25	Sequence 25, Appl
c 768	37	1.0	646	10	US-09-771-209-25	Sequence 25, Appl
c 769	37	1.0	647	9	US-10-198-846-2767	Sequence 2767, Ap
c 770	37	1.0	647	9	US-10-198-846-8338	Sequence 8338, Ap
c 771	37	1.0	648	9	US-10-198-846-8163	Sequence 8163, Ap
772	37	1.0	650	9	US-10-198-846-6060	Sequence 6060, Ap
c 773	37	1.0	650	9	US-10-198-846-9306	Sequence 9306, Ap
c 774	37	1.0	650	10	US-09-955-866-15	Sequence 15, Appl
c 775	37	1.0	651	9	US-10-198-846-8980	Sequence 8980, Ap
c 776	37	1.0	654	9	US-10-198-846-2091	Sequence 2091, Ap
777	37	1.0	655	9	US-10-198-846-9659	Sequence 9659, Ap
778	37	1.0	655	10	US-09-880-107-3489	Sequence 3489, Ap
c 779	37	1.0	657	9	US-10-198-846-8304	Sequence 8304, Ap
780	37	1.0	657	10	US-09-880-107-3487	Sequence 3487, Ap
c 781	37	1.0	657	10	US-09-880-107-3487	Sequence 3487, Ap
782	37	1.0	661	10	US-09-880-107-3488	Sequence 3488, Ap
c 783	37	1.0	661	10	US-09-880-107-3488	Sequence 3488, Ap
c 784	37	1.0	663	9	US-10-198-846-9197	Sequence 9197, Ap
c 785	37	1.0	664	9	US-10-000-256A-10	Sequence 10, Appl
786	37	1.0	664	9	US-10-198-846-2402	Sequence 2402, Ap
c 787	37	1.0	664	9	US-10-198-846-8856	Sequence 8856, Ap
788	37	1.0	665	9	US-10-198-846-13821	Sequence 13821, A
789	37	1.0	666	9	US-10-198-846-8497	Sequence 8497, Ap
c 790	37	1.0	667	12	US-10-001-870-92	Sequence 92, Appl
c 791	37	1.0	672	9	US-10-198-846-7865	Sequence 7865, Ap
792	37	1.0	672	9	US-10-198-846-8818	Sequence 8818, Ap
793	37	1.0	672	9	US-10-198-846-9524	Sequence 9524, Ap
794	37	1.0	675	9	US-10-198-846-8672	Sequence 8672, Ap
795	37	1.0	678	9	US-10-198-846-12844	Sequence 12844, A
c 796	37	1.0	679	9	US-10-198-846-9169	Sequence 9169, Ap
c 797	37	1.0	684	9	US-10-198-846-2063	Sequence 2063, Ap
c 798	37	1.0	688	9	US-10-080-980-8	Sequence 8, Appli
799	37	1.0	695	9	US-10-016-157A-69	Sequence 69, Appl
800	37	1.0	698	9	US-10-001-835-50	Sequence 50, Appl
c 801	37	1.0	701	9	US-10-198-846-2832	Sequence 2832, Ap
802	37	1.0	702	9	US-10-198-846-2127	Sequence 2127, Ap
c 803	37	1.0	702	9	US-10-198-846-2153	Sequence 2153, Ap
c 804	37	1.0	702	9	US-10-198-846-7891	Sequence 7891, Ap
c 805	37	1.0	704	9	US-10-198-846-3574	Sequence 3574, Ap
806	37	1.0	706	9	US-10-198-846-8653	Sequence 8653, Ap
c 807	37	1.0	707	9	US-10-198-846-8343	Sequence 8343, Ap
808	37	1.0	709	9	US-10-198-846-2420	Sequence 2420, Ap
c 809	37	1.0	709	9	US-10-198-846-2445	Sequence 2445, Ap
c 810	37	1.0	709	9	US-10-198-846-6290	Sequence 6290, Ap
811	37	1.0	710	9	US-10-198-846-2422	Sequence 2422, Ap
c 812	37	1.0	710	9	US-10-198-846-3573	Sequence 3573, Ap
c 813	37	1.0	712	9	US-10-198-846-2859	Sequence 2859, Ap
814	37	1.0	712	10	US-09-834-975-804	Sequence 804, App
815	37	1.0	713	9	US-09-989-920-39	Sequence 39, Appl
c 816	37	1.0	716	9	US-10-198-846-3572	Sequence 3572, Ap
817	37	1.0	716	9	US-10-198-846-3587	Sequence 3587, Ap
c 818	37	1.0	716	9	US-10-198-846-3587	Sequence 3587, Ap
c 819	37	1.0	719	9	US-10-198-846-3579	Sequence 3579, Ap
c 820	37	1.0	720	9	US-10-198-846-3593	Sequence 3593, Ap
c 821	37	1.0	721	9	US-10-198-846-5137	Sequence 5137, Ap
822	37	1.0	721	9	US-10-198-846-8725	Sequence 8725, Ap

c 823	37	1.0	721	9	US-10-198-846-8725	Sequence 8725, Ap
c 824	37	1.0	724	9	US-10-016-157A-93	Sequence 93, Appl
c 825	37	1.0	725	9	US-10-198-846-5119	Sequence 5119, Ap
c 826	37	1.0	726	9	US-10-000-256A-11	Sequence 11, Appl
c 827	37	1.0	727	9	US-10-198-846-2421	Sequence 2421, Ap
828	37	1.0	727	12	US-10-001-879-84	Sequence 84, Appl
829	37	1.0	729	9	US-10-198-846-5123	Sequence 5123, Ap
830	37	1.0	733	9	US-10-034-934-27	Sequence 27, Appl
c 831	37	1.0	733	9	US-10-034-934-27	Sequence 27, Appl
832	37	1.0	733	9	US-10-198-846-3580	Sequence 3580, Ap
c 833	37	1.0	733	9	US-10-198-846-9379	Sequence 9379, Ap
834	37	1.0	736	10	US-09-833-381-1010	Sequence 1010, Ap
c 835	37	1.0	736	10	US-09-833-381-1010	Sequence 1010, Ap
c 836	37	1.0	737	9	US-10-198-846-3741	Sequence 3741, Ap
837	37	1.0	744	9	US-09-954-531-1036	Sequence 1036, Ap
c 838	37	1.0	744	9	US-10-198-846-8944	Sequence 8944, Ap
839	37	1.0	747	10	US-09-919-580-928	Sequence 928, App
c 840	37	1.0	749	9	US-10-198-846-8973	Sequence 8973, Ap
841	37	1.0	751	10	US-09-833-381-924	Sequence 924, App
842	37	1.0	758	9	US-10-198-846-5122	Sequence 5122, Ap
c 843	37	1.0	758	9	US-10-198-846-5122	Sequence 5122, Ap
844	37	1.0	759	9	US-10-198-846-9651	Sequence 9651, Ap
c 845	37	1.0	759	9	US-10-198-846-9651	Sequence 9651, Ap
846	37	1.0	762	9	US-10-198-846-10368	Sequence 10368, A
847	37	1.0	764	10	US-09-910-943-398	Sequence 398, App
848	37	1.0	768	9	US-10-198-846-8094	Sequence 8094, Ap
c 849	37	1.0	768	9	US-10-198-846-8094	Sequence 8094, Ap
850	37	1.0	768	9	US-10-198-846-8966	Sequence 8966, Ap
c 851	37	1.0	768	9	US-10-198-846-8966	Sequence 8966, Ap
c 852	37	1.0	771	9	US-10-002-344A-112	Sequence 112, App
c 853	37	1.0	773	9	US-10-007-280A-38	Sequence 38, Appl
c 854	37	1.0	777	12	US-10-001-879-63	Sequence 63, Appl
c 855	37	1.0	778	9	US-10-198-846-9608	Sequence 9608, Ap
c 856	37	1.0	781	9	US-10-198-846-9089	Sequence 9089, Ap
c 857	37	1.0	783	9	US-10-198-846-6256	Sequence 6256, Ap
c 858	37	1.0	784	9	US-10-198-846-9626	Sequence 9626, Ap
c 859	37	1.0	784	10	US-09-833-381-1255	Sequence 1255, Ap
c 860	37	1.0	786	9	US-10-198-846-4405	Sequence 4405, Ap
861	37	1.0	787	9	US-09-989-920-145	Sequence 145, App
c 862	37	1.0	787	9	US-09-989-920-145	Sequence 145, App
c 863	37	1.0	788	9	US-10-198-846-10966	Sequence 10966, A
864	37	1.0	789	9	US-10-198-846-7451	Sequence 7451, Ap
c 865	37	1.0	789	9	US-10-198-846-7451	Sequence 7451, Ap
866	37	1.0	793	9	US-10-198-846-6887	Sequence 6887, Ap
c 867	37	1.0	793	9	US-10-198-846-6887	Sequence 6887, Ap
868	37	1.0	795	9	US-10-198-846-9053	Sequence 9053, Ap
869	37	1.0	797	10	US-09-954-456-1241	Sequence 1241, Ap
c 870	37	1.0	799	9	US-10-198-846-3566	Sequence 3566, Ap
c 871	37	1.0	800	9	US-10-198-846-6258	Sequence 6258, Ap
872	37	1.0	801	9	US-10-082-830-92	Sequence 92, Appl
c 873	37	1.0	801	9	US-10-198-846-4420	Sequence 4420, Ap
c 874	37	1.0	801	9	US-10-198-846-6257	Sequence 6257, Ap
c 875	37	1.0	801	9	US-10-198-846-9262	Sequence 9262, Ap
876	37	1.0	801	9	US-10-198-846-9632	Sequence 9632, Ap
c 877	37	1.0	804	9	US-10-198-846-9072	Sequence 9072, Ap
c 878	37	1.0	804	9	US-10-198-846-9654	Sequence 9654, Ap
879	37	1.0	805	9	US-10-198-846-9061	Sequence 9061, Ap
c 880	37	1.0	810	9	US-10-198-846-7424	Sequence 7424, Ap
c 881	37	1.0	810	9	US-10-198-846-9545	Sequence 9545, Ap
882	37	1.0	813	9	US-10-198-846-3034	Sequence 3034, Ap
c 883	37	1.0	813	9	US-10-198-846-6277	Sequence 6277, Ap
c 884	37	1.0	814	9	US-10-198-846-6047	Sequence 6047, Ap
c 885	37	1.0	814	9	US-10-198-846-9036	Sequence 9036, Ap
886	37	1.0	814	9	US-10-198-846-9642	Sequence 9642, Ap
c 887	37	1.0	814	9	US-10-198-846-9642	Sequence 9642, Ap
888	37	1.0	814	9	US-10-198-846-12769	Sequence 12769, A
889	37	1.0	815	9	US-10-001-857-111	Sequence 111, App
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c 895	37	1.0	819	9	US-10-198-846-3094	Sequence 3094, Ap
c 896	37	1.0	819	9	US-10-198-846-6058	Sequence 6058, Ap
c 897	37	1.0	820	9	US-10-016-634A-26	Sequence 26, Appl
898	37	1.0	822	9	US-10-001-876-5	Sequence 5, Appli
c 899	37	1.0	823	9	US-10-198-846-6962	Sequence 6962, Ap
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c 902	37	1.0	825	9	US-10-198-846-6068	Sequence 6068, Ap
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c 904	37	1.0	827	9	US-10-198-846-6040	Sequence 6040, Ap
905	37	1.0	828	9	US-10-198-846-3044	Sequence 3044, Ap
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c 909	37	1.0	828	9	US-10-198-846-6278	Sequence 6278, Ap
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912	37	1.0	829	9	US-10-198-846-3032	Sequence 3032, Ap
913	37	1.0	829	9	US-10-198-846-3045	Sequence 3045, Ap
914	37	1.0	829	9	US-10-198-846-9564	Sequence 9564, Ap
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917	37	1.0	830	9	US-10-198-846-6633	Sequence 6633, Ap
918	37	1.0	831	9	US-10-001-887-58	Sequence 58, Appl
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931	37	1.0	839	9	US-09-954-531-197	Sequence 197, App
932	37	1.0	839	9	US-10-205-841-21	Sequence 21, Appl
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938	37	1.0	841	9	US-10-198-846-3092	Sequence 3092, Ap
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c 955	37	1.0	847	9	US-10-198-846-4990	Sequence 4990, Ap
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c 962	37	1.0	848	9	US-10-198-846-3306	Sequence 3306, Ap
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965	37	1.0	848	9	US-10-198-846-5016	Sequence 5016, Ap
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c 967	37	1.0	850	9	US-10-198-846-3316	Sequence 3316, Ap
968	37	1.0	851	9	US-10-198-846-2156	Sequence 2156, Ap

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972	37	1.0	852	9	US-10-198-846-6037	Sequence 6037, Ap
973	37	1.0	853	9	US-10-198-846-6122	Sequence 6122, Ap
974	37	1.0	853	9	US-10-198-846-7571	Sequence 7571, Ap
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977	37	1.0	854	9	US-10-198-846-3599	Sequence 3599, Ap
c 978	37	1.0	854	9	US-10-198-846-3599	Sequence 3599, Ap
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983	37	1.0	855	9	US-10-042-406-2	Sequence 2, Appli
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c 986	37	1.0	855	9	US-10-042-492-2	Sequence 2, Appli
c 987	37	1.0	855	9	US-10-198-846-3301	Sequence 3301, Ap
988	37	1.0	855	9	US-10-198-846-6045	Sequence 6045, Ap
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991	37	1.0	856	9	US-10-198-846-3334	Sequence 3334, Ap
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c 993	37	1.0	856	9	US-10-198-846-4963	Sequence 4963, Ap
994	37	1.0	857	9	US-10-198-846-3048	Sequence 3048, Ap
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996	37	1.0	857	9	US-10-198-846-6115	Sequence 6115, Ap
997	37	1.0	857	9	US-10-198-846-6632	Sequence 6632, Ap
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ALIGNMENTS

RESULT 1
US-10-198-846-13651
; Sequence 13651, Application US/10198846
; Publication No. US20030099974A1
; GENERAL INFORMATION:
; APPLICANT: Lillie, James
; APPLICANT: Xu, Yongyao
; APPLICANT: Wang, Youzhen
; APPLICANT: Steinmann, Kathleen
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS
; TITLE OF INVENTION: FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF BREAST CANCER
; FILE REFERENCE: MRI-049
; CURRENT APPLICATION NUMBER: US/10/198,846
; CURRENT FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/306,220
; PRIOR FILING DATE: 2001-07-18
; NUMBER OF SEQ ID NOS: 14084
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 13651
; LENGTH: 3897
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 3878, 3879, 3880, 3881, 3882, 3883, 3884, 3885, 3886, 3887,
; LOCATION: 3888, 3889, 3890, 3891, 3892, 3893, 3894, 3895, 3896, 3897
; OTHER INFORMATION: n = A,T,C or G
US-10-198-846-13651

Query Match 57.8%; Score 2174; DB 9; Length 3897;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2344; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

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Qy         25 AACAACAACAAAAAAAAATCCTCATCAAATCCTCACCTAAGCTTTCAGTGTATCCAGATC 84
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Qy       1885 ATGGGCCTGTATGAGACAGGAAAAACCAACAGGTTTATCTGAAGGACCCCAGGTAAGATG 1944
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Qy       2124 CTTTCATCGGTGCCTGGTACTCTGGCAAATGATGATGGGGTGGGAGACTTTCCATTAAAT 2183
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Qy       2304 GCACGCTGCCTGCCAAAGTAGTCCTGGCAGCTGGACCATCTCTGTAGGATCGTAAAAAAA 2363
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Qy       2364 TAGAAA 2369
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Db       2476 TAGAAA 2481
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RESULT 2
US-10-044-090-638
; Sequence 638, Application US/10044090
; Patent No. US20020137081A1
; GENERAL INFORMATION:
; APPLICANT: Olga Bandman
; TITLE OF INVENTION: GENES DIFFERENTIALLY EXPRESSED IN VASCULAR TISSUE ACTIVATION
; FILE REFERENCE: PA-0028 US
; CURRENT APPLICATION NUMBER: US/10/044,090
; CURRENT FILING DATE: 2002-01-09
; NUMBER OF SEQ ID NOS: 850
; SOFTWARE: PERL Program
; SEQ ID NO 638
; LENGTH: 3765
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. US20020137081A1 331181.1
; NAME/KEY: unsure
; LOCATION: 2378, 3184, 3187, 3194
; OTHER INFORMATION: a, t, c, g, or other
US-10-044-090-638

Query Match 56.6%; Score 2129; DB 12; Length 3765;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2369; Conservative 0; Mismatches 0; Indels 2; Gaps 2;

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Qy          1 GGTGGCAGCAGCAGCATCACACGTAACAACAACAAAAAAAAATCCTCATCAAATCCTCAC 60
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Db          1 GGTGGCAGCAGCAGCATCACACGTAACAACAACAAAAAAAAATCCTCATCAAATCCTCAC 60

Qy         61 CTAAGCTTTCAGTGTATCCAGATCCACATCTTCACTCAAGCCAGGAGAGGGAAAGAGGAA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CTAAGCTTTCAGTGTATCCAGATCCACATCTTCACTCAAGCCAGGAGAGGGAAAGAGGAA 120

Qy        121 AGGGGGGCAGGAAAAAAAAAAAAACCCAACAACTTAGCGGAAACTTCTCAGAGAATGCTCC 180
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Db        121 AGGGGGGCAGGAAAAAAAAAAAAACCCAACAACTTAGCGGAAACTTCTCAGAGAATGCTCC 180

Qy        181 AAAACTCAGCAGTGCTTCTGGTGCTGGTGATCAGTGCTTCTGCAACCCATGAGGCGGAGC 240
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Db        181 AAAACTCAGCAGTGCTTCTGGTGCTGGTGATCAGTGCTTCTGCAACCCATGAGGCGGAGC 240

Qy        241 AGAATGACTCTGTGAGCCCCAGGAAATCCCGAGTGGCGGCTCAAAACTCAGCTGAAGTGG 300
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Qy        301 TTCGTTGCCTCAACAGTGCTCTACAGGTCGGCTGCGGGGCTTTTGCATGCCTGGAAAACT 360
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Qy        361 CCACCTGTGACACAGATGGGATGTATGACATCTGTAAATCCTTCTTGTACAGCGCTGCTA 420
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Db        361 CCACCTGTGACACAGATGGGATGTATGACATCTGTAAATCCTTCTTGTACAGCGCTGCTA 420

Qy        421 AATTTGACACTCAGGGAAAAGCATTCGTCAAAGAGAGCTTAAAATGCATCGCCAACGGGG 480
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Qy        481 TCACCTCCAAGGTCTTCCTCGCCATTCGGAGGTGCTCCACTTTCCAAAGGATGATTGCTG 540
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Db        541 AGGTGCAGGAAGAGTGCTACAGCAAGCTGAATGTGTGCAGCATCGCCAAGCGGAACCCTG 600

Qy        601 AAGCCATCACTGAGGTCGTCCAGCTGCCCAATCACTTCTCCAACAGATACTATAACAGAC 660
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Db        601 AAGCCATCACTGAGGTCGTCCAGCTGCCCAATCACTTCTCCAACAGATACTATAACAGAC 660

Qy        661 TTGTCCGAAGCCTGCTGGAATGTGATGAAGACACAGTCAGCACAATCAGAGACAGCCTGA 720
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Db        661 TTGTCCGAAGCCTGCTGGAATGTGATGAAGACACAGTCAGCACAATCAGAGACAGCCTGA 720

Qy        721 TGGAGAAAATTGGGCCTAACATGGCCAGCCTCTTCCACATCCTGCAGACAGACCACTGTG 780
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Db        721 TGGAGAAAATTGGGCCTAACATGGCCAGCCTCTTCCACATCCTGCAGACAGACCACTGTG 780

Qy        781 CCCAAACACACCCACGAGCTGACTTCAACAGGAGACGCACCAATGAGCCGCAGAAGCTGA 840
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Db        781 CCCAAACACACCCACGAGCTGACTTCAACAGGAGACGCACCAATGAGCCGCAGAAGCTGA 840

Qy        841 AAGTCCTCCTCAGGAACCTCCGAGGTGAGGAGGACTCTCCCTCCCACATCAAACGCACAT 900
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Db        841 AAGTCCTCCTCAGGAACCTCCGAGGTGAGGAGGACTCTCCCTCCCACATCAAACGCACAT 900

Qy        901 CCCATGAGAGTGCATAACCAGGGAGAGGTTATTCACAACCTCACCAAACTAGTATCATTT 960
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Db        901 CCCATGAGAGTGCATAACCAGGGAGAGGTTATTCACAACCTCACCAAACTAGTATCATTT 960

Qy        961 TAGGGGTGTTGACACACCAGTTTTGAGTGTACTGTGCCTGGTTTGATTTTTTTAAAGTAG 1020
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Db        961 TAGGGGTGTTGACACACCAGTTTTGAGTGTACTGTGCCTGGTTTGATTTTTTTAAAGTAG 1020

Qy       1021 TTCCTATTTTCTATCCCCCTTAAAGAAAATTGCATGAAACTAGGCTTCTGTAATCAATAT 1080
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Db       1021 TTCCTATTTTCTATCCCCCTTAAAGAAAATTGCATGAAACTAGGCTTCTGTAATCAATAT 1080

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Qy       1261 GTGGATCCCTTTAGAACGGTTGCCCCAGTAGAGTTAGCTGATAAGGAAACTTTATTTAAA 1320
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Db       1261 GTGGATCCCTTTAGAACGGTTGCCCCAGTAGAGTTAGCTGATAAGGAAACTTTATTTAAA 1320

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Qy       1381 CCATGGACGAATATGAATGTCACATTTGAATTCTTGATCTCTAATGAGCTAGTGTCTTAT 1440
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Db       1381 CCATGGACGAATATGAATGTCACATTTGAATTCTTGATCTCTAATGAGCTAGTGTCTTAT 1440

Qy       1441 GGTCTTGATCCTCCAATGTCTAATTTTCTTTCCGACACATTTACCAAATTGCTTGAGCCT 1500
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Qy       1501 GGCTGTCCAACCAGACTTTGAGCCTGCATCTTCTTGCATCTAATGAAAAACAAAAAGCTA 1560
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Db       1621 ACCAGAGAATCTTAAGGTCTAACTGTGGAATATAAATAGCTGAAAACTAATGTACTGTAC 1680

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Qy       1801 CCAGATATCCACATAAATGCTCCTTGTGGCCTTTTTTATAACTAAGGGGGTAGAAGTAGT 1860
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Qy       1861 TTTAATTCAACATCAAAACTTAAGATGGGCCTGTATGAGACAGGAAAAACCAACAGGTTT 1920
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Db       1861 TTTAATTCAACATCAAAACTTAAGATGGGCCTGTATGAGACAGGAAAAACCAACAGGTTT 1920

Qy       1921 ATCTGAAGGACCCCAGGTAAGATGTTAATCTCCCAGCCCACCTCAACCCAGAGGCTACTC 1980
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Db       1921 ATCTGAAGGACCCCAGGTAAGATGTTAATCTCCCAGCCCACCTCAACCCAGAGGCTACTC 1980

Qy       1981 TTGACTTAGACCTATACTGAAAGATCTCTGTCACATCCAACTGGAAATTCCAGGAACCAA 2040
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Qy       2041 AAAGAGCA-CCCTATGGGCTTGGACCACTTACAGTGTGATAAGGCCTACTATACATTAGG 2099
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Db       2101 AAGTGGCAGTTCTTTACTCGTCCCCTTTTCATCGGTGCCTGGTACTCTGGCAAATGATGA 2160

Qy       2159 TGGGGTGGGAGACTTTCCATTAAATCAATCAGGAATGAGTCAATCAGCCTTTAGGTCTTT 2218
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Db       2161 TGGGGTGGGAGACTTTCCATTAAATCAATCAGGAATGAGTCAATCAGCCTTTAGGTCTTT 2220

Qy       2219 AGTCCGGGGGACTTGGGGCTGAGAGAGTATAAATAACCCTGGGCTGTCCAGCCTTAATAG 2278
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Db       2221 AGTCCGGGGGACTTGGGGCTGAGAGAGTATAAATAACCCTGGGCTGTCCAGCCTTAATAG 2280

Qy       2279 ACTTCTCTTACATTTTCGTCCTGTAGCACGCTGCCTGCCAAAGTAGTCCTGGCAGCTGGA 2338
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Db       2281 ACTTCTCTTACATTTTCGTCCTGTAGCACGCTGCCTGCCAAAGTAGTCCTGGCAGCTGGA 2340

Qy       2339 CCATCTCTGTAGGATCGTAAAAAAATAGAAA 2369
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Db       2341 CCATCTCTGTAGGATCGTAAAAAAATAGAAA 2371
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RESULT 3
US-09-925-300-486
; Sequence 486, Application US/09925300
; Patent No. US20020151681A1
; GENERAL INFORMATION:
; APPLICANT: Craig Rosen,
; APPLICANT: Steve Ruben
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA101
; CURRENT APPLICATION NUMBER: US/09/925,300
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05988
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1890
; SOFTWARE: PatentIn Ver. 2.0

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; SEQ ID NO 486
;   LENGTH: 2572
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc feature
;   LOCATION: (823)
;   OTHER INFORMATION: n equals a,t,g, or c
US-09-925-300-486

  Query Match             48.7%;  Score 1831;  DB 10;  Length 2572;
  Best Local Similarity   99.8%;  Pred. No. 0;
  Matches 2221;  Conservative    0;  Mismatches    3;  Indels    2;  Gaps    2;

Qy         37 AAAAAATCCTCATCAAATCCTCACCTAAGCTTTCAGTGTATCCAGATCCACATCTTCACT  96
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Qy        157 CGGAAACTTCTCAGAGAATGCTCCAAAACTCAGCAGTGCTTCTGGTGCTGGTGATCAGTG 216
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Db        308 CTTCTGCAACCCATGAGGCGGAGCAGAATGACTCTGTGAGCCCCAGGAAATCCCGAGTGG 367

Qy        277 CGGCTCAAAACTCAGCTGAAGTGGTTCGTTGCCTCAACAGTGCTCTACAGGTCGGCTGCG 336
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Db        368 CGGCTCAAAACTCAGCTGAAGTGGTTCGTTGCCTCAACAGTGCTCTACAGGTCGGCTGCG 427

Qy        337 GGGCTTTTGCATGCCTGGAAAACTCCACCTGTGACACAGATGGGATGTATGACATCTGTA 396
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Db        428 GGGCTTTTGCATGCCTGGAAAACTCCACCTGTGACACAGATGGGATGTATGACATCTGTA 487

Qy        397 AATCCTTCTTGTACAGCGCTGCTAAATTTGACACTCAGGGAAAAGCATTCGTCAAAGAGA 456
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        488 AATCCTTCTTGTACAGCGCTGCTAAATTTGACACTCAGGGAAAAGCATTCGTCAAAGAGA 547

Qy        457 GCTTAAAATGCATCGCCAACGGGGTCACCTCCAAGGTCTTCCTCGCCATTCGGAGGTGCT 516
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Db        548 GCTTAAAATGCATCGCCAACGGGGTCACCTCCAAGGTCTTCCTCGCCATTCGGAGGTGCT 607

Qy        517 CCACTTTCCAAAGGATGATTGCTGAGGTGCAGGAAGAGTGCTACAGCAAGCTGAATGTGT 576
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Db        608 CCACTTTCCAAAGGATGATTGCTGAGGTGCAGGAAGAGTGCTACAGCAAGCTGAATGTGT 667

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Db        728 TCTCCAACAGATACTATAACAGACTTGTCCGAAGCCTGCTGGAATGTGATGAAGACACAG 787

Qy        697 TCAGCACAATCAGAGACAGCCTGATGGAGAAAATT-GGGCCTAACATGGCCAGCCTCTTC 755
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Db        788 TCAGCACAATCAGAGACAGCCTGATGGAGRAAATTNGGGCCTAACATGGCCAGCCTCTTC 847

Qy        756 CACATCCTGCAGACAGACCACTGTGCCCAAACACACCCACGAGCTGACTTCAACAGGAGA 815
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Db        848 CACATCCTGCAGACAGACCACTGTGCCCAAACACACCCACGAGCTGACTTCAACAGGAGA 907

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Qy        876 TCTCCCTCCCACATCAAACGCACATCCCATGAGAGTGCATAACCAGGGAGAGGTTATTCA 935
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Db        968 TCTCCCTCCCACATCAAACGCACATCCCATGAGAGTGCATAACCAGGGAGAGGTTATTCA 1027

Qy        936 CAACCTCACCAAACTAGTATCATTTTAGGGGTGTTGACACACCAGTTTTGAGTGTACTGT 995
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Db       1028 CAACCTCACCAAACTAGTATCATTTTAGGGGTGTTGACACACCARTTTTGAGTGTACTGT 1087

Qy        996 GCCTGGTTTGATTTTTTTAAAGTAGTTCCTATTTTCTATCCCCCTTAAAGAAAATTGCAT 1055
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Db       1088 GCCTGGTTTGATTTTTTTAAAGTAGTTCCTATTTTCTATCCCCCTTAAAGAAAATTGCAT 1147

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Db       1148 GAAACTAGGCTTCTGTAATCAATATCCCAACATTCTGCAATGGCAGCATTCCCACCAACA 1207

Qy       1116 AAATCCATGTGACCATTCTGCCTCTCCTCAGGAGAAAGTACCCTCTTTTACCAACTTCCT 1175
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Db       1208 AAATCCATGTGACCATTCTGCCTCTCCTCAGGAGAAAGTACCCTCTTTTACCAACTTCCT 1267

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Db       1268 CTGCCATGTTTTTCCCCTGCTCCCCTGAGACCACCCCCAAACACAAAACATTCATGTAAC 1327

Qy       1236 TCTCCAGCCATTGTAATTTGAAGATGTGGATCCCTTTAGAACGGTTGCCCCAGTAGAGTT 1295
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Db       1328 TCTCCAGCCATTGTAATTTGAAGATGTGGATCCCTTTAGAACGGTTGCCCCAGTAGAGTT 1387

Qy       1296 AGCTGATAAGGAAACTTTATTTAAATGCATGTCTTAAATGCTCATAAAGATGTTAAATGG 1355
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Db       1388 AGCTGATAAGGAAACTTTATTTAAATGCATGTCTTAAATGCTCATAAAGATGTTAAATGG 1447

Qy       1356 AATTCGTGTTATGAATCTGTGCTGGCCATGGACGAATATGAATGTCACATTTGAATTCTT 1415
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Db       1448 AATTCGTGTTATGAATCTGTGCTGGCCATGGACGAATATGAATGTCACATTTGAATTCTT 1507

Qy       1416 GATCTCTAATGAGCTAGTGTCTTATGGTCTTGATCCTCCAATGTCTAATTTTCTTTCCGA 1475
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Db       1568 CACATTTACCAAATTGCTTGAGCCTGGCTGTCCAACCAGACTTTGAGCCTGCATCTTCTT 1627

Qy       1536 GCATCTAATGAAAAACAAAAAGCTAACATCTTTACGTACTGTAACTGCTCAGAGCTTTAA 1595
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Db       1628 GCATCTAATGAAAAACAAAAAGCTAACATCTTTACGTACTGTAACTGCTCAGAGCTTTAA 1687

Qy       1596 AAGTATCTTTAACAATTGTCTTAAAACCAGAGAATCTTAAGGTCTAACTGTGGAATATAA 1655
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Db       1688 AAGTATCTTTAACAATTGTCTTAAAACCAGAGAATCTTAAGGTCTAACTGTGGAATATAA 1747

Qy       1656 ATAGCTGAAAACTAATGTACTGTACATAAATTCCAGAGGACTCTGCTTAAACAAAGCAGT 1715
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Db       1748 ATAGCTGAAAACTAATGTACTGTACATAAATTCCAGAGGACTCTGCTTAAACAAAGCAGT 1807

Qy       1716 ATATAATAACTTTATTGCATATAGATTTAGTTTTGTAACTTAGCTTTATTTTTCTTTTCC 1775
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Db       1808 ATATAATAACTTTATTGCATATAGATTTAGTTTTGTAACTTAGCTTTATTTTTCTTTTCC 1867

Qy       1776 TGGGAATGGAATAACTATCTCACTTCCAGATATCCACATAAATGCTCCTTGTGGCCTTTT 1835
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Db       1868 TGGGAATGGAATAACTATCTCACTTCCAGATATCCACATAAATGCTCCTTGTGGCCTTTT 1927

Qy       1836 TTATAACTAAGGGGGTAGAAGTAGTTTTAATTCAACATCAAAACTTAAGATGGGCCTGTA 1895
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Qy       1896 TGAGACAGGAAAAACCAACAGGTTTATCTGAAGGACCCCAGGTAAGATGTTAATCTCCCA 1955
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Qy       1956 GCCCACCTCAACCCAGAGGCTACTCTTGACTTAGACCTATACTGAAAGATCTCTGTCACA 2015
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Qy       2016 TCCAACTGGAAATTCCAGGAACCAAAAAGAGCA-CCCTATGGGCTTGGACCACTTACAGT 2074
             ||||||||| |||||||||||||||||||||||| |||||||||||||||||||||||||||
Db       2108 TCCAACTGGRAATTCCAGGAACCAAAAAGAGCATCCCTATGGGCTTGGACCACTTACAGT 2167

Qy       2075 GTGATAAGGCCTACTATACATTAGGAAGTGGCAGTTCTTTACTCGTCCCCTTTCATCGGT 2134
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2168 GTGATAAGGCCTACTATACATTAGGAAGTGGCAGTTCTTTACTCGTCCCCTTTCATCGGT 2227

Qy       2135 GCCTGGTACTCTGGCAAATGATGATGGGGTGGGAGACTTTCCATTAAATCAATCAGGAAT 2194
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2228 GCCTGGTACTCTGGCAAATGATGATGGGGTGGGAGACTTTCCATTAAATCAATCAGGAAT 2287

Qy       2195 GAGTCAATCAGCCTTTAGGTCTTTAGTCCGGGGGACTTGGGGCTGAGAGAGTATAAATAA 2254
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2288 GAGTCAATCAGCCTTTAGGTCTTTAGTCCGGGGGACTTGGGGCTGAGAGAGTATAAATAA 2347

Qy       2255 CCCTGG 2260
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Db       2348 CCCTGG 2353
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RESULT 4
US-09-840-989A-1
; Sequence 1, Application US/09840989A
; Patent No. US20020042372A1
; GENERAL INFORMATION:
; APPLICANT: Olsen et al.
; TITLE OF INVENTION: Stanniocalcin Polynucleotides, Polypeptides, and Methods Based Th
; FILE REFERENCE: PF108P2
; CURRENT APPLICATION NUMBER: US/09/840,989A
; CURRENT FILING DATE: 2001-04-25
; PRIOR APPLICATION NUMBER: PCT/US00/29432
; PRIOR FILING DATE: 2000-10-26
; PRIOR APPLICATION NUMBER: US 60/161,740
; PRIOR FILING DATE: 1999-10-27
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 1283
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (45)..(788)
; OTHER INFORMATION:
; NAME/KEY: misc_feature
; LOCATION: (857)..(857)
; OTHER INFORMATION: n is equal to a, t, c, or g.
; NAME/KEY: misc_feature
; LOCATION: (1254)..(1254)
; OTHER INFORMATION: n is equal to a, t, c, or g.
; NAME/KEY: misc_feature
; LOCATION: (1279)..(1279)
; OTHER INFORMATION: n is equal to a, t, c, or g.
US-09-840-989A-1

Query Match 21.6%; Score 814; DB 10; Length 1283;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 964; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Qy        132 AAAAAAAAAAAACCCAACAACTTAGCGGAAACTTCTCAGAGAATGCTCCAAAACTCAGCA 191
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          3 AAAAAAAAAAAACCCAACAACTTAGCGGAAACTTCTCAGAGAATGCTCCAAAACTCAGCA 62

Qy        192 GTGCTTCTGGTGCTGGTGATCAGTGCTTCTGCAACCCATGAGGCGGAGCAGAATGACTCT 251
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         63 GTGCTTCTGGTGCTGGTGATCAGTGCTTCTGCAACCCATGAGGCGGAGCAGAATGACTCT 122

Qy        252 GTGAGCCCCAGGAAATCCCGAGTGGCGGCTCAAAACTCAGCTGAAGTGGTTCGTTGCCTC 311
              |||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db        123 GTGAGCCCCAGGAAATCCCGAGTGGCGGCCCAAAACTCAGCTGAAGTGGTTCGTTGCCTC 182

Qy        312 AACAGTGCTCTACAGGTCGGCTGCGGGGCTTTTGCATGCCTGGAAAACTCCACCTGTGAC 371
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        183 AACAGTGCTCTACAGGTCGGCTGCGGGGCTTTTGCATGCCTGGAAAACTCCACCTGTGAC 242

Qy        372 ACAGATGGGATGTATGACATCTGTAAATCCTTCTTGTACAGCGCTGCTAAATTTGACACT 431
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        243 ACAGATGGGATGTATGACATCTGTAAATCCTTCTTGTACAGCGCTGCTAAATTTGACACT 302

Qy        432 CAGGGAAAAGCATTCGTCAAAGAGAGCTTAAAATGCATCGCCAACGGGGTCACCTCCAAG 491
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        303 CAGGGAAAAGCATTCGTCAAAGAGAGCTTAAAATGCATCGCCAACGGGGTCACCTCCAAG 362

Qy        492 GTCTTCCTCGCCATTCGGAGGTGCTCCACTTTCCAAAGGATGATTGCTGAGGTGCAGGAA 551
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        363 GTCTTCCTCGCCATTCGGAGGTGCTCCACTTTCCAAAGGATGATTGCTGAGGTGCAGGAA 422

Qy        552 GAGTGCTACAGCAAGCTGAATGTGTGCAGCATCGCCAAGCGGAACCCTGAAGCCATCACT 611
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        423 GAGTGCTACAGCAAGCTGAATGTGTGCAGCATCGCCAAGCGGAACCCTGAAGCCATCACT 482

Qy        612 GAGGTCGTCCAGCTGCCCAATCACTTCTCCAACAGATACTATAACAGACTTGTCCGAAGC 671
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        483 GAGGTCGTCCAGCTGCCCAATCACTTCTCCAACAGATACTATAACAGACTTGTCCGAAGC 542

Qy        672 CTGCTGGAATGTGATGAAGACACAGTCAGCACAATCAGAGACAGCCTGATGGAGAAAATT 731
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        543 CTGCTGGAATGTGATGAAGACACAGTCAGCACAATCAGAGACAGCCTGATGGAGAAAATT 602

Qy        732 GGGCCTAACATGGCCAGCCTCTTCCACATCCTGCAGACAGACCACTGTGCCCAAACACAC 791
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        603 GGGCCTAACATGGCCAGCCTCTTCCACATCCTGCAGACAGACCACTGTGCCCAAACACAC 662

Qy        792 CCACGAGCTGACTTCAACAGGAGACGCACCAATGAGCCGCAGAAGCTGAAAGTCCTCCTC 851
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        663 CCACGAGCTGACTTCAACAGGAGACGCACCAATGAGCCGCAGAAGCTGAAAGTCCTCCTC 722

Qy        852 AGGAACCTCCGAGGTGAGGAGGACTCTCCCTCCCACATCAAACGCACATCCCATGAGAGT 911
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        723 AGGAACCTCCGAGGTGAGGAGGACTCTCCCTCCCACATCAAACGCACATCCCATGAGAGT 782

Qy        912 GCATAACCAGGGAGAGGTTATTCACAACCTCACCAAACTAGTATCATTTTAGGGGTGTTG 971
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        783 GCATAACCAGGGAGAGGTTATTCACAACCTCACCAAACTAGTATCATTTTAGGGGTGTTG 842

Qy        972 ACACACCAGTTTTGAGTGTACTGTGCCTGGTTTGATTTTTTTAAAGTAGTTCCTATTTTC 1031
              ||||||||||||||| |||||||||||||||||| |||||||||||||||||||||||||||
Db        843 ACACACCAGTTTTGNGTGTACTGTGCCTGGTTTGGTTTTTTTAAAGTAGTTCCTATTTTC 902

Qy       1032 TATCCCCCTTAAAGAAAATTGCATGAAACTAGGCTTCTGTAATCAATATCCCAACATTCT 1091
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        903 TATCCCCCTTAAAGAAAATTGCATGAAACTAGGCTTCTGTAATCAATATCCCAACATTCT 962

Qy       1092 GCAATGG 1098
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Db        963 GCAATGG 969
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RESULT 5
US-10-116-051-1
; Sequence 1, Application US/10116051
; Patent No. US20020146791A1
; GENERAL INFORMATION:
; APPLICANT: Olsen et al.
; TITLE OF INVENTION: CORPUSCLES OF STANNIUS PROTEIN, STANNIOCALCIN
; FILE REFERENCE: PF108P1D1C1
; CURRENT APPLICATION NUMBER: US/10/116,051
; CURRENT FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: 09/312,610
; PRIOR FILING DATE: 1999-05-17
; PRIOR APPLICATION NUMBER: 08/431,117
; PRIOR FILING DATE: 1995-04-28
; PRIOR APPLICATION NUMBER: 08/208,005
; PRIOR FILING DATE: 1994-03-08
; NUMBER OF SEQ ID NOS: 10

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;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
;   LENGTH: 771
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-116-051-1

  Query Match             19.1%;  Score 720;  DB 12;  Length 771;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches  770;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        159 GAAACTTCTCAGAGAATGCTCCAAAACTCAGCAGTGCTTCTGGTGCTGGTGATCAGTGCT 218
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GAAACTTCTCAGAGAATGCTCCAAAACTCAGCAGTGCTTCTGGTGCTGGTGATCAGTGCT 60

Qy        219 TCTGCAACCCATGAGGCGGAGCAGAATGACTCTGTGAGCCCCAGGAAATCCCGAGTGGCG 278
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TCTGCAACCCATGAGGCGGAGCAGAATGACTCTGTGAGCCCCAGGAAATCCCGAGTGGCG 120

Qy        279 GCTCAAAACTCAGCTGAAGTGGTTCGTTGCCTCAACAGTGCTCTACAGGTCGGCTGCGGG 338
              || ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GCCCAAAACTCAGCTGAAGTGGTTCGTTGCCTCAACAGTGCTCTACAGGTCGGCTGCGGG 180

Qy        339 GCTTTTGCATGCCTGGAAAACTCCACCTGTGACACAGATGGGATGTATGACATCTGTAAA 398
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GCTTTTGCATGCCTGGAAAACTCCACCTGTGACACAGATGGGATGTATGACATCTGTAAA 240

Qy        399 TCCTTCTTGTACAGCGCTGCTAAATTTGACACTCAGGGAAAAGCATTCGTCAAAGAGAGC 458
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TCCTTCTTGTACAGCGCTGCTAAATTTGACACTCAGGGAAAAGCATTCGTCAAAGAGAGC 300

Qy        459 TTAAAATGCATCGCCAACGGGGTCACCTCCAAGGTCTTCCTCGCCATTCGGAGGTGCTCC 518
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TTAAAATGCATCGCCAACGGGGTCACCTCCAAGGTCTTCCTCGCCATTCGGAGGTGCTCC 360

Qy        519 ACTTTCCAAAGGATGATTGCTGAGGTGCAGGAAGAGTGCTACAGCAAGCTGAATGTGTGC 578
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 ACTTTCCAAAGGATGATTGCTGAGGTGCAGGAAGAGTGCTACAGCAAGCTGAATGTGTGC 420

Qy        579 AGCATCGCCAAGCGGAACCCTGAAGCCATCACTGAGGTCGTCCAGCTGCCCAATCACTTC 638
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 AGCATCGCCAAGCGGAACCCTGAAGCCATCACTGAGGTCGTCCAGCTGCCCAATCACTTC 480

Qy        639 TCCAACAGATACTATAACAGACTTGTCCGAAGCCTGCTGGAATGTGATGAAGACACAGTC 698
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 TCCAACAGATACTATAACAGACTTGTCCGAAGCCTGCTGGAATGTGATGAAGACACAGTC 540

Qy        699 AGCACAATCAGAGACAGCCTGATGGAGAAAATTGGGCCTAACATGGCCAGCCTCTTCCAC 758
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 AGCACAATCAGAGACAGCCTGATGGAGAAAATTGGGCCTAACATGGCCAGCCTCTTCCAC 600

Qy        759 ATCCTGCAGACAGACCACTGTGCCCAAACACACCCACGAGCTGACTTCAACAGGAGACGC 818
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 ATCCTGCAGACAGACCACTGTGCCCAAACACACCCACGAGCTGACTTCAACAGGAGACGC 660

Qy        819 ACCAATGAGCCGCAGAAGCTGAAAGTCCTCCTCAGGAACCTCCGAGGTGAGGAGGACTCT 878
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 ACCAATGAGCCGCAGAAGCTGAAAGTCCTCCTCAGGAACCTCCGAGGTGAGGAGGACTCT 720

Qy        879 CCCTCCCACATCAAACGCACATCCCATGAGAGTGCATAACCAGGGAGAGGT 929
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 CCCTCCCACATCAAACGCACATCCCATGAGAGTGCATAACCAGGGAGAGGT 771


RESULT 6
US-09-778-320-149
; Sequence 149, Application US/09778320
; Patent No. US20010034052A1
; GENERAL INFORMATION:
;  APPLICANT:  Dillon, Davin C.
;  APPLICANT:  Day, Craig H.
;  APPLICANT:  Jiang, Yuqiu
;  APPLICANT:  Houghton, Raymond L.
;  APPLICANT:  Mitcham, Jennifer
;  APPLICANT:  Wang, TongTong
;  APPLICANT:  McNeill, Patricia D.
;  TITLE OF INVENTION:  COMPOSITIONS AND METHODS FOR THE THERAPY AND
;  TITLE OF INVENTION:  DIAGNOSIS OF BREAST CANCER
;  FILE REFERENCE:  210121.491C5
;  CURRENT APPLICATION NUMBER: US/09/778,320
;  CURRENT FILING DATE:  2001-02-06
;  NUMBER OF SEQ ID NOS:  301
;  SOFTWARE:  FastSEQ for Windows Version 3.0
; SEQ ID NO 149
;   LENGTH: 585
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(585)
;   OTHER INFORMATION: n=A,T,C or G
US-09-778-320-149

  Query Match             13.1%;  Score 494;  DB 10;  Length 585;
  Best Local Similarity   100.0%;  Pred. No. 8.3e-241;
  Matches  494;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        435 GGAAAAGCATTCGTCAAAGAGAGCTTAAAATGCATCGCCAACGGGGTCACCTCCAAGGTC 494
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         33 GGAAAAGCATTCGTCAAAGAGAGCTTAAAATGCATCGCCAACGGGGTCACCTCCAAGGTC 92

Qy        495 TTCCTCGCCATTCGGAGGTGCTCCACTTTCCAAAGGATGATTGCTGAGGTGCAGGAAGAG 554
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         93 TTCCTCGCCATTCGGAGGTGCTCCACTTTCCAAAGGATGATTGCTGAGGTGCAGGAAGAG 152

Qy        555 TGCTACAGCAAGCTGAATGTGTGCAGCATCGCCAAGCGGAACCCTGAAGCCATCACTGAG 614
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        153 TGCTACAGCAAGCTGAATGTGTGCAGCATCGCCAAGCGGAACCCTGAAGCCATCACTGAG 212

Qy        615 GTCGTCCAGCTGCCCAATCACTTCTCCAACAGATACTATAACAGACTTGTCCGAAGCCTG 674
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        213 GTCGTCCAGCTGCCCAATCACTTCTCCAACAGATACTATAACAGACTTGTCCGAAGCCTG 272

Qy        675 CTGGAATGTGATGAAGACACAGTCAGCACAATCAGAGACAGCCTGATGGAGAAAATTGGG 734
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        273 CTGGAATGTGATGAAGACACAGTCAGCACAATCAGAGACAGCCTGATGGAGAAAATTGGG 332

Qy        735 CCTAACATGGCCAGCCTCTTCCACATCCTGCAGACAGACCACTGTGCCCAAACACACCCA 794
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        333 CCTAACATGGCCAGCCTCTTCCACATCCTGCAGACAGACCACTGTGCCCAAACACACCCA 392

Qy        795 CGAGCTGACTTCAACAGGAGACGCACCAATGAGCCGCAGAAGCTGAAAGTCCTCCTCAGG 854
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        393 CGAGCTGACTTCAACAGGAGACGCACCAATGAGCCGCAGAAGCTGAAAGTCCTCCTCAGG 452

Qy        855 AACCTCCGAGGTGAGGAGGACTCTCCCTCCCACATCAAACGCACATCCCATGAGAGTGCA 914
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        453 AACCTCCGAGGTGAGGAGGACTCTCCCTCCCACATCAAACGCACATCCCATGAGAGTGCA 512

Qy        915 TAACCAGGGAGAGG 928
              ||||||||||||||
Db        513 TAACCAGGGAGAGG 526


RESULT 7
US-09-910-689-149
; Sequence 149, Application US/09910689
; Patent No. US20020081609A1
; GENERAL INFORMATION:
;  APPLICANT: Dillon, Davin C.
;  APPLICANT:  Day, Craig H.
;  APPLICANT:  Jiang, Yuqiu
;  APPLICANT:  Houghton, Raymond L.
;  APPLICANT:  Mitcham, Jennifer
;  APPLICANT:  Wang, Tongtong
;  APPLICANT:  McNeill, Patricia D.
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;  APPLICANT:  Harlocker, Susan L.
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
;  TITLE OF INVENTION:  DIAGNOSIS OF BREAST CANCER
;  FILE REFERENCE: 210121.491C6
;  CURRENT APPLICATION NUMBER: US/09/910,689
;  CURRENT FILING DATE:  2001-07-20
;  NUMBER OF SEQ ID NOS: 307
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 149
;   LENGTH: 585
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: 10, 30, 32, 527, 565
;   OTHER INFORMATION: n = A,T,C or G
US-09-910-689-149

  Query Match             13.1%;  Score 494;  DB 10;  Length 585;
  Best Local Similarity   100.0%;  Pred. No. 8.3e-241;
  Matches  494;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        435 GGAAAAGCATTCGTCAAAGAGAGCTTAAAATGCATCGCCAACGGGGTCACCTCCAAGGTC 494
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         33 GGAAAAGCATTCGTCAAAGAGAGCTTAAAATGCATCGCCAACGGGGTCACCTCCAAGGTC 92

Qy        495 TTCCTCGCCATTCGGAGGTGCTCCACTTTCCAAAGGATGATTGCTGAGGTGCAGGAAGAG 554
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         93 TTCCTCGCCATTCGGAGGTGCTCCACTTTCCAAAGGATGATTGCTGAGGTGCAGGAAGAG 152

Qy        555 TGCTACAGCAAGCTGAATGTGTGCAGCATCGCCAAGCGGAACCCTGAAGCCATCACTGAG 614
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        153 TGCTACAGCAAGCTGAATGTGTGCAGCATCGCCAAGCGGAACCCTGAAGCCATCACTGAG 212

Qy        615 GTCGTCCAGCTGCCCAATCACTTCTCCAACAGATACTATAACAGACTTGTCCGAAGCCTG 674
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        213 GTCGTCCAGCTGCCCAATCACTTCTCCAACAGATACTATAACAGACTTGTCCGAAGCCTG 272

Qy        675 CTGGAATGTGATGAAGACACAGTCAGCACAATCAGAGACAGCCTGATGGAGAAAATTGGG 734
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        273 CTGGAATGTGATGAAGACACAGTCAGCACAATCAGAGACAGCCTGATGGAGAAAATTGGG 332

Qy        735 CCTAACATGGCCAGCCTCTTCCACATCCTGCAGACAGACCACTGTGCCCAAACACACCCA 794
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        333 CCTAACATGGCCAGCCTCTTCCACATCCTGCAGACAGACCACTGTGCCCAAACACACCCA 392

Qy        795 CGAGCTGACTTCAACAGGAGACGCACCAATGAGCCGCAGAAGCTGAAAGTCCTCCTCAGG 854
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        393 CGAGCTGACTTCAACAGGAGACGCACCAATGAGCCGCAGAAGCTGAAAGTCCTCCTCAGG 452

Qy        855 AACCTCCGAGGTGAGGAGGACTCTCCCTCCCACATCAAACGCACATCCCATGAGAGTGCA 914
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        453 AACCTCCGAGGTGAGGAGGACTCTCCCTCCCACATCAAACGCACATCCCATGAGAGTGCA 512

Qy        915 TAACCAGGGAGAGG 928
              ||||||||||||||
Db        513 TAACCAGGGAGAGG 526


RESULT 8
US-10-010-742-149
; Sequence 149, Application US/10010742
; Patent No. US20020146727A1
; GENERAL INFORMATION:
;  APPLICANT: Dillon, Davin C.
;  APPLICANT:  Day, Craig H.
;  APPLICANT:  Jiang, Yuqiu
;  APPLICANT:  Houghton, Raymond L.
;  APPLICANT:  Mitcham, Jennifer L.
;  APPLICANT:  Wang, Tongtong
;  APPLICANT:  McNeill, Patricia D.
;  APPLICANT:  Harlocker, Susan L.
;  APPLICANT:  Bennington, Angela Ann
;  APPLICANT:  Zehentner, Barbara
;  APPLICANT:  Fanger, Gary R.
;  APPLICANT:  Retter, Marc W.
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
;  TITLE OF INVENTION:  DIAGNOSIS OF BREAST CANCER
;  FILE REFERENCE: 210121.491C7
;  CURRENT APPLICATION NUMBER: US/10/010,742
;  CURRENT FILING DATE:  2001-11-30
;  NUMBER OF SEQ ID NOS: 307
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 149
;   LENGTH: 585
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: 10, 30, 32, 527, 565
;   OTHER INFORMATION: n = A,T,C or G
US-10-010-742-149

  Query Match             13.1%;  Score 494;  DB 12;  Length 585;
  Best Local Similarity   100.0%;  Pred. No. 8.3e-241;
  Matches  494;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        435 GGAAAAGCATTCGTCAAAGAGAGCTTAAAATGCATCGCCAACGGGGTCACCTCCAAGGTC 494
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         33 GGAAAAGCATTCGTCAAAGAGAGCTTAAAATGCATCGCCAACGGGGTCACCTCCAAGGTC 92

Qy        495 TTCCTCGCCATTCGGAGGTGCTCCACTTTCCAAAGGATGATTGCTGAGGTGCAGGAAGAG 554
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         93 TTCCTCGCCATTCGGAGGTGCTCCACTTTCCAAAGGATGATTGCTGAGGTGCAGGAAGAG 152

Qy        555 TGCTACAGCAAGCTGAATGTGTGCAGCATCGCCAAGCGGAACCCTGAAGCCATCACTGAG 614
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        153 TGCTACAGCAAGCTGAATGTGTGCAGCATCGCCAAGCGGAACCCTGAAGCCATCACTGAG 212

Qy        615 GTCGTCCAGCTGCCCAATCACTTCTCCAACAGATACTATAACAGACTTGTCCGAAGCCTG 674
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        213 GTCGTCCAGCTGCCCAATCACTTCTCCAACAGATACTATAACAGACTTGTCCGAAGCCTG 272

Qy        675 CTGGAATGTGATGAAGACACAGTCAGCACAATCAGAGACAGCCTGATGGAGAAAATTGGG 734
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        273 CTGGAATGTGATGAAGACACAGTCAGCACAATCAGAGACAGCCTGATGGAGAAAATTGGG 332

Qy        735 CCTAACATGGCCAGCCTCTTCCACATCCTGCAGACAGACCACTGTGCCCAAACACACCCA 794
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        333 CCTAACATGGCCAGCCTCTTCCACATCCTGCAGACAGACCACTGTGCCCAAACACACCCA 392

Qy        795 CGAGCTGACTTCAACAGGAGACGCACCAATGAGCCGCAGAAGCTGAAAGTCCTCCTCAGG 854
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        393 CGAGCTGACTTCAACAGGAGACGCACCAATGAGCCGCAGAAGCTGAAAGTCCTCCTCAGG 452

Qy        855 AACCTCCGAGGTGAGGAGGACTCTCCCTCCCACATCAAACGCACATCCCATGAGAGTGCA 914
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        453 AACCTCCGAGGTGAGGAGGACTCTCCCTCCCACATCAAACGCACATCCCATGAGAGTGCA 512

Qy        915 TAACCAGGGAGAGG 928
              ||||||||||||||
Db        513 TAACCAGGGAGAGG 526


RESULT 9
US-10-060-036-2677/c
; Sequence 2677, Application US/10060036
; Publication No. US20030073144A1
; GENERAL INFORMATION:
;  APPLICANT: Benson, Darin R.
;  APPLICANT:  Kalos, Michael D.
;  APPLICANT:  Lodes, Michael J.
;  APPLICANT:  Persing, David H.
;  APPLICANT:  Hepler, William T.
;  APPLICANT:  Jiang, Yuqiu
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
```

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;  TITLE OF INVENTION:  AND DIAGNOSIS OF PANCREATIC CANCER
;  FILE REFERENCE: 210121.566
;  CURRENT APPLICATION NUMBER: US/10/060,036
;  CURRENT FILING DATE:  2002-01-30
;  NUMBER OF SEQ ID NOS: 4560
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2677
;   LENGTH: 473
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-060-036-2677

  Query Match            12.3%;  Score 462;  DB 9;  Length 473;
  Best Local Similarity  100.0%;  Pred. No. 1.6e-224;
  Matches  462;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        518 CACTTTCCAAAGGATGATTGCTGAGGTGCAGGAAGAGTGCTACAGCAAGCTGAATGTGTG 577
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        473 CACTTTCCAAAGGATGATTGCTGAGGTGCAGGAAGAGTGCTACAGCAAGCTGAATGTGTG 414

Qy        578 CAGCATCGCCAAGCGGAACCCTGAAGCCATCACTGAGGTCGTCCAGCTGCCCAATCACTT 637
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        413 CAGCATCGCCAAGCGGAACCCTGAAGCCATCACTGAGGTCGTCCAGCTGCCCAATCACTT 354

Qy        638 CTCCAACAGATACTATAACAGACTTGTCCGAAGCCTGCTGGAATGTGATGAAGACACAGT 697
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        353 CTCCAACAGATACTATAACAGACTTGTCCGAAGCCTGCTGGAATGTGATGAAGACACAGT 294

Qy        698 CAGCACAATCAGAGACAGCCTGATGGAGAAAATTGGGCCTAACATGGCCAGCCTCTTCCA 757
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        293 CAGCACAATCAGAGACAGCCTGATGGAGAAAATTGGGCCTAACATGGCCAGCCTCTTCCA 234

Qy        758 CATCCTGCAGACAGACCACTGTGCCCAAACACACCCACGAGCTGACTTCAACAGGAGACG 817
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        233 CATCCTGCAGACAGACCACTGTGCCCAAACACACCCACGAGCTGACTTCAACAGGAGACG 174

Qy        818 CACCAATGAGCCGCAGAAGCTGAAAGTCCTCCTCAGGAACCTCCGAGGTGAGGAGGACTC 877
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        173 CACCAATGAGCCGCAGAAGCTGAAAGTCCTCCTCAGGAACCTCCGAGGTGAGGAGGACTC 114

Qy        878 TCCCTCCCACATCAAACGCACATCCCATGAGAGTGCATAACCAGGGAGAGGTTATTCACA 937
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        113 TCCCTCCCACATCAAACGCACATCCCATGAGAGTGCATAACCAGGGAGAGGTTATTCACA 54

Qy        938 ACCTCACCAAACTAGTATCATTTTAGGGGTGTTGACACACCA 979
              |||||||||||||||||||||||||||||||||||||||||
Db         53 ACCTCACCAAACTAGTATCATTTTAGGGGTGTTGACACACCA 12


RESULT 10
US-09-918-995-33032
; Sequence 33032, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
;  APPLICANT: Hyseq, Inc.
;  TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
;  TITLE OF INVENTION:  FROM VARIOUS cDNA LIBRARIES
;  FILE REFERENCE: 20411-756
;  CURRENT APPLICATION NUMBER: US/09/918,995
;  CURRENT FILING DATE:  2001-07-30
;  PRIOR APPLICATION NUMBER: US/09/235,076
;  PRIOR FILING DATE: 1999-01-20
;  NUMBER OF SEQ ID NOS: 38054
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 33032
;   LENGTH: 436
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-918-995-33032

  Query Match            11.6%;  Score 436;  DB 9;  Length 436;
  Best Local Similarity  100.0%;  Pred. No. 2.8e-211;
  Matches  436;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        686 TGAAGACACAGTCAGCACAATCAGAGACAGCCTGATGGAGAAAATTGGGCCTAACATGGC 745
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 TGAAGACACAGTCAGCACAATCAGAGACAGCCTGATGGAGAAAATTGGGCCTAACATGGC 60

Qy        746 CAGCCTCTTCCACATCCTGCAGACAGACCACTGTGCCCAAACACACCCACGAGCTGACTT 805
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CAGCCTCTTCCACATCCTGCAGACAGACCACTGTGCCCAAACACACCCACGAGCTGACTT 120

Qy        806 CAACAGGAGACGCACCAATGAGCCGCAGAAGCTGAAAGTCCTCCTCAGGAACCTCCGAGG 865
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CAACAGGAGACGCACCAATGAGCCGCAGAAGCTGAAAGTCCTCCTCAGGAACCTCCGAGG 180

Qy        866 TGAGGAGGACTCTCCCTCCCACATCAAACGCACATCCCATGAGAGTGCATAACCAGGGAG 925
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TGAGGAGGACTCTCCCTCCCACATCAAACGCACATCCCATGAGAGTGCATAACCAGGGAG 240

Qy        926 AGGTTATTCACAACCTCACCAAACTAGTATCATTTTAGGGGTGTTGACACACCAGTTTTG 985
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AGGTTATTCACAACCTCACCAAACTAGTATCATTTTAGGGGTGTTGACACACCAGTTTTG 300

Qy        986 AGTGTACTGTGCCTGGTTTGATTTTTTTAAAGTAGTTCCTATTTTCTATCCCCCTTAAAG 1045
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 AGTGTACTGTGCCTGGTTTGATTTTTTTAAAGTAGTTCCTATTTTCTATCCCCCTTAAAG 360

Qy       1046 AAAATTGCATGAAACTAGGCTTCTGTAATCAATATCCCAACATTCTGCAATGGCAGCATT 1105
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AAAATTGCATGAAACTAGGCTTCTGTAATCAATATCCCAACATTCTGCAATGGCAGCATT 420

Qy       1106 CCCACCAACAAAATCC 1121
              ||||||||||||||||
Db        421 CCCACCAACAAAATCC 436


RESULT 11
US-09-736-457-4/c
; Sequence 4, Application US/09736457
; Patent No. US20020168637A1
; GENERAL INFORMATION:
;  APPLICANT:  Wang, Tongtong
;  APPLICANT:  Bangur, Chaitanya S.
;  APPLICANT:  Lodes, Michael A.
;  APPLICANT:  Fanger, Gary
;  APPLICANT:  Vedvick, Tom
;  APPLICANT:  Carter, Darrick
;  APPLICANT:  Retter, Marc
;  APPLICANT:  Mannion, Jane
;  APPLICANT:  Fan, Liqun
;  APPLICANT:  Wang, Aijun
;  TITLE OF INVENTION:  COMPOSITIONS AND METHODS FOR THE THERAPY AND
;  TITLE OF INVENTION:  DIAGNOSIS OF LUNG CANCER
;  FILE REFERENCE:  210121.478C15
;  CURRENT APPLICATION NUMBER: US/09/736,457
;  CURRENT FILING DATE:  2000-12-13
;  NUMBER OF SEQ ID NOS:  1864
;  SOFTWARE:  FastSEQ for Windows Version 3.0
; SEQ ID NO 4
;   LENGTH: 510
;   TYPE: DNA
;   ORGANISM: Homo sapien
US-09-736-457-4

  Query Match            10.8%;  Score 405;  DB 9;  Length 510;
  Best Local Similarity  100.0%;  Pred. No. 1.8e-195;
  Matches  405;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1644 TGTGGAATATAAATAGCTGAAAACTAATGTACTGTACATAAATTCCAGAGGACTCTGCTT 1703
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        441 TGTGGAATATAAATAGCTGAAAACTAATGTACTGTACATAAATTCCAGAGGACTCTGCTT 382

Qy       1704 AAACAAAGCAGTATATAATAACTTTATTGCATATAGATTTAGTTTTGTAACTTAGCTTTA 1763
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        381 AAACAAAGCAGTATATAATAACTTTATTGCATATAGATTTAGTTTTGTAACTTAGCTTTA 322
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Qy       1764 TTTTTCTTTTCCTGGGAATGGAATAACTATCTCACTTCCAGATATCCACATAAATGCTCC 1823
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        321 TTTTTCTTTTCCTGGGAATGGAATAACTATCTCACTTCCAGATATCCACATAAATGCTCC 262

Qy       1824 TTGTGGCCTTTTTTATAACTAAGGGGGTAGAAGTAGTTTTAATTCAACATCAAAACTTAA 1883
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        261 TTGTGGCCTTTTTTATAACTAAGGGGGTAGAAGTAGTTTTAATTCAACATCAAAACTTAA 202

Qy       1884 GATGGGCCTGTATGAGACAGGAAAAACCAACAGGTTTATCTGAAGGACCCCAGGTAAGAT 1943
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        201 GATGGGCCTGTATGAGACAGGAAAAACCAACAGGTTTATCTGAAGGACCCCAGGTAAGAT 142

Qy       1944 GTTAATCTCCCAGCCCACCTCAACCCAGAGGCTACTCTTGACTTAGACCTATACTGAAAG 2003
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        141 GTTAATCTCCCAGCCCACCTCAACCCAGAGGCTACTCTTGACTTAGACCTATACTGAAAG 82

Qy       2004 ATCTCTGTCACATCCAACTGGAAATTCCAGGAACCAAAAAGAGCA 2048
             |||||||||||||||||||||||||||||||||||||||||||||
Db          81 ATCTCTGTCACATCCAACTGGAAATTCCAGGAACCAAAAAGAGCA 37
```

RESULT 12
US-09-902-941-4/c
; Sequence 4, Application US/09902941
; Patent No. US20020172952A1
; GENERAL INFORMATION:
; APPLICANT: Henderson, Robert A.
; APPLICANT: Wang, Tongtong
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Johnson, Jeffrey C.
; APPLICANT: Retter, Marc W.
; APPLICANT: Marnerakis, Margarita
; APPLICANT: Carter, Darrick
; APPLICANT: Fanger, Gary R.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: McNabb, Andria
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.478C17
; CURRENT APPLICATION NUMBER: US/09/902,941
; CURRENT FILING DATE: 2001-07-10
; NUMBER OF SEQ ID NOS: 2002
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 510
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-902-941-4

Query Match 10.8%; Score 405; DB 9; Length 510;
Best Local Similarity 100.0%; Pred. No. 1.8e-195;
Matches 405; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy       1644 TGTGGAATATAAATAGCTGAAAACTAATGTACTGTACATAAATTCCAGAGGACTCTGCTT 1703
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        441 TGTGGAATATAAATAGCTGAAAACTAATGTACTGTACATAAATTCCAGAGGACTCTGCTT 382

Qy       1704 AAACAAAGCAGTATATAATAACTTTATTGCATATAGATTTAGTTTTGTAACTTAGCTTTA 1763
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        381 AAACAAAGCAGTATATAATAACTTTATTGCATATAGATTTAGTTTTGTAACTTAGCTTTA 322

Qy       1764 TTTTTCTTTTCCTGGGAATGGAATAACTATCTCACTTCCAGATATCCACATAAATGCTCC 1823
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        321 TTTTTCTTTTCCTGGGAATGGAATAACTATCTCACTTCCAGATATCCACATAAATGCTCC 262

Qy       1824 TTGTGGCCTTTTTTATAACTAAGGGGGTAGAAGTAGTTTTAATTCAACATCAAAACTTAA 1883
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        261 TTGTGGCCTTTTTTATAACTAAGGGGGTAGAAGTAGTTTTAATTCAACATCAAAACTTAA 202

Qy       1884 GATGGGCCTGTATGAGACAGGAAAAACCAACAGGTTTATCTGAAGGACCCCAGGTAAGAT 1943
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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```
Db        201 GATGGGCCTGTATGAGACAGGAAAAACCAACAGGTTTATCTGAAGGACCCCAGGTAAGAT 142

Qy       1944 GTTAATCTCCCAGCCCACCTCAACCCAGAGGCTACTCTTGACTTAGACCTATACTGAAAG 2003
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        141 GTTAATCTCCCAGCCCACCTCAACCCAGAGGCTACTCTTGACTTAGACCTATACTGAAAG 82

Qy       2004 ATCTCTGTCACATCCAACTGGAAATTCCAGGAACCAAAAAGAGCA 2048
             |||||||||||||||||||||||||||||||||||||||||||||
Db          81 ATCTCTGTCACATCCAACTGGAAATTCCAGGAACCAAAAAGAGCA 37
```

RESULT 13
US-09-849-626-4/c
; Sequence 4, Application US/09849626
; Publication No. US20020197669A1
; GENERAL INFORMATION:
; APPLICANT: Bangur, Chaitanya
; APPLICANT: Fanger, Gary
; APPLICANT: Wang, Aijun
; APPLICANT: Wang, Tongtong
; APPLICANT: Switzer, Anne
; APPLICANT: McNeill, Patricia
; APPLICANT: Clapper, Jonathan
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.478C16
; CURRENT APPLICATION NUMBER: US/09/849,626
; CURRENT FILING DATE: 2001-05-03
; NUMBER OF SEQ ID NOS: 1926
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 510
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-849-626-4

Query Match 10.8%; Score 405; DB 9; Length 510;
Best Local Similarity 100.0%; Pred. No. 1.8e-195;
Matches 405; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy       1644 TGTGGAATATAAATAGCTGAAAACTAATGTACTGTACATAAATTCCAGAGGACTCTGCTT 1703
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        441 TGTGGAATATAAATAGCTGAAAACTAATGTACTGTACATAAATTCCAGAGGACTCTGCTT 382

Qy       1704 AAACAAAGCAGTATATAATAACTTTATTGCATATAGATTTAGTTTTGTAACTTAGCTTTA 1763
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        381 AAACAAAGCAGTATATAATAACTTTATTGCATATAGATTTAGTTTTGTAACTTAGCTTTA 322

Qy       1764 TTTTTCTTTTCCTGGGAATGGAATAACTATCTCACTTCCAGATATCCACATAAATGCTCC 1823
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        321 TTTTTCTTTTCCTGGGAATGGAATAACTATCTCACTTCCAGATATCCACATAAATGCTCC 262

Qy       1824 TTGTGGCCTTTTTTATAACTAAGGGGGTAGAAGTAGTTTTAATTCAACATCAAAACTTAA 1883
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        261 TTGTGGCCTTTTTTATAACTAAGGGGGTAGAAGTAGTTTTAATTCAACATCAAAACTTAA 202

Qy       1884 GATGGGCCTGTATGAGACAGGAAAAACCAACAGGTTTATCTGAAGGACCCCAGGTAAGAT 1943
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        201 GATGGGCCTGTATGAGACAGGAAAAACCAACAGGTTTATCTGAAGGACCCCAGGTAAGAT 142

Qy       1944 GTTAATCTCCCAGCCCACCTCAACCCAGAGGCTACTCTTGACTTAGACCTATACTGAAAG 2003
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        141 GTTAATCTCCCAGCCCACCTCAACCCAGAGGCTACTCTTGACTTAGACCTATACTGAAAG 82

Qy       2004 ATCTCTGTCACATCCAACTGGAAATTCCAGGAACCAAAAAGAGCA 2048
             |||||||||||||||||||||||||||||||||||||||||||||
Db          81 ATCTCTGTCACATCCAACTGGAAATTCCAGGAACCAAAAAGAGCA 37
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RESULT 14
US-10-017-754-4/c
; Sequence 4, Application US/10017754
; Publication No. US20030054363A1

```
; GENERAL INFORMATION:
;  APPLICANT: Henderson, Robert A.
;  APPLICANT:  Wang, Tongtong
;  APPLICANT:  Watanabe, Yoshihiro
;  APPLICANT:  Johnson, Jeffrey C.
;  APPLICANT:  Retter, Marc W.
;  APPLICANT:  Marnerakis, Margarita
;  APPLICANT:  Carter, Darrick
;  APPLICANT:  Fanger, Gary R.
;  APPLICANT:  Vedvick, Thomas S.
;  APPLICANT:  Bangur, Chaitanya S.
;  APPLICANT:  McNabb, Andria
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
;  TITLE OF INVENTION:  AND DIAGNOSIS OF LUNG CANCER
;  FILE REFERENCE: 210121.478C18
;  CURRENT APPLICATION NUMBER: US/10/017,754
;  CURRENT FILING DATE:  2001-10-29
;  NUMBER OF SEQ ID NOS: 2004
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
;   LENGTH: 510
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-017-754-4

  Query Match             10.8%;  Score 405;  DB 9;  Length 510;
  Best Local Similarity   100.0%;  Pred. No. 1.8e-195;
  Matches  405;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1644 TGTGGAATATAAATAGCTGAAAACTAATGTACTGTACATAAATTCCAGAGGACTCTGCTT 1703
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        441 TGTGGAATATAAATAGCTGAAAACTAATGTACTGTACATAAATTCCAGAGGACTCTGCTT 382

Qy       1704 AAACAAAGCAGTATATAATAACTTTATTGCATATAGATTTAGTTTTGTAACTTAGCTTTA 1763
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        381 AAACAAAGCAGTATATAATAACTTTATTGCATATAGATTTAGTTTTGTAACTTAGCTTTA 322

Qy       1764 TTTTTCTTTTCCTGGGAATGGAATAACTATCTCACTTCCAGATATCCACATAAATGCTCC 1823
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        321 TTTTTCTTTTCCTGGGAATGGAATAACTATCTCACTTCCAGATATCCACATAAATGCTCC 262

Qy       1824 TTGTGGCCTTTTTTATAACTAAGGGGGTAGAAGTAGTTTTAATTCAACATCAAAACTTAA 1883
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        261 TTGTGGCCTTTTTTATAACTAAGGGGGTAGAAGTAGTTTTAATTCAACATCAAAACTTAA 202

Qy       1884 GATGGGCCTGTATGAGACAGGAAAAACCAACAGGTTTATCTGAAGGACCCCAGGTAAGAT 1943
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        201 GATGGGCCTGTATGAGACAGGAAAAACCAACAGGTTTATCTGAAGGACCCCAGGTAAGAT 142

Qy       1944 GTTAATCTCCCAGCCCACCTCAACCCAGAGGCTACTCTTGACTTAGACCTATACTGAAAG 2003
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        141 GTTAATCTCCCAGCCCACCTCAACCCAGAGGCTACTCTTGACTTAGACCTATACTGAAAG 82

Qy       2004 ATCTCTGTCACATCCAACTGGAAATTCCAGGAACCAAAAAGAGCA 2048
             |||||||||||||||||||||||||||||||||||||||||||||
Db          81 ATCTCTGTCACATCCAACTGGAAATTCCAGGAACCAAAAAGAGCA 37


RESULT 15
US-09-864-761-21309/c
; Sequence 21309, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
;  APPLICANT: Penn, Sharron G.
;  APPLICANT:  Rank, David R.
;  APPLICANT:  Hanzel, David K.
;  APPLICANT:  Chen, Wensheng
;  TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
;  TITLE OF INVENTION:  GENE EXPRESSION ANALYSIS BY MICROARRAY
;  FILE REFERENCE: Aeomica-X-1
;  CURRENT APPLICATION NUMBER: US/09/864,761
;  CURRENT FILING DATE:  2001-05-23
;  PRIOR APPLICATION NUMBER: US 60/180,312
;  PRIOR FILING DATE: 2000-02-04
;  PRIOR APPLICATION NUMBER: US 60/207,456
;  PRIOR FILING DATE: 2000-05-26
;  PRIOR APPLICATION NUMBER: US 09/632,366
;  PRIOR FILING DATE: 2000-08-03
;  PRIOR APPLICATION NUMBER: GB 24263.6
;  PRIOR FILING DATE: 2000-10-04
;  PRIOR APPLICATION NUMBER: US 60/236,359
;  PRIOR FILING DATE: 2000-09-27
;  PRIOR APPLICATION NUMBER: PCT/US01/00666
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00667
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00664
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00669
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00665
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00668
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00663
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00662
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00661
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00670
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: US 60/234,687
;  PRIOR FILING DATE: 2000-09-21
;  PRIOR APPLICATION NUMBER: US 09/608,408
;  PRIOR FILING DATE: 2000-06-30
;  PRIOR APPLICATION NUMBER: US 09/774,203
;  PRIOR FILING DATE: 2001-01-29
;  NUMBER OF SEQ ID NOS: 49117
;  SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 21309
;   LENGTH: 219
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: MAP TO AC012119.1
;   OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.7
;   OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 2.4
;   OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 2.8
;   OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 2.8
;   OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 2.4
;   OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 3.1
;   OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 1.8
;   OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.7
;   OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 2.2
;   OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 2.7
;   OTHER INFORMATION: SWISSPROT HIT: P52823, EVALUE 2.00e-36
;   OTHER INFORMATION: NT HIT: AF098463.1, EVALUE 1.00e-120
;   OTHER INFORMATION: EST_HUMAN HIT: AW954342.1, EVALUE 1.00e-116
US-09-864-761-21309

 *Query Match             5.6%;  Score 212;  DB 10;  Length 219;
  Best Local Similarity   100.0%;  Pred. No. 3.3e-97;
  Matches  212;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        435 GGAAAAGCATTCGTCAAAGAGAGCTTAAAATGCATCGCCAACGGGGTCACCTCCAAGGTC 494
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        219 GGAAAAGCATTCGTCAAAGAGAGCTTAAAATGCATCGCCAACGGGGTCACCTCCAAGGTC 160

Qy        495 TTCCTCGCCATTCGGAGGTGCTCCACTTTCCAAAGGATGATTGCTGAGGTGCAGGAAGAG 554
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        159 TTCCTCGCCATTCGGAGGTGCTCCACTTTCCAAAGGATGATTGCTGAGGTGCAGGAAGAG 100

Qy        555 TGCTACAGCAAGCTGAATGTGTGCAGCATCGCCAAGCGGAACCCTGAAGCCATCACTGAG 614
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         99 TGCTACAGCAAGCTGAATGTGTGCAGCATCGCCAAGCGGAACCCTGAAGCCATCACTGAG 40
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Qy        615 GTCGTCCAGCTGCCCAATCACTTCTCCAACAG 646
              ||||||||||||||||||||||||||||||||
Db         39 GTCGTCCAGCTGCCCAATCACTTCTCCAACAG 8
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Search completed: June 12, 2003, 19:53:54
Job time : 500 secs